50th Annual Meeting of the Phycological Society of America

August 10-13

Drexel University
Philadelphia, PA

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

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Naomi Phillips, Arcadia University

PROGRAM DIRECTOR FOR 2015:

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Meeting acknowledgements

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

Rick McCourt, Local Organizer and general go-to person extraordinaire

Naomi Phillips, Co-Local Organizer, also extraordinaire

Patrick T. Martone, Bold and Lewin Award Coordinator and enthusiast

John Hall, Naomi Phillips and Elizabeth Lacey for their excellent field trip leading

Chris MacTaggart who provided the awesome image for this year's meeting!

The excellent staff at Drexel and the Academy of Natural Sciences

Our fantastic workshop organizers:
- Cyanobacterial taxonomy: Jeff Johansen
- Taxonomy under the scope: Juliet Brodie and Eunsoo Kim

Alyson Norwich, Chelsea Villanueva, and Yasmine Zakaria (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:
- Polar Phycology: Kate Schoenrock
- Green Algae: Louise Lewis and Rick McCourt
- Brown Algae: Naomi Phillips
- Biofuels and Applied Phycology: Milton Sommerfeld

General Philadelphia Information

Getting Around Philadelphia

The dorms are a few minutes away by foot from the PSA meeting venue at Drexel. Hotels in University City are roughly the same distance. There are many restaurants, delis, and food trucks nearby for eating.

If you're staying in Center City, it's a little over 1 mile to the Drexel campus. Walking in Philadelphia is easy and, with good weather, it is a pleasant 20-30 minute walk from many Center City hotels to the Drexel campus, with a picturesque transit of the Schuylkill River.

Public transportation is available between Center City and the meeting venue. The subway runs every 5 minutes or so, and the trip takes 5 minutes. The fare is $2.25 cash one way (discounted to $1.80 for a token, available in packs of 2 or more).

Taxis and Uber are also available (ca. $10 and up).

Center City hotels are closer to many, but not all of the museums, in particular Independence Hall and the Liberty Bell. The Philly Phlash (http://www.visitphilly.com/tours/philadelphia/phlash/) is a public shuttle service that runs to many of the popular tourist sites from Independence Hall to the Art Museum (i.e., the Rocky Steps) and is cheap--$2 per ride, or $5 for an all-day pass.

Biking and Walking

Philadelphia is a bicycle-friendly city and was ranked #6 in the top-10 bike cities in the US, the highest ranking for a big city. There are a number of bike lanes and trails. Philly Bike Share is scheduled to begin in spring 2015 with 600 bikes at 60 locations, and it might be functioning by the time of PSA's meeting. Proposed stations include several in Center City and one on the Drexel campus.

The PSA meeting will be on the Drexel campus, which is immediately adjacent to the University of Pennsylvania. On campus there are some nice walks and the outstanding Penn Museum of Archeology. Also nearby is a river trail that runs for > 6 miles on either side of the Schuylkill River from South Street to the Philadelphia Art Museum and beyond--great for a walk, run, or bike ride. For the true bike enthusiast or marathoner, the trail runs all the way to Valley Forge National Historic Park about 21 miles northwest of Philly.

Hospitals

The Hospital of the University of Pennsylvania and Children's Hospital of Philadelphia are less than a mile away from the meeting venue. Both are ranked among the best in the nation.

Getting to the meeting

Flights:

- Philadelphia International airport (~ 8 miles to Drexel University, Center of Campus is at 3141 Chestnut Street, Philadelphia, PA 19104). Addresses of the dorm and hotels are below.
- Newark, NJ (~90 miles to Drexel University).

From Philadelphia airport:

- Trains run ~ every 30 minutes to 30th Street Station, Philadelphia's main train station. Train platforms at the airport are near baggage claim area, clearly marked. From 30th Street Station it's a short taxi ride or 5-10 minute walk to Drexel University, 3141 Chestnut Street, Philadelphia, PA 19104. The dorm is a few minutes further. See address below.
- Airport Taxi: About $28.00 plus tip, one way to University City. Pickup is outside baggage claim.

Driving from the airport and other places:

- See driving directions on Drexel's web page.
- Or, check Google maps, and follow directions to Drexel University or Race Street Residences, addresses below.
- Parking: The Drexel Parking Garage (Lot G) is at 34th and Market Street. Parking Map showing Garage (G). ***Note: If you need parking and have not signed up on the meeting registration site, please contact Rick McCourt prior to arrival, rmm45@drexel.edu.***

Dormitory and Event Locations

Campus Map

See attached page, and online at Drexel University City Campus Map

Dormitory

The dormitory is the Race Street Residences, also called Race Street Hall.
3300 Race Street, Philadelphia, PA 19104
Front Desk: 215-571-3103
http://www.drexel.edu/dbs/universityHousing/undergraduate-housing/residence-halls/raceStreet/

Workshops, August 8, 2015

The microscopy workshop and Cyanobacteria workshop will both be held at the Academy of Natural Sciences. **Preregistration is required.** You will be sent details by email.

Pre-Meeting Field Trips, Sunday, August 9, 2015.
Reregistration is required for the two trips. Details will be provided by email.

Plenary Lectures and Presented Talks
Sessions will be in the Creese Student Center in Behrakis Grand Hall, or in the Mandell Theater. Though technically these are in two different buildings, they are close by each other and the buildings are connected.

- *Creese Student Center*: 3141 Chestnut St, Philadelphia, PA 19104
  Phone:(215) 895-2000. http://www.drexel.edu/dbs/studentCenters/creeseCenter/
- *Mandell Theater*: 33rd and Chestnut, in a building connected to Creese Student Center. http://www.drexel.edu/westphal/resources/MandellTheater/

Poster Session and Auction, Monday evening, August 10, 6-9 pm
Location TBA in program.
Poster setup will be from 4-6 pm. Easels and poster boards provided, size 30 in. x 40 in.

Film Showing: "Beneath the Tide." Tuesday, August 11, 2015, 5-6 pm.
This will be shown in the Mandell Theater.

Career Workshop. Led by Dr. Steven Murray, Provost of Cal State Los Angeles. Location TBA in program.

Banquet Wednesday evening, August 12, 2015, 6:30-9:30 pm.
Academy of Natural Sciences of Drexel
1900 Benjamin Franklin Parkway
Philadelphia, PA 19118
Pickup and dropoff will be near the Creese Student Center at an exact location to be announced at the meeting. Attendees may choose to walk there (approxm. 25 minutes). Return bus service will begin at 9:00 pm.

Food

Philadelphia is foodie heaven. There are many guides, online and off. The food section of the *Philadelphia Inquirer* is excellent, and Craig Laban, is very good and has many recommendations online. If you don't gain weight during your visit, you're just not trying.

You will be in the heart of two urban campuses (Drexel and the University of Pennsylvania, or Penn), so food and drink are not a problem. There are so many places of various cuisines and prices to eat well in Philly that it's hard to recommend some with the risk of you missing something you'd love. That said, there are a few nearby the dorm and meeting venues that are worth noting. I'll also mention a couple a bit further away that might be worth a taxi or Uber ride.

Sabrina's - http://sabrinascafe.com/ 227 N
34th St, Philadelphia, PA 19104 (215) 222-
1022

Breakfast and Lunch.
Several restaurants by this name, but it's not a chain. This one is very close to the Race Street Hall, slightly upscale, a place to sit down and stuff yourself. Themed breakfast and lunch menus are quite entertaining and change weekly. For vegans, vegetarians, omnivores, and carnivores.

Food Trucks --- Google "University City Food Trucks" or click here.
These are parked all over, on 34th, 33rd, and on streets around the meeting venue and dorms. Virtually any cuisine, for any diet-from all fruit to Halal to vegan to more meat kebabs and exotic tacos. Open from breakfast through late night. Inexpensive and tasty.

Sansom Street - Between 35th and 36th street, near the Penn bookstore
This is a mini-restaurant row worth checking out. You won't go wrong, from Baby Blues BBQ to the foodie classic White Dog Cafe, Doc Magrogan's Oyster House, and the New Deck Tavern. A little further away is the upscale Pod, which looks something like the milk bar from Clockwork Orange-amazing sushi and Asian fusion in a unique space-age setting.

Miscellaneous: *Han*
Dynasty Viet Nam Cafe
Marigold Kitchen
Zavino's (next door to the meeting)

Center City

You'll want to take a taxi or Uber over and back from Drexel, but there are some great places across the Schuylkill River (pronounced "Skoo-kill"). The best are inaccessible without reservations months in advance (Laurel, Townsend, Vetri, Zahav), and will max out your credit card, but there are others worthwhile. Percy Street Barbecue is worth a visit for carnivores and beer lovers, and is right on South Street so you can find many places nearby. The Reading Street Terminal is in a revamped huge train station, accessible by subway and has dozens of places for authentic Philly food. Try the Bassett's Ice Cream for dessert (40% of your daily recommended dose of saturated fat).

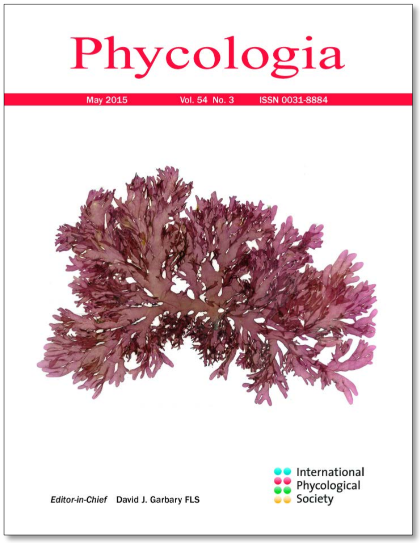
Cheesesteaks

For those with excessively healthy cholesterol levels, we can take care of that in Philly with just one of these items. Gino's, Pats, Jim's- if the name has one person's first name in it, it's probably good. Everyone has a favorite, so Google "Philly Cheesesteak" and go for it. The big decision is whether you want it with onions and cheez-whiz or Provalone. Most places have in-house defibrillators.

PSA is Proud to present the premier screening of *Beneath the Tide*, a documentary film about algal aquaculture in Africa. The film will premier on Tuesday, August 11 (5:00-6:00), with a question and answer period with the Director, Kat Zoula (**Mandell Theater in Creese Student Center)**

BENEATH THE TIDE

a documentary by Kat Zoula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• CELEBRATING 50 YEARS •

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HIGHEST IMPACT FACTOR IN JOURNAL HISTORY

Published on behalf of the Phycological Society of America

Phycological Society of America

50th Anniversary Virtual Issue

In celebration of the 50th year of publication, the *Journal of Phycology* is pleased to present you a special Virtual Issue edited by Co-Editor-in-Chief and Managing Editor Michael Graham. The Virtual Issue features a historical collection of phycological contributions marking important milestones of the Journal's history, accompanied with a special editorial.

READ THE ISSUE FOR FREE HERE

Available on iTunes

iPad Air Giveaway

Don't forget to pick up your raffle tickets at Registration to **win a brand new iPad Air,** to be given away at the Monday Night PSA Auction!

About the Journal

The Journal of Phycology covers all aspects of basic and applied research on algae to provide a common medium for the ecologist, physiologist, cell biologist, molecular biologist, morphologist, oceanographer, taxonomist, geneticist, and biochemist.

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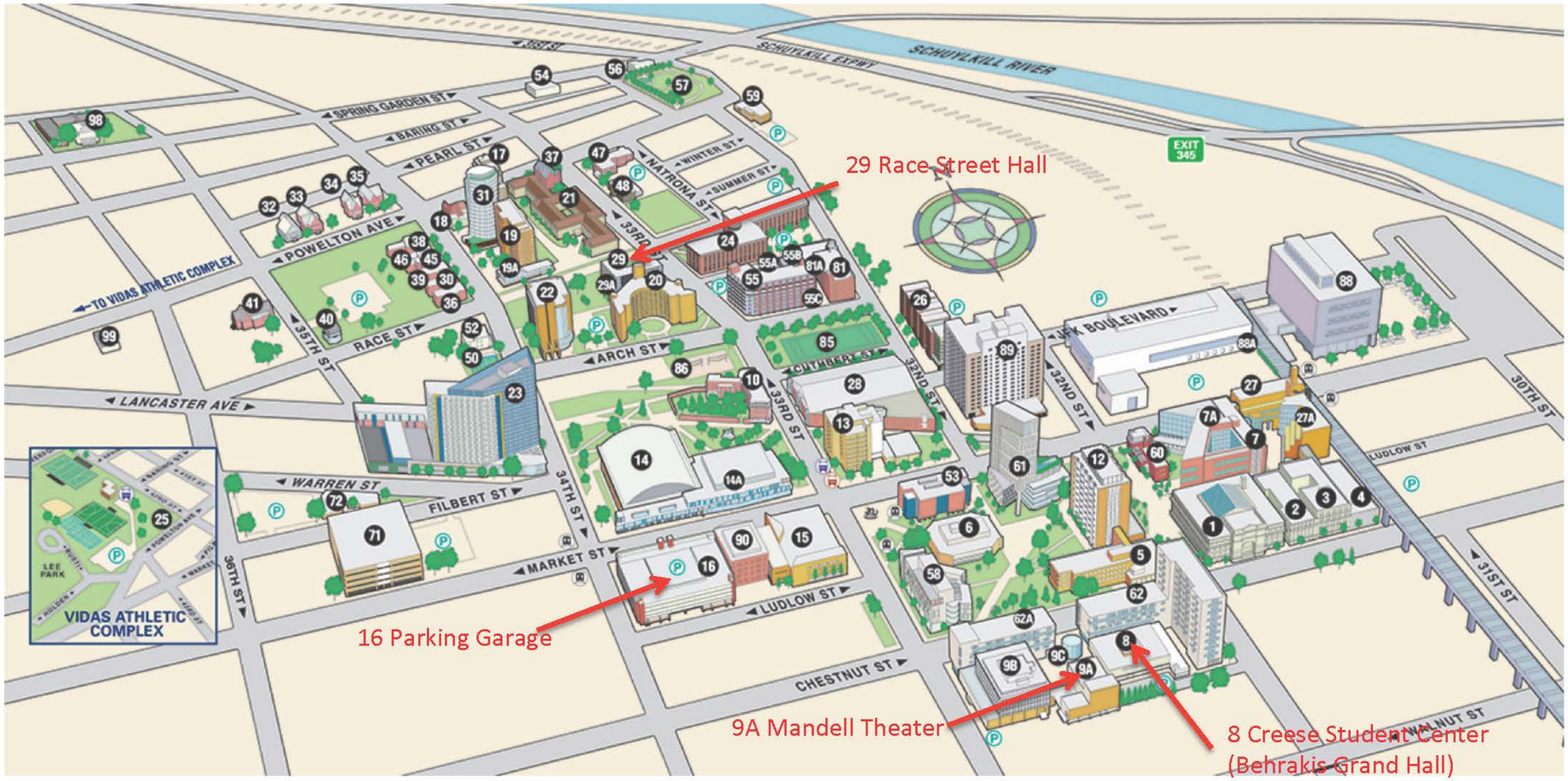

29 Race Street Hall

16 Parking Garage

9A Mandell Theater

8 Creese Student Center
(Behrakis Grand Hall)

Saturday, August 8

PSA Board of Trustees (4:00-6:00 pm) **Liberty View** (McAlister Hall, connected to the Creese Student Center. Take elevator near Drexel Bookstore to the 6th Floor).

Microscopy Workshop: Identification and Systematics of Cyanobacteria (Academy of Natural Sciences of Drexel, 1900 Benjamin Franklin Parkway, Philadelphia, PA, 191031; 9:30-5:30): Dr. Jeff Johansen (John Carroll University)

> Meet at Security Desk at 19th Street Entrance of ANSP at approximately 9:15 am. You will be escorted to the workshop.

Microscopy Workshop: Taxonomy under the scope, (Academy of Natural Sciences of Drexel, 1900 Benjamin Franklin Parkway, Philadelphia, PA, 19103;12:30-5:30): Drs. Juliet Brodie (NHM of London, filamentous red algae) and Eunsoo Kim, American Museum of Natural History)

> Meet at Security Desk at 19th Street Entrance of ANSP at approximately 12:15 pm. You will be escorted to the workshop.

Please note these workshops will be at the Academy of Natural Sciences of Drexel, in Center City (address provided above). Further details will be provided to participants.

Sunday, August 9

PSA Executive Committee (9:00-5:00 pm): **Liberty View** (McAlister Hall, connected to the Creese Student Center. Take elevator near Drexel Bookstore to the 6th Floor).

Marine algal fieldtrip (9:00-5:00)- Naomi Phillips and Elizabeth Lacey

Freshwater fieldtrip (9:00-5:00)- John Hall (Field trip participants will receive information from the trip leaders on meeting place and trip details).

Arrival and registration (registration desk open after noon): Balcony outside Behrakis Grand Hall, Creese Student Center Lobby (Hours to be announced, approximately 3:00 pm - 6:00 pm)

PSA Opening Reception (6:00-8:00 pm): **008 Behrakis Grand Hall, Creese Student Center**

Please note: Speakers for the sessions in Mandell Theater each day should provide their PowerPoint presentations on a USB drive to the Mandell staff by 7:30 a.m.

Monday, August 10

07:00-08:00 Continental Breakfast, Behrakis Grand Hall North

8:00 Opening Remarks (Rick Zechman, PSA President and Rick McCourt, Local Organizer)

8:15 ***Plenary Session-*** *Algal Sensory Photoreceptors and their Adaptation to Optogenetic Application* (Peter Hegemann, Humboldt University) (**Mandell Theater, Creese Student Center)**

***Bold Award Competition* I (Mandell Theater, Creese Student Center)**
Session moderator: Patrick Martone, University of British Columbia

9:30 SYSTEMATICS, PHYLOGENY AND EVOLUTION OF THE FILAMENTOUS RED ALGAE: GENUS *POLYSPHONIA SENSU LATO*
Bustamante, D. E., Department of Marine Life Science, Chosun University, Gwangju 501-759, Korea, Republic Of Korea

9:45 COMPARATIVE PLASTID GENOME ANALYSIS FROM THREE NEMALIOPHYCIDAE RED ALGAE
Cho, C. H., Department of Biological Sciences, Sungkyunkwan University, Republic Of Korea

10:00 ON THE RED ALGAL GENUS GRATELOUPIA IN THE GULF OF MEXICO, FEATURING THE ORGANELLAR GENOMES OF *GRATELOUPIA TAIWANENSIS* (RHODOPHYTA)
DePriest, M. S., The University of Alabama, USA

10:15 STRIKING A BALANCE BETWEEN PHOTOTROPHY AND HETEROTROPHY IN THE MIXOTROPHIC CHRYSOPHYTE *DINOBRYON* SP.
DeVaul, S. B., Temple University, USA

10:30 DARK SURVIVAL AND RECOVERY OF A FOREIGN ORGANELLE-RETAINING DINOFLAGELLATE AND ITS HAPTOPHYTE PREY AND PLASTID SOURCE FOLLOWING A SIMULATED AUSTRAL WINTER
Sellers, C. G., Temple University, USA, cgsellers@temple.edu
Gast, R. J., Woods Hole Oceanographic Institution, USA, rgast@whoi.edu
Sanders, R. W., Temple University, USA, robert.sanders@temple.edu

10:45-11:15 COFFEE BREAK

Bold Award Competition II (Mandell Theater, Creese Student Center)

Session moderator: Patrick Martone, University of British Columbia

11:15 PHYLOGENY AND FUNCTION: THE ROLE OF THE EUKARYOTIC INITIATION FACTOR 4E IN CONTROL OF GENE EXPRESSION IN DINOFLAGELLATES
Jones, G. D., University of Maryland, Baltimore, USA

11:30 EXAMINING THE MOLECULAR PHYLOGENY AND TAXONOMY OF THE RED ALGAL ORDER HALYMENIALES (FLORIDEOPHYCEAE) IN AUSTRALIA TO BETTER CONCEIVE ITS BIODIVERSITY
Kraft, L. K., University of New Brunswick, Canada

11:45 EVOLUTION OF RED ALGAL PLASTID GENOMES WITH A WIDE RANGE GENOMIC COMPREHENSION
Lee, J. M., Sungkyunkwan University, Republic Of Korea

12:00 MORPHOLOGY AND MOLECULAR STUDIES ON LARGE *NEIDIUM* SPECIES OF NORTH AMERICA, INCLUDING AN EXAMINATION OF EHRENBERG'S TYPES
Lefebvre, K. E., University of Ottawa, Canada

12:15 DIATOM FRUSTULES AS A MECHANICAL DEFENSE AGAINST PREDATION BY HETEROTROPHIC DINOFLAGELLATES
Spillane, T., Western Washington University, USA

12:30 ILLUMINATING CRITICAL FACTORS WHEN CONSIDERING WASTEWATER FOR ULTRA-PRODUCTIVE MICROALGAL CULTURE
Wray, J. T., Arizona State University, USA

12:45-1:45 LUNCH BREAK (wherever the Fates may lead)

Phylogeny and Systematics I (Mandell Theater, Creese Student Center)

Session moderator: Juliet Brodie, NHM of London

1:45 MORPHOLOGICAL AND MOLECULAR ASSESSMENT OF *AVRAINVILLEA* (ULVOPHYCEAE, CHLOROPHYTA) AND IMPLICATIONS FOR INVASIVE SPECIES MANAGEMENT
Wade, R. M., Department of Botany, University of Hawaii at Manoa, USA, rmwade@hawaii.edu
Tang, Y., Department of Botany, University of Hawaii at Manoa, USA, tangyue2@hawaii.edu
Sherwood, A. R., Department of Botany, University of Hawaii at Manoa, Hawaii, USA, asherwoo@hawaii.edu

2:00 DNA BARCODE ASSESSMENT OF THE GENUS *RHODYMENIA* (RHODYMENIACEAE, RHODYMENIALES) FROM AUSTRALIA REVEALS CRYPTIC AND OVERLOOKED SPECIES DIVERSITY
Filloramo, G. V., University of New Brunswick, Canada, gina.filloramo@gmail.com

Saunders, G. W., University of New Brunswick, Canada, gws@unb.ca

2:15 *SPOROLITHON PTYCHOIDES* (SPOROLITHALES, RHODOPHYTA): GENERITYPE SPECIES OF TYPE GENUS OF THE ORDER ASSESSED BY SEQUENCING TYPE AND TOPOTYPE MATERIAL
Gabrielson, P. W., University of North Carolina, Chapel Hill, USA, drseaweed@hotmail.com
Hughey, J. R., Hartnell College, USA, jhughey@hartnell.edu
Richards, J., University of Louisiana at Lafayette, USA, jlr0420@louisiana.edu
Sauvage, T., University of Louisiana at Lafayette, USA, tomsauv@gmail.com
Schmidt, W., University of Louisiana at Lafayette, USA, weschmidt01@yahoo.com
Fredericq, S., University of Louisiana at Lafayette, USA, sfredericq@yahoo.com

2:30 FROM FOSSILS TO DNA: DEFINING THE DIATOM GENUS *BIDDULPHIA* GRAY
Ashworth, M. P., University of Texas, Austin, USA, mashworth@utexas.edu
Sims, P. A., Natural History Museum, London, United Kingdom

2:45 MOLECULAR 'FISHING' REVEALS *KALLYMENICOLA* GEN. NOV. INCLUDING THREE NEW HOST-SPECIFIC ENDO/EPIPHYTIC SPECIES OF MEIODISCACEAE (PALMARIALES).
Evans, J. R., University of New Brunswick, Canada, joshua.evans@unb.ca
Saunders, G. W., University of New Brunswick, Canada, gws@unb.ca

3:00 PHYLOGENY OF *NANNOCHLOROPSIS* (EUSTIGMATOPHYCEAE), INCLUDING STRAINS FROM THE AUSTRALIAN NATIONAL ALGAE CULTURE COLLECTION
Fawley, M. W., University of Arkansas at Monticello, USA, fawleym@uamont.edu Jameson, I., Australian National Algae Culture Collection, Australia, Ian.Jameson@csiro.au
Fawley, K. P., University of Arkansas at Monticello, USA, fawleym@uamont.edu

***Harmful Algal Blooms* (Behrakis Grand Hall, Creese Student Center)**

Session moderator: Rick Zechman, Humboldt State University

1:30 MICROPLASTICS AND HARMFUL ALGAL BLOOMS – HOW WOULD THEY INTERACT?
Yokota, K., SUNY Oneonta Biological Field Station, USA, Kiyoko.Yokota@oneonta.edu
Hastings, C., Rochester Institute of Technology, USA, cjh8615@rit.edu
Davidson, E. G., SUNY Oneonta Biological Field Station, USA, davidson.emilygrace@gmail.com
Waterfield, H. A., SUNY Oneonta Biological Field Station, USA, Holly.Waterfield@oneonta.edu
Kwietniewski, E. J., SUNY Oneonta Biological Field Station, USA, kwieej62@suny.oneonta.edu

1:45 RELATIONSHIP BETWEEN BACTERIAL COMMUNITY STRUCTURE AND BLOOM DYNAMICS OF *COCHLODINIUM POLYKRIKOIDES* IN KOREAN COASTAL WATERS
PARK, B., Hanyang university, Republic Of Korea, parkbs911@gmail.com
KIM, J., Hanyang university, Republic Of Korea, ikart00@nate.com

JOO, J., Hanyang university, Republic Of Korea, rabbit-016@hanmail.net
LEE, H., Hanyang university, Republic Of Korea, fmfqh@hanmail.net
Han, S., Hanyang university, , outofsoul7@gmail.com
GOBLER, C. J., Stony Brook University, USA, christopher.gobler@stonybrook.edu
BAEK, S., Korea Institute of Ocean Science and Technology/South Sea Institute, Republic Of Korea, baeksh@kiost.ac
HAN, M., Hanyang university, Republic Of Korea, hanms@hanyang.ac.kr

2:00 IDENTIFICATION OF THE SPECIES RESPONSIBLE FOR PARALYTIC SHELLFISH POISONING IN ALASKA
Litaker, R. W., NOAA, National Ocean Service, Beaufort Laboratory, Beaufort, NC, wayne.litaker@noaa.gov
Vandersea, M.W., NOAA, National Ocean Service, Beaufort Laboratory, Beaufort, NC, USA
Kibler, S.R., NOAA, National Ocean Service, Beaufort Laboratory, Beaufort, NC, USA
Hondolero, D.E., NOAA, National Ocean Service, Kasitsna Bay Laboratory, Homer, AK, USA
Holderied, K., NOAA, National Ocean Service, Kasitsna Bay Laboratory, Homer, AK, USA
Tester, P.A., NOAA, National Ocean Service, Beaufort Laboratory, Beaufort, NC, USA

2:15 COMPETITION IN MACROALGAL BLOOMS: THREE SPECIES OF BLADE-FORMING ULVA INHIBIT THE GROWTH OF CO-OCCURRING MACROALGAE THROUGH ALLELOPATHY
Green, L. A., University of Rhode Island, USA, lindsaygreen@uri.edu
MacKechnie, F., University of Rhode Island, USA, fionamack3@hotmail.com
Thornber, C. S., University of Rhode Island, USA, thornber@uri.edu
Licht, S., University of Rhode Island, USA, slicht@uri.edu

3:15- 3:45 AFTERNOON COFFEE BREAK

***Population/Distribution/Large Scale Phycology* I (Mandell Theater, Creese Student Center)**

Session moderator: Steven Murray, University of California, Fullerton

3:45 THE IMPORTANCE OF GENOTYPE IN *MACROCYSTIS PYRIFERA* FORM AND FUNCTION
Camus, C., Consorcio BalBiofuels & CeBiB, Chile, ccamus@balchile.com
Faugeron, S., Centro de Conservación Marina and CeBiB, Facultad de Ciencias Biológicas, P. Universidad de Chile, Chile, sfaugeron@bio.puc.cl
Buschmann, A. H., Centro i-mar & CeBiB, Universidad de Los Lagos, Puerto Montt, Chile, abuschma@ulagos.cl

4:00 SPATIAL AND TEMPORAL VARIATION IN ULVOID PROPAGULE AVAILABILITY IN SAN FRANCISCO BAY
Romero, R., University of California, Berkeley, USA, rromero@berkeley.edu

4:15 THE MACROALGAL HERBARIUM DIGITIZATION PROJECT
Neefus, C. D., University of New Hampshire, USA, chris.neefus@unh.edu

4:30 CYANOBACTERIA FROM THE LAPLAND BIOSPHERE RESERVE, RUSSIA
Shalygin, S. S., John Carroll University, Polar-Alpine Botanical Garden-Institute, USA, sshalygin18@jcu.edu

4:45 WHAT IS HAPPENING TO THE LARGE BROWN SEAWEEDS IN THE NORTHEASTERN ATLANTIC IN A RAPIDLY CHANGING ENVIRONMENT?
Brodie, J. Natural History Museum, Department of Life Sciences, London SW7 5BD;
Williamson, C., Natural History Museum, Department of Life Sciences, London SW7 5BD, and Institute of Zoology, Zoological Society of London, Regent's Park, London, NW1 4RY;
Yesson, C., Natural History Museum, Department of Life Sciences, London SW7 5BD and School of Earth and Ocean Sciences, Cardiff University, Main Building, Park Place, Cardiff, CF10 3YE, UK

5:00 THE MEDITERRANEAN RED ALGAL GENUS *FELICINIA* (HALYMENIALES, RHODOPHYTA) IS NOT AN ENDEMIC TAXON
Wilson, K., University of Louisiana at Lafayette, USA, kew0851@louisiana.edu
Arakaki, N., Universidad Cientifica del Sur, Lima, Peru, natyarakaki@yahoo.com Schmidt, W. E., University of Louisiana at Lafayette, USA, william.schmidt.algae@gmail.com
Fredericq, S., University of Louisiana at Lafayette, USA, slf9209@louisiana.edu

***Applied Phycology* I (Behrakis Grand Hall, Creese Student Center)**

Session moderator: Milton Sommerfeld, Arizona State University

3:45 DIATOM COMMUNITY STRUCTURE ON IN-SERVICE SHIP HULLS
Hunsucker, K. Z., Florida Institute of Technology, USA, khunsucker@fit.edu
Swain, G. W., Florida Institute of Technology, USA, swain@fit.edu

4:00 A FUNGAL ORIGIN FOR THE GROWTH PROMOTING EFFECTS OF EXTRACTS OF *ASCOPHYLLUM NODOSUM*?
Van de Reep, S., St. Francis Xavier University, Canada, x2011bfo@stfx.ca
MacNeil, K. E., St. Francis Xavier University, Canada, kmacneil@stfx.ca
Garbary, D. J., St. Francis Xavier University, Canada, dgarbary@gmail.com

4:15 FUNCTIONAL EXPRESSION OF FETUIN/ASIALOFETUIN SPECIFIC ALGAL LECTIN DOMAINS IN *ESCHERICHIA COLI*
Han, J. W., National Marine Biodiversity Institute of Korea, Republic Of Korea, jwhan@mabik.re.kr
Jung, M. G., Kongju National University, Republic Of Korea, mgjung@kongju.ac.kr
Shim, E. Y., Kongju National University, Republic Of Korea, tlasud@kongju.ac.kr
Shim, J. B., Kongju National University, Republic Of Korea, matthew80@kongju.ac.kr
Kim, G. H., Kongju National University, Republic Of Korea, ghkim@kongju.ac.kr

4:30 SENSATIONAL SEAWEEDS: A NON-MAJORS INTRODUCTION TO MARINE MACROALGAE
Lacey, E. A., Stockton University, USA, elizabeth.lacey@stockton.edu

4:45 A DIATOM-BASED BIOLOGICAL CONDITION GRADIENT (BCG) APPROACH FOR ASSESSING STREAM IMPAIRMENT
Charles, D. F., Academy of Natural Sciences of Drexel University, USA, charles@ansp.org
Hausmann, S., Academy of Natural Sciences of Drexel University, USA, sh843@drexel.edu
Belton, T. J., New Jersey Department of Environmental Protection, USA, Thomas.Belton@dep.nj.gov
Gerritsen, J., Tetra Tech, Inc., USA, Jeroen.Gerritsen@tetratech.com

5:00 THE DEVELOPMENT OF NUTRIENT CRITERIA USING THE BIOLOGICAL CONDITION GRADIENT (BCG) APROACH
Hausmann, S., Academy of Natural Sciences of Drexel University, USA, Sonja.Hausmann@drexel.edu
Charles, D. F., Academy of Natural Sciences of Drexel University, USA, dfc63@drexel.edu
Belton, T., 2Office of Science, Department of Environmental Protection New Jersey, Thomas.Belton@dep.nj.gov
Gerritsen, J., Tetra Tech, Inc., USA, Jeroen.Gerritsen@tetratech.com

Monday Evening

PSA Poster Session (6:00-8:00) **(Behrakis Grand Hall)** Poster set up will take place from 3:00-6:00 pm.

PSA Auction (8:00-10:00) (**Behrakis Grand Hall)**

Tuesday, August 11

07:00-08:00 Luxurious Continental Breakfast, Behrakis Grand Hall North

8:00 ***Plenary Session:*** *Giant Clams As Solar Flux Transformers: Lessons for Algal Culture* (Dr. Alison Sweeney, University of Pennsylvania) (**Mandell Theater, Creese Student Center)**

Please note that only presenting authors are listed for invited symposia; full citations with co-authors may be found in the abstract portion of the program guide.

Morning Symposium: POLAR PHYCOLOGY (Mandell Theater, Creese Student Center)

Session moderator: Charles Amsler, University of Alabama, Birmingham

9:15 ALLIES, CHEATERS, & THIEVES: MACROALGAL-MESOGRAZER INTERACTIONS ALONG THE WESTERN ANTARCTIC PENINSULA (Amsler, C.D., University of Alabama at Birmingham, USA, amsler@uab.edu)

10:00-10:30 COFFEE BREAK

10:30 THE ARCTIC'S SECRET GARDEN: LANDFAST SEA ICE COMMUNITIES AND THEIR CONTRIBUTION TO THE UNDERLYING MARINE ECOSYSTEM (Aumack, C. F., Lamont-Doherty Earth Observatory of Columbia University, USA, aumackcr@gmail.com)

11:05 PHYSIOLOGIAL ACCLIMATION OF ANTARCTIC MACROALGAE TO CLIMATE CHANGE: EFFECTS OF UV RADIATION AND INCREASING SEAWATER TEMPERATURE (Rautenberger, R., Universidad Austral de Chile, Chile, ralf.rautenberger@uach.cl)

11:40 COMMUNITY ECOLOGY OF ISOLATED KELP BEDS IN THE ALASKA ARCTIC (Konar, B., School of Fisheries and Ocean Sciences, University of Alaska, Fairbanks)

12:15-1:30 LUNCH BREAK (wherever the winds blow)

12:15-1:30 *JOURNAL OF PHYCOLOGY* EDITORIAL LUNCH (Skyview Room, MacAlister Hall, connected to Creese Student Center. Take elevator near Drexel Bookstore to 6th floor)

Ecology I (Mandell Theater, Creese Student Center)

Session moderator: Tim Nelson, Seattle Pacific University

1:30 A METAGENOMIC ANALYSIS OF SUMMER AND WINTER PROTISTAN PLANKTON IN THE LOWER HUDSON RIVER

Sprung, B., American Museum of Natural History, USA, bsprung@gmail.com
Liberato, A., American Museum of Natural History, USA, allieliberato@gmail.com
Scheinbach, S., American Museum of Natural History, USA, judisaul@aol.com
Yang, A., American Museum of Natural History, USA, ayang@amnh.org
Kim, E., American Museum of Natural History, USA, ekim1@amnh.org
Levandowsky, M., Pace University, USA, mlevandowsky@gmail.com

1:45 STINKING UP THE BEACH: VARIABLE RATES OF DECAY AND DECOMPOSITION OF NATIVE AND INVASIVE SEAWEEDS IN BAYNES SOUND, BRITISH COLUMBIA

Pawluk, K. A., University of Victoria, Canada, kpawluk@uvic.ca
Cross, S. F., Vancouver Island University, Canada, sfcross@SEAvisionGroup.ca

2:00 SHIP HULL TRANSPORT OF MARINE DIATOMS THROUGH FRESHWATER

Sweat, L. H., Florida Institute of Technology, USA, hsweat2007@my.fit.edu
Swain, G. W., Florida Institute of Technology, USA, swain@fit.edu
Johnson, K. B., Florida Institute of Technology, USA, johnson@fit.edu

2:15 A METHODOLOGICAL ASSESSMENT OF EPIPHYTE REMOVAL FROM MARINE SEAGRASSES

Zimba, P. V., TAMU-CC, USA, paul.zimba@tamucc.edu

2:30 WHAT KILLED DRIFT MACROALGAE PRIOR TO THE SEAGRASS DIE-OFF CAUSED BY THE 2011 SUPERBLOOM IN THE INDIAN RIVER LAGOON, FLORIDA?

Hanisak, M. D., FAU Harbor Branch, USA, dhanisak@fau.edu
Wills, P. S., FAU Harbor Branch, USA, pwills2@fau.edu
Robinson, C., FAU Harbor Branch, USA, crobinso@fau.edu
Chamberlain, R., St. Johns River Water Management District, USA, rchamber@sjrwmd.com
Green, W., St. Johns River Water Management District, USA, whitcgreen@gmail.com
Morris, L., St. Johns River Water Management District, USA, lmorris@sjrwmd.com

***Cell and Molecular Biology* (Behrakis Grand Hall, Creese Student Center)**

Session moderator: Deborah Robertson, Clark University

1:30 CELL BIOLOGY OF EPIDERMAL SHEDDING IN THE MARINE BROWN ALGA *ASCOPHYLLUM NODOSUM*

Halat, L. S., St. Francis Xavier University, Canada, laryssahalat@gmail.com
Galway, M. E., St. Francis Xavier University, Canada, mgalway@stfx.ca
Garbary, D.J., St. Francis Xavier University, Canada, dgarbary@gmail.com

1:45 THE FLAGELLAR APPARATUS OF CYANOPHORA

Heiss, A. A., American Museum of Natural History, USA, aheiss@amnh.org
Kim, E., American Museum of Natural History, USA, ekim1@amnh.org

2:00 MOLECULAR CHARACTERIZATION OF SOME CYANOBACTERIAL SPECIES IN A COASTAL LAGOON, SOUTH-WEST, NIGERIA
Akagha, S. C., University of Lagos, Nigeria, sandraakagha@yahoo.com
Yin, K., Sun Yat-Sen University, China, yinkd@mail.sysu.edu.cn

2:15 PUTATIVE SNP MARKERS FROM TRANSCRIPTOMES FOR POPULATION STRUCTURE IN *PORPHYRA UMBILICALIS* (RHODOPHYTA)
Cao, Y., University of New Hampshire, USA, yov2@wildcats.unh.edu
Green, L. A., University of Rhode Island, USA, lindsaygreen@mail.uri.edu
Eriksen, R., United States Department of Agriculture, USA, renee.eriksen@ars.usda.gov
Klein, A. S., University of New Hampshire, USA, Anita.Klein@unh.edu

2:30 SEASONAL PATTERNS OF NITRATE UPTAKE AND EXPRESSION OF NITRATE ASSIMILATING ENZYMES IN *FUCUS VESICULOSUS*.
Johnson, C.H. Clark University, Worcester MA,
Young, E.B. University of Wisconsin, Milwaukee. Milwaukee, WI, ebyoung@uwm.edu
Robertson, D.L. Clark University, Worcester, MA, debrobertson@clarku.edu

2:45- 3:15 AFTERNOON COFFEE BREAK

Phylogeny and Systematics II (Mandell Theater, Creese Student Center)

Session moderator: Jeff Johansen, John Carroll University

3:15 DECIPHERING *DISTROMIUM* DIVERSITY FROM THE DEEP: UNIQUE MESOPHOTIC SPECIES FROM THE HAWAIIAN ARCHIPELAGO
Spalding, H. L., Department of Botany, University of Hawaii at Manoa, USA, hspaldin@hawaii.edu
Tsuda, R. T., Bernice Pauahi Bishop Museum, USA, roy.tsuda@bishopmuseum.org
Sherwood, A. R., Department of Botany, University of Hawaii at Manoa, asherwoo@hawaii.edu

3:30 POLYPHYLY IN *SCYTONEMA* (NOSTOCALES, CYANOBACTERA): PHYLOGENETIC SEPARATION OF THE *S. HYALINUM* GROUP FROM THE TYPE SPECIES S. HOFFMANII
Pietrasiak, N., John Carroll University, USA, npietrasiak@jcu.edu
Johansen, J. R., John Carroll University, USA, johansen@jcu.edu
Bohunicka, M., University of South Bohemia, Czech Republic, kreveta4@seznam.cz
Mares, J., Institute of Botany, Academy of Sciences of the Czech Republic, Czech Republic, jan.mares@centrum.cz

3:45 THE AMANSIEAE (RHODOMELACEAE) REVISITED: A MULTIGENE APPROACH
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

4:00 NEXT GEN TAXONOMIC DESCRIPTIONS FOR MICROBIAL EUKARYOTES
Thessen, A. E., The Ronin Institute for Independent Scholarship, USA, annethessen@gmail.com

4:15 HOW MANY SPECIES OF *BANGIA* OCCUR ON THE WEST COAST OF NORTH AMERICA?
Lindstrom, S. C., University of British Columbia, Canada, Sandra.Lindstrom@botany.ubc.ca

4:30 *DOLICHOSPERMUM HANII* SP. NOV. (CYANOPHYCEAE); A NEW SPECIES FROM HAN RIVER, KOREA.
Choi, H. J., Hanyang University, Republic Of Korea, hjchoi426@hanyang.ac.kr
Kim, J. H., Hanyang University, Republic Of Korea, chedar@hanyang.ac.kr
Kang, Y. H., Wonju Regional Environment Office, Republic Of Korea, korea1975@korea.kr
Lee, H. W., Hanyang University, Republic Of Korea, fmfqh@hanmail.net
Han, S. R., Hanyang University, Republic Of Korea, outofsoul@gmail.com
Han, M. S., Hanyang University, Republic Of Korea, hanms@hanyang.ac.kr

4:45 TAXON-SPECIFIC CHARACTER EVALUATION IN DINOPHYSALES (DINOPHYCEAE), TOWARDS IMPROVED TAXONOMY AND SYSTEMATICS.
Hoppenrath, M., Senckenberg am Meer, DZMB, Germany, mhoppenrath@senckenberg.de
Wilke, T., Carl von Ossietzky University, Germany, tanja.wilke@uni-oldenburg.de
Zinssmeister, C., Senckenberg am Meer, DZMB, Germany, czinssmeister@senckenberg.de

5:00 ASSESSING THE EVOLUTIONARY HISTORY OF THE CLASS SYNUROPHYCEAE USING FOSSIL REMAINS, MOLECULAR APPROACHES AND MORPHOMETRIC ANALYSES
Siver, P. A., Connecticut College, USA, pasiv@conncoll.edu
Jo, B. Y., Chungnam National University, Republic Of Korea, shinw@cnu.ac.kr
Shin, W., Chungnam National University, Republic Of Korea, shinw@cnu.ac.kr
Kim, J. I., Chungnam National University, Republic Of Korea, shinw@cnu.ac.kr
Lott, A. M., Connecticut College, USA, aliz@conncoll.edu
Wolfe, A. P., University of Alberta, Canada, awolfe@ualberta.ca

Evolution (Behrakis Grand Hall, Creese Student Center)

Session moderator: Eric Linton, Central Michigan University

3:15 BARCODE GENE EVOLUTION IS OUTPACED BY MORPHOLOGICAL EVOLUTION IN THE FRESHWATER THALASSIOSIRALES: EVIDENCE FOR RECENT, RAPID RADIATIONS
Theriot, E., University of Texas, USA, etheriot@austin.utexas.edu
Ashworth, M., University of Texas, USA
Brady, M., University of Texas, USA
Goertzen, L., Auburn University, USA
Nakov, T., University of Arkansas, USA

3:30 COMPARATIVE DNA SEQUENCE ANALYSIS OF *PYRAMIMONAS PARKEAE* CHLOROPLAST GENOMES
Satjarak, A., University of Wisconsin-Madison, USA, satjarak@wisc.edu

Graham, L., University of Wisconsin-Madison, USA, lkgraham@wisc.edu

3:45 A POLYPHYLETIC ARCHAEPLASTIDA (PLANTAE) BASED ON ANALYSES OF CORE TRANSCRIPTIONAL MACHINERY
Perry, J. B., East Carolina University, USA, perryj07@students.ecu.edu
Stiller, J. W., East Carolina University, USA, stillerj@ecu.edu

4:00 FEATURES OF DINOFLAGELLATE MOLECULAR EVOLUTION
Bachvaroff, T. R., University of Maryland Center for Environmental Science, USA, bachvarofft@umces.edu
Williams, E., University of Maryland Center for Environmental Science, USA, williamse@umces.edu
Jagus, R., University of Maryland Center for Environmental Science, USA, jagus@umces.edu

4:15 RECENT MOBILITY OF PLASTID ENCODED GROUP II INTRONS AND TWINTRONS IN FIVE STRAINS OF THE UNICELLULAR RED ALGA *PORPHYRIDIUM*
Price, D. C., Rutgers, The State University, USA, d.price@rutgers.edu
Perrineau, M. M., Rutgers, The State University, USA, marie-mathilde.perrineau@hotmail.fr
Mohr, G., University of Texas at Austin, USA, georgius@austin.utexas.edu
Bhattacharya, D., Rutgers, The State University, USA, debash.bhattacharya@gmail.com

4:30 METABOLIC CONNECTIVITY AS A DRIVER OF HOST AND PLASTID ENDOSYMBIONT INTEGRATION
Bhattacharya, D., Rutgers University, New Brunswick, United States, USA, debash.bhattacharya@gmail.com
Karkar, S., Rutgers University, New Brunswick, United States, USA, karkar.slim@gmail.com
Facchinelli, F., Heinrich-Heine Universität, Düsseldorf, Germany, Germany, Fabio.Facchinelli@uni-duesseldorf.de
Price, D. C., Rutgers University, New Brunswick, United States, USA, dana.price@gmail.com
Weber, A. P., Heinrich-Heine Universität, Düsseldorf, Germany, Germany, Andreas.Weber@uni-duesseldorf.de

4:45 EVIDENCE FOR RECENT AND RAPID RADIATION OF THE MODERN FRESHWATER THALASSASIORALES FLORA
Theriot, E. C., University of Texas, USA, etheriot@austin.utexas.edu
Ashworth, M., University of Texas, USA, mashworth@utexas.edu
Brady, M., University of Texas, USA, mariska.brady@gmail.com
Goertzen, L., Auburn University, USA, goertlr@auburn.edu
Nakov, T., University of Arkansas, USA, teofiln@gmail.com

5:00 THE TETRAPYRROLE SYNTHESIS PATHWAY AS A MODEL OF HORIZONTAL GENE TRANSFER IN EUGLENOIDS
Lakey, B. D., Michigan State University, USA, lakeybry@msu.edu
Triemer, R. E., Michigan State University, USA, triemer@msu.edu

Tuesday Evening

PSA Movie Extravaganza: Beneath the Tide - With a question and answer period with the Director, Kat Zoula (5:00-6:00) Camera and cinematography by Sri Jiva Southall (**Mandell Theater, Creese Student Center)**

Workshop: How to Apply and Interview for An Academic Position (6:15-7:15): Steven Murray **(Behrakis Grand Hall)**

PSA Student Social (Emily Johnson) (8:00-???)

Wednesday, August 12

07:00-08:00 Continental Breakfast, Behrakis Grand Hall North

8:00 ***Plenary Session:*** *And so we beat on: Swimming behavior of algal cells and an engineering view of flagella in viscoelastic fluids* (Dr. Paulo Arratia, University of Pennsylvania) **(Mandell Theater, Creese Student Center)**

Please note that only presenting authors are listed for invited symposia; full citations with co-authors may be found in the abstract portion of the program guide.

Morning symposium: UNRAVELING THE ENIGMATIC GREEN ALGAE

(Mandell Theater, Creese Student Center)

Symposium moderator: Louise Lewis, University of Connecticut

9:15 MUTATION RATES IN PLASTID GENOMES: THEY'RE LOWER THAN YOU MIGHT THINK.
Smith, D. R., University of Western Ontario, Canada, dsmit242@uwo.ca

9:40 SIGNALING THE EVOLUTION OF MULTICELLULARITY IN THE CHAROPHYTE LINEAGE.
Delwiche, C.F., University of Maryland – College Park

10:05-10:35 COFFEE BREAK

10:35 SMALL, GREEN, AND PARAPHYLETIC: A REVIEW OF THE GENOMIC AND PHYLOGENETIC RELATIONSHIPS OF PRASINOPHYTE GREEN ALGAE.
Gottschalk, S. D., Fordham University, USA, sgottschalk@fordham.edu

11:00 WHEN ONE TREE IS NOT ENOUGH: THE COMPLEX MOLECULAR EVOLUTION OF CHLOROPHYCEAN GREEN ALGAE.
Lewis, L.A., University of Connecticut, U.S.A., louise.lewis@uconn.edu

11:25 AN ASSESSMENT OF THE CURRENT STATE OF KNOWLEDGE OF THE ULVOPHYCEAE
Lam, D.W., University of Alabama, USA, dwlam@ua.edu

11:50 EVOLUTION OF ORGANELLAR GENOMES IN CHAROPHYTIC GREEN ALGAE.
Karol, K.G., The Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, New York

12:15-1:30 LUNCH BREAK (as the wind blows)

Genomics I (Mandell Theater, Creese Student Center)

Session moderator: Chris Lane, University of Rhode Island

1:30 COMPARATIVE GENOMICS OF A BACTERIVOROUS GREEN ALGA REVEALS EVOLUTIONARY CAUSALITIES AND CONSEQUENCES OF PHAGO-MIXOTROPHIC MODES OF NUTRITION
Burns, J. A., American Museum of Natural History, USA, jburns@amnh.org
Paasch, A., AMNH, USA, apaasch@amnh.org
Narechania, A., AMNH, USA, anarechania@amnh.org
Kim, E., AMNH, USA, ekim1@amnh.org

1:45 GENOME REDUCTION DRIVES ALGAL EVOLUTION AND BIODIVERSITY
Qiu, H., Rutgers University, USA, huan.qiu.bio@gmail.com
Bhattacharya, D., Rutgers University, USA, debash.bhattacharya@gmail.com

2:00 THE CHLOROPLAST AND MITOCHONDRIAL GENOMES OF THE TUBULAR GREEN MACROALGA *ULVA* SP. (ULVOPHYCEAE, CHLOROPHYTA)
Melton, J. T., Department of Biological Sciences, The University of Alabama, Tuscaloosa, Alabama 35487-0345, USA, melto006@crimson.ua.edu
Leliaert, F., Marine Biology Research Group, Department of Biology, Ghent University, Ghent, Belgium, frederik.leliaert@gmail.com
Tronholm, A., Smithsonian Marine Station at Fort Pierce, 701 Seaway Drive, Fort Pierce, Florida 34949, USA, atronholm@gmail.com
Lopez-Bautista, J. M., Department of Biological Sciences, The University of Alabama, Tuscaloosa, Alabama 35487-0345, USA, jlopez@ua.edu

2:15 ANALYSIS OF *SYMBIODINIUM* GENOMES REVEALS REMARKABLE DIVERGENCE
Chan, C. X., The University of Queensland, Australia, c.chan1@uq.edu.au
Stephens, T. G., The University of Queensland, Australia, timothy.stephens1@uq.net.au
Forêt, S., The Australian National University, Australia, sylvain.foret@anu.edu.au
Morrow, K., Australian Institute of Marine Science, Australia, k.morrow@aims.gov.au
Bourne, D. G., Australian Institute of Marine Science, Australia, d.bourne@aims.gov.au
Voolstra, C. R., King Abdullah University of Science and Technology, Saudi Arabia, christian.voolstra@kaust.edu.sa
Leggat, W., James Cook University, Australia, bill.leggat@jcu.edu.au
Miller, D. J., James Cook University, Australia, david.miller@jcu.edu.au
Ragan, M. A., The University of Queensland, Australia, m.ragan@uq.edu.au

2:30 TWINTRONS OF THE EUGLENOPHYTA - A COMPREHENSIVE COMPARATIVE ANALYSIS
Bennett, M. S., Michigan State University, USA, benne124@msu.edu
Triemer, R. E., Michigan State University, USA, triemer@msu.edu

2:45 GENOME EVOLUTION IN RED ALGAE ON THE PATH TO PARASITISM

Salomaki, E. D., University of Rhode Island, USA, eric.salomaki@gmail.com
Lane, C. E., University of Rhode Island, USA, clane@uri.edu

Population/Distribution/Large Scale Phycology II (Behrakis Grand Hall, Creese Student Center)

Session moderator: Kirsten Müller, University of Waterloo

1:30 CYANOBACTERIA FROM THE LAPLAND BIOSPHERE RESERVE, RUSSIA
Shalygin, S. S., John Carroll University, Polar-Alpine Botanical Garden-Institute, USA, sshalygin18@jcu.edu

1:45 INVESTIGATING SPECIES DIVERSITY WITHIN THE RED ALGAL GENERA *ANTITHAMNIONELLA*, *HOLLENBERGIA* AND *SCAGELIA* (CERAMIALES, RHODOPHYTA) IN CANADA
Bruce, M., University of New Brunswick, Canada, meghann.bruce@gmail.com
Saunders, G., University of New Brunswick, Canada, gws@unb.ca

2:00 VIEWING RHODOLITHS AS DIVERSITY-RICH HOLOBIONTS
Fredericq, S., University of Louisiana at Lafayette, USA, slf9209@louisiana.edu
Sauvage, T., University of Louisiana at Lafayette, USA, tomsauv@gmail.com
Schmidt, W. E., University of Louisiana at Lafayette, USA, william.schmidt.algae@gmail.com

2:15 FACTORS SHAPING PHOTOTROPH-DOMINATED MICROBIAL COMMUNITIES ALONG OAHU'S WINWARD COAST
Johnston, E. T., University of Hawaii at Manoa, USA, ej363707@gmail.com
Sherwood, A. R., University of Hawaii at Manoa, USA, asherwoo@hawaii.edu

2:30 EFFECTS OF OCEAN ACIDIFICATION ON PHYTOPLANKTON PHOTOSYNTHESIS
Morris, J. J., University of Alabama at Birmingham, USA, evolve@uab.edu

2:45 LIMITS TO THE POSITIVE EFFECT OF OCEAN ACIDIFICATION ON MACROALGAL PRODUCTION
Kübler, J. E., CSUN, USA, janet.kubler@csun.edu
Nisumaa, A. M., CSUN, Estonia, annemarin@gmail.com
Scoma, S., CSUN, USA, samuel.scoma.496@my.csun.edu
Dudgeon, S. R., CSUN, USA, steve.dudgeon@csun.edu

3:00- 3:30 AFTERNOON COFFEE BREAK

Applied Phycology Special Symposium I: Biofuels and Bioproducts (Behrakis Grand Hall, Creese Student Center)

Session moderator: Milton Sommerfeld, Arizona State University

3:30 **Plenary talk: examining biological challenges in algal biofuels and bioproduct generation**
Polle, J. E., Brooklyn College of CUNY, USA, jpolle@brooklyn.cuny.edu

4:00 EFFECTS OF DIFFERENT AMMONIUM SALTS ON MEDIUM PH CHANGE, GROWTH AND LIPID ACCUMULATION OF *ACUTODESMUS BERNARDII* UNDER BATCH AND FE-BATCH CUTURES
Zhou, Z., Jinan University, China, air9137@126.com
Gao, B., Jinan University, China, gaobaoyan1211@126.com
Li, X., Jinan University, China
Li, A., Jinan University, China, tiger@jnu.edu.cn
Zhang, C., Jinan University, China, tzhangcw@jnu.edu.cn

4:15 EARLY DETECTION OF A MAJOR ZOOPLANKTON GRAZER IN ALGAE CULTURE
Wang, Y., Arizona Center for Technology and Innovation, Environment and Resource Management, ASU, USA, ywang187@asu.edu
Keller, M. C., Arizona Center for Technology and Innovation, Environment and Resource Management, ASU, USA, Maria.Castillokeller@asu.edu
Sommerfeld, M., Arizona Center for Technology and Innovation, Environment and Resource Management, ASU, USA, Milton.Sommerfeld@asu.edu

4:30 CONTROL OF CHITIN AND LIPID PRODUCTION IN THE PHOTOSYNTHETIC DIATOM *CYCLOTELLA* SP. BY CO-LIMITATION OF SILICON AND NITRATE IN BATCH AND FED-BATCH CULTIVATION
Chiriboga, O., Oregon State University, USA, chiriboo@onid.oregonstate.edu
Chotyakul, N., Oregon State University, USA, nattaporn.chotyakul@oregonstate.edu
Wu, X., Oregon State University, USA, sarawu1989@gmail.com
Durst, B., Oregon State University, USA, bob.durst@oregonstate.edu
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4:45 METAGENOMIC ANALYSIS ON THE INFECTION PROCESS OF *PYROPIA* (=*PORPHYRA*) DISEASES
Kim, G. H., Kongju National University, Republic Of Korea, ghkim@kongju.ac.kr

Genomics II (Mandell Theater, Creese Student Center)

Session moderator: Eric Linton, Central Michigan University (Go MAC!)

3:30 TEMPO AND MODE OF DIATOM PLASTID GENOME EVOLUTION
Yu, M., The University of Texas at Austin, USA, annaymj_2010@utexas.edu
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Theriot, E. C., Texas Memorial Museum, USA, etheriot@austin.utexas.edu
Sabir, J. S., King Abdulaziz University, Saudi Arabia, jsabir2622@gmail.com
Jansen, R. K., The University of Texas at Austin, USA, jansen@austin.utexas.edu

3:45 CHLOROPLAST GENOMICS OF *TRACHELOMONAS ELLIPSODALIS* (EUGLENACEAE) AND *PHACUS ORBICULARIS* (PHACACEAE)

Kasiborski, B. A., Central Michigan University, Department of Biology, Mount Pleasant, MI 48859, USA, kasib1b@cmich.edu

Linton, E. W., Central Michigan University, Department of Biology, Mount Pleasant, MI 48859, USA, eric.linton@cmich.edu

4:00 THE UNEXPECTED EXTREMOPHILE: TOLERANCE TO FLUCTUATING SALINITY IN THE GREEN ALGA *PICOCHLORUM*

Foflonker, F., Department of Biochemistry and Microbiology

Ananyev, G., Waksman Institute of Microbiology and Department of Chemistry and Chemical Biology

Qiu, H., Department of Ecology, Evolution and Natural Resources

Morrison, A., Department of Marine and Coastal Sciences, Rutgers University, NJ, USA

Dismukes, G.C., Waksman Institute of Microbiology

Bhattacharya, D., Department of Ecology, Evolution and Natural Resources and Department of Marine and Coastal Sciences, Rutgers University, NJ, USA

Wednesday Evening

PSA Business Meeting (4:45-5:45) (**Mandell Theater, Creese Student Center)**

Luxurious PSA Banquet (6:30-9:30) **Academy of Natural Sciences of Drexel University. 1900 Benjamin Franklin Parkway, Philadelphia, PA 19103** (Bus transportation provided, beginning at 6:00 pm from Drexel to Academy, and return beginning at 9:00 pm. Pickup and dropoff will be near the Creese Student Center, at exact location to be announced at the meeting. Attendees may walk from Drexel to the Academy, approximately 20-25 minutes; maps will be provided)

Thursday, August 13

07:00-08:00 Continental Breakfast, Behrakis Grand Hall North

8:00 ***Plenary Session:*** *Algae and Climate Change* (Dr. Susan Kilham, Drexel University)

Please note that only presenting authors are listed for invited symposia; full citations with co-authors may be found in the abstract portion of the program guide

Morning Symposium I: Brown Algal Tree of Life (Mandell Theater, Creese Student Center)

Session moderator: Naomi Phillips, Arcadia University

9:15 USING ECTOCARPUS GENOMICS TO INVESTIGATE THE EMERGENCE OF COMPLEX MULTICELLULARITY IN THE BROWN ALGAE
Cock, J. M., CNRS, France, cock@sb-roscoff.fr

9:35 KELP GENOME EVOLUTION
Yoon, H. S., Sungkyunkwan University, Republic Of Korea, hsyoon2011@skku.edu

10:00-10:30 COFFEE BREAK

10:30 BROWN ALGAL ORGANELLAR GENOMES: OVERALL PATTERNS AND INSIGHTS FROM HETEROKONTS
Phillips, N., Biology Department, Arcadia University, USA, phillipsn@arcadia.edu

10:50 ENIGMATIC BROWN ALGAE
Parente, M. I., CIBIO, Portugal, nelaparente@hotmail.com

11:10 MYSTERIES IN FRESHWATER BROWN ALGAL EVOLUTION AND ECOLOGY
Wehr, J. D., Fordham University, USA, wehr@fordham.edu

11:30 REVIEWING SPECIES RELATIONSHIPS IN BROWN MACROALGAE (PHAEOPHYCEAE) IN THE MOLECULAR ERA
Camacho, O., University of Louisiana at Lafayette, USA, omc1833@louisiana.edu

11:50 WHAT MAKES ECTOCARPUS CELLS ROUNDER?
Charrier, Bénédicte, Morphogenesis of MacroAlgae, NRS-UPMC Station Biologique, ROSCOFF-FRANCE

12:00 LUNCH BREAK/ADJOURNMENT

Morning Symposium II: Biofuels, Bioproducts, and Bioremediation - Algae for the 21st Century (Behrakis Grand Hall, Creese Student Center)

Session: Large-Scale Cultivation of Microalgae with Commercial Potential: Products and Processes (Schonna Manning-session leader)
9:00 INTRODUCTION TO ATP^3, AZCATI AND UTEX
Sommerfeld, M., Arizona State University, USA, milton.sommerfeld@asu.edu

9:05 INTRODUCTION TO WORKSHOP AND HISTORICAL PERSPECTIVE
Manning, S., University of Texas, USA, Shonna.Manning@asu.edu

9:15 COMMODITY AND HIGH-VALUE PRODUCTS FROM MICROALGAE
Manning, S., University of Texas, USA, Shonna.Manning@asu.edu

9:30 MODERN SYSTEMS FOR CULTURING MICROALGAE AT LARGE SCALE
Sommerfeld, M., Arizona State University, USA, milton.sommerfeld@asu.edu

9:45 MANAGING MICROALGAL CULTURES AT THE PRODUCTION SCALE
Dempster. T., Arizona State University, USA, dempster@asu.edu

10:00 -10:30 COFFEE BREAK

Session: Applied Phycology: Bioremediation (Thomas Dempster-session leader)

10:30 **Plenary Talk:** OPTIMIZING POLYCULTURE CULTIVATION AND WASTEWATER TREATMENT IN LARGE-SCALE OFFSHORE PHOTOBIOREACTORS
Novoveska, L., Algae Systems LLC, USA, lnovoveska@algaesystems.com
Sundstrom, E. R., Algae Systems LLC, USA, esundstrom@algaesystems.com
Atwood, M., Algae Systems LLC, USA, matwood@algaesystems.com

11:00 MICROALGAE: HARNESSING DIVERSE METABOLISMS FOR ENVIRONMENTAL REMEDIATION AND WASTE STREAM TREATMENT
Price, J.R., Department of Engineering, Drexel University, Philadelphia, PA, USA
Sales, C.M. Department of Engineering, Drexel University, Philadelphia, PA, USA

11:15 USING ALGAE TO BIOREMEDIATE DISCHARGE WATERS FROM POWER PLANTS
Puruhito, E., Arizona State University, USA, emil.puruhito@asu.edu
Sommerfeld, M., Arizona State University, USA, milton.sommerfeld@asu.edu

11:30 Discussion

12:00 LUNCH BREAK/ADJOURNMENT

Abstracts

Please note that presenting authors are underlined.

Invited Symposia

Plenary Talks

PHOTOSYMBIOTIC GIANT CLAMS ARE TRANSFORMERS OF SOLAR FLUX
Sweeney, A. University of Pennsylvania

Giant tridacnid clams, like reef-building corals, harbor and exchange nutrients with the photosynthetic dinoflagellate *Symbiodinium*. These clams are also notable for their iridescent color patterns, caused by clam cells called iridocytes. These cells are unusual compared to iridocytes in other taxa, having a structure that is a superposition of sub-wavelength scale layers with a super-wavelength scale sphere. We recently showed that, in combination with a pillared geometry of the dinoflagellates within the clam mantle tissue, these iridocytes function to reshape and propagate incident solar radiance deep into the the system. This phenomenon results in a remarkably deep photic zone inside the animal, producing even illumination at about 10% of the intensity of downwelling sunlight along the sides of the algal pillars. This down-regulation of solar flux relative to irradiances on shallow reefs is approximately what is needed to reduce or eliminate non-photochemical quenching in *Symbiodinium*. Algae in clams are therefore likely able to use all of the energy present in high-intensity downwelling sunlight for photosynthesis while avoiding the photodamage that would result without this evolved system in place. This talk will outline our initial description of the system, and our ongoing work on the species complex in Palau. We are currently investigating the ecological responsiveness of iridocyte/algal system in various tridacnid species, as well as possible *Symbiodinium* clade/iridocyte interactions. Insights gained from the clam system may also inform efforts to produce algal-based chemicals and fuels more efficiently.

ALGAL PHOTORECEPTORS AND THEIR OPTOGENETIC APPLICATION
Hegemann, P., Exp. Biophysics, Humboldt-Universität zu Berlin, Hegemann@rz.hu-berlin.de

Many years back in 1985 we began to study light-induced movement responses in the green model algae *Chlamydomons reinhardtii* and *Volvox carteri* by application of various biophysical techniques[1]. We observed that the photoreceptor currents of the algal eye (eyespot) exhibits a rhodopsin action spectrum and that the rise of the current is extremely fast after a short light flash. These two observations lead to the proposal that the rhodopsin photoreceptor and the photoreceptor channel are a single protein complex or even constituted by a single protein[2,3]. Due to the fact that *Chlamydomonas* contains at least 10 rhodopsins, biochemical purification of the photoreceptor protein was impossible. Only based on a novel cDNA library we were able to identify rhodopsin sequences and the expression of rhodopsin 3 and 4 (COP3 and COP4) in *Xenopus* oocytes allowed us to prove that these two photoreceptors are functioning as directly light-gated ion channels that we named Channelrhodopsin 1 and 2 (ChR1 and ChR2)[4,5]. After we had expressed ChR2 in human embryo kidney cells (HEK) many neuroscientist began to use ChR2 for selective stimulation of neuronal cells with light[6,7]. Since the algal photoreceptor expressed so well in neurons, other groups started to apply ChR2 to living animals including *C.elegans*, *Drosophila*, Zebrafish, and mouse. At least three ophthalmology teams got the permission to express ChR2 in the human eyes for curing blindness at least to some extent. My own group studied these unusual photoreceptors and modified absorption, kinetics, and ion selectivity in such as way that the ChR palette is now widely applicable to many different biological problems within a new field that is now named Optogenetics [8]. Over the years we also identified another uncharacterized group of rhodopsins that are directly linked to a kinase, a response regulator, and in many cases a guanylyl- or adenylyl cyclase. We named the family histidine kinase rhodopsins (HRKs)[1]. Some of these photoreceptors are bimodal switchable by UV and blue light and we expect that these photoreceptors measure the UV/blue ratio and are involved in developmental adaptation, seasonal adaptation etc.. Green algae also contain phototropin, a flavin-based photoreceptor that regulates sexuality, the size of the algal eye, and the amount of ChR1 and ChR2 that is expressed in the eye. And finally, *C.reinhardii* contains at least three cryptochromes that are involved in developmental processes, although the details are not clear so far. To further study the photoreceptor function in more detail, a nuclear gene targeting system for green algae is urgently needed. I will discuss the current knowledge of several nuclear targeting approaches involving ssDNA, zink finger nucleases and CRISPR/CAS9.

AND SO WE BEAT ON: SWIMMING BEHAVIOR OF ALGAL CELLS & AN ENGINEERING VIEW OF FLAGELLA IN COMPLEX FLUIDS

Arratia, P.E., Dept. Mechanical Engineering & Applied Mechanics, University of Pennsylvania

Due to their small size (less than a millimeter), microorganisms such as bacteria, sperm cells, and various kinds of algal cells must overcome fluid forces that are predominantly viscous in order to achieve any net motion (e.g. swim forward). While much attention has been recently devoted to swimming of microorganisms in simple Newtonian fluids like water[1], many microorganisms encounter fluids that contain (bio)-polymers and/or particles such as soil, intestinal fluid, and human mucus. The material properties (or rheology) of such fluids are often complex and can strongly affect an organism's motility behavior. A major challenge is to understand the mechanism of propulsion in media that exhibit both solid- and fluid-like behavior, such as viscoelastic fluids.

In this talk, I will discuss recent experiments on the swimming behavior of *Chlamydomonas reinhardtii* in model viscoelastic fluids using boundary-tracking methods[2]. Experiments are performed using a high-speed camera in a thin fluid layer, which allows for precise tracking of the algae body and flagellum with good spatial and temporal resolution. We find that fluid elasticity hinders the cell's overall swimming speed but leads to a surprising increase in the cell's flagellum beating frequency. The beating kinematics and flagellum waveforms are also significantly modified by fluid elasticity. A mathematical model is developed to capture the main features of the frequency behavior. Overall, our results demonstrate (i) that the spreading and motility of algal cells can be controlled by tuning fluid properties and (ii) the intimate link between swimming kinematics and fluid rheology.

Polar Phycology

ALLIES, CHEATERS, & THIEVES: MACROALGAL-MESOGRAZER INTERACTIONS ALONG THE WESTERN ANTARCTIC PENINSULA

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McClintock, J. B., University of Alabama at Birmingham, USA
Baker, B. J., University of South Florida, USA

Macroalgae dominate the hard benthos along the Western Antarctic Peninsula to depths of up to 40 m or more. Most of the macroalgae are chemically defended from a variety of macro- and mesograzers but harbor very high densities of amphipod mesograzers. The amphipods benefit from living on the large, chemically-defended macroalgae because they gain refuge from fish which are their primary predators. Most amphipod species do not consume most of the macroalgal species, but are of benefit to the macroalgae by keeping them relatively clean of epiphytic microalgae and filamentous macroalgae. One amphipod species does consume some of the chemically defended red algal species and is able to sequester algal metabolites for its own use as defenses against fish. This is the first known incidence of defensive metabolite sequestration in marine arthropods. Feeding rates of this amphipod on its preferred chemically defended host vary noticeably between experiments with algae from different collection sites. A combined genetic and chemical analysis of the alga from different collection sites revealed that it divides into two closely related phylogroups, not distinct enough to be considered separate species, each of which is further divided into one of five chemogroups. The chemogroups are largely collection-site specific except for differences between individuals of the two phylogroups.

THE ARCTIC'S SECRET GARDEN: LANDFAST SEA ICE COMMUNITIES AND THEIR CONTRIBUTION TO THE UNDERLYING MARINE ECOSYSTEM

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Juhl, A. R., Lamont-Doherty Earth Observatory of Columbia University, USA, andyjuhl@ldeo.columbia.edu

Sea-ice environments support a diverse interstitial algal community that contributes to annual polar production and, upon export, provides nutritious material to underlying ecosystems prior to spring bloom development in the open water. However, both the ecological and biogeochemical connections between sea ice derived material and the underlying marine systems are relatively unknown. In Spring 2011-2014, a series of field and laboratory experiments were conducted to further investigate community dynamics within the sea ice along with the ultimate fate of this material once it leaves the ice. Whether materials exported are primarily consumed by pelagic or benthic organisms is related to residence time in the water column, a capricious characteristic that can be influenced both by biotic (algal composition, EPS concentration) and abiotic (nutrient dynamics, overlying snow cover) factors. Results indicate that community composition, vertical orientation within the ice, and sinking velocity are all related to overlying snow depth and distance from the ice-water interface. This suggests that algal production within sea ice, carbon flux from sea ice, and the availability of this material to various marine organisms can be significantly influenced by local climate related shifts in temperature and precipitation.

PHYSIOLOGIAL ACCLIMATION OF ANTARCTIC MACROALGAE TO CLIMATE CHANGE: EFFECTS OF UV RADIATION AND INCREASING SEAWATER TEMPERATURE

Rautenberger, R., Universidad Austral de Chile, Chile, ralf.rautenberger@uach.cl

Marine macroalgae, which are endemic in the Antarctic, are strongly adapted to the low seawater temperatures ranging between -1.8 and +2°C as well as to the low light conditions in their subtidal habitats. These characteristics can make them particular sensitive to climate change in Antarctica. Enhanced ultraviolet-B (UV-B: 280-315nm) radiation resulting from the annual ozone hole over Antarctica in spring and high solar radiation in summer affects photosynthesis of macroalgae. Projected ocean warming can have an overall effect on macroalgal metabolism such that their ability to cope with UV-B stress might be favoured. In this talk I am going to present results of present research in stress physiology to show how Antarctic macroalgae are able to acclimate to these major environmental factors. The impact of changing temperatures on UV stress tolerance will be of particular interest. I further will put these results into the context of climate change to draw possible future consequences for Antarctic coastal ecosystems. This talk gives an overview about the progress in phycological research in Antarctica.

COMMUNITY ECOLOGY OF ISOLATED KELP BEDS IN THE ALASKA ARCTIC

Konar, B., School of Fisheries and Ocean Sciences, University of Alaska, Fairbanks, Fairbanks, AK
Iken, K., Institute of Marine Science, University of Alaska, Fairbanks, Fairbanks, AK

Rocky habitat dominated by kelps is rare in the nearshore Arctic, but where they occur, these habitats are known to be distinct biodiversity hotspots. These boulder regions are ecologically important because they support benthic primary producers with tightly linked food webs and relatively high biodiversity compared to non-boulder, soft sediment dominated areas. Here, we present a community description of macroalgal-dominated boulder fields in the Alaska Arctic from the Chukchi to Beaufort seas. Our results show that these nearshore boulder communities share many of their community elements but each also has dominant members that are infrequent at the other locations. This indicates that dispersal and exchange among these isolated communities may be limited and local recruitment may be crucial. However, recruitment is extremely slow in these regions and may be adversely affected by increasing climate warming trends, river runoff, coastal erosion and local oil and gas exploration. This may result in a much decreased resilience to these drivers or delayed recovery from disturbances such as ice scour.

Green Algal Tree of Life

MUTATION RATES IN PLASTID GENOMES: THEY'RE LOWER THAN YOU MIGHT THINK

Smith, D. R., University of Western Ontario, Canada, dsmit242@uwo.ca

Within plastid-bearing species, the mutation rate of the plastid genome is often assumed to be greater than that of the mitochondrial genome. This assumption is based on early, pioneering studies of land plant molecular evolution, which uncovered higher rates of synonymous substitution in plastid versus mitochondrial DNAs. However, much of the plastid-containing eukaryotic diversity falls outside of land plants, and the patterns of plastid DNA evolution for embryophytes do not necessarily reflect those of other groups. Recent analyses of plastid and mitochondrial substitution rates in diverse lineages have uncovered very different trends than those recorded for land plants. In this presentation, I explore these new data and argue that for many protists the plastid mutation rate is lower than that of the mitochondrion, including groups with primary or secondary plastids as well as nonphotosynthetic algae. These findings have far-reaching implications for how we view plastid genomes and how their sequences are used for evolutionary analyses, and might ultimately reflect a general tendency toward more efficient DNA repair mechanisms in plastids than in mitochondria.

SMALL, GREEN, AND PARAPHYLETIC: A REVIEW OF THE GENOMIC AND PHYLOGENETIC RELATIONSHIPS OF PRASINOPHYTE GREEN ALGAE

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Karol, K. G., The Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, USA, kkarol@nybg.org

At least seven distinct clades are now thought to comprise the prasinophytes - a paraphyletic grouping of unicellular planktonic green algae within the Chlorophyta. With the sequencing of *Scherffelia* and *Tetraselmis* in Clade IV (Chlorodendrales) reported here, plastid genomes are now available for all seven clades of prasinophytes. The genomes of *Scherffelia* and *Tetraselmis* are 137,163 bp and 176,680 bp in length respectively. Each genome contains a large single copy, a small single copy and an inverted repeat. The small single copy is reduced to 3,385 bp in *Scherffelia* and 1,350 bp in *Tetraselmis*. Plastid genome architecture - including the loss, expansion, or reduction of small single copies and inverted repeats - has changed markedly across the seven clades of prasinophytes. These architectural changes provide new perspectives and context for the evolution of the Chlorophyta.

WHEN ONE TREE IS NOT ENOUGH: THE COMPLEX MOLECULAR EVOLUTION OF CHLOROPHYCEAN GREEN ALGAE.

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Nine chloroplast genomes were newly sequenced to increase phylogenetic resolution in the chlorophycean order Sphaeropleales. Like other plastid genomes reported for green algae, the genomes vary considerably in gene arrangement and size, ranging from 102 - 220 kb, and with 1 - 32 introns. The cp genomes of all species contain the same set of protein-coding genes with the exception of *Neochloris aquatica*, which lacks the *chlB*, *chlL*, and *chlN* genes. Of the remaining protein-coding genes, 56 were used for phylogenetic inference and the concatenated data set yielded a fully resolved, well-supported phylogeny. However, topologies from individual genes were in strong conflict despite high support for all nodes in the concatenated analysis. An amino acid analysis was conducted and yielded a different, but also highly supported concatenated topology. We tested if this disagreement was due to saturation, but omission of 3rd codon positions or even 50% of the most rapidly evolving sites did not remove the conflict. Further investigation of the data revealed strong differences in molecular evolution of the genes that might contribute to conflict among genes. Codon usage bias was strong in certain taxa (esp. *Mychonastes homosphaera*), confounding their position in the phylogeny, but ambiguation of problematic codons or removal of such “rogue” taxa did not remove conflict. Other known sources of systematic error were investigated, including heterotachy, incomplete lineage sorting, and horizontal gene transfer. The phenomenon extends to other orders of Chlorophyceae, but its occurrence in other green classes is a matter of future investigation.

AN ASSESSMENT OF THE CURRENT STATE OF KNOWLEDGE OF THE ULVOPHYCEAE

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The Ulvophyceae include some of the most conspicuous green algal organisms. They exhibit a vast array of diversity and run the gamut from seaweeds to freshwater filaments, and even include microscopic terrestrial forms. In order to study the evolution and taxonomy of this enigmatic class of autotrophs, we implemented an integrative approach. Both field collected and cultured specimens were examined using both light and electron microscopy. Additionally, molecular phylogenies based on plastid and mitochondrial genome data were inferred. Complete mitochondrial and chloroplast genomes for *Ulva* sp. inferred sister relationship between the orders Ulvales and Ulotrichales. The chloroplast genomes of *Bryopsis plumosa* and *Tydemania expeditions* are currently some of the most gene dense in the “core Chlorophyta” and include examples of HGT. Phylogenomic analyses of the Antarctic ulvophycean *Lambia antarctica* confirm that this species is in the order Bryopsidales (suborder Bryopsidineae). Furthermore, these results support the idea that homoplasty (only chloroplasts) vs. heteroplasty (chloroplasts and amyloplasts) are key features in the evolution of Bryopsidales. Preliminary phylogenomic assessments based on the aforementioned *de novo* genomes suggest that the Ulvophyceae is not monophyletic.

EVOLUTION OF ORGANELLAR GENOMES IN CHAROPHYTIC GREEN ALGAE.

Karol, K.G., The Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, New York
Hall, J.D., Department of Plant Science and Landscape Architecture, University of Maryland, College Park, MD
Pérez, W., The Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, New York
McCourt, R.M., Academy of Natural Sciences of Drexel University, Philadelphia, Pennsylvania

Land plants evolved from an ancient lineage that includes the charophytic green algae. The most species-rich lineages of extant charophytes are the conjugating green algae (Zygnematophyceae) and the Characeae (stoneworts). In order to better understand evolutionary relationships throughout the charophytes, the Green Algal Tree of Life (GrAToL) project has sequenced

dozens of organellar genomes from these lineages. Patterns of genome evolution differ markedly among the lineages of charophytes. Plastid genomes of Characeae are remarkably syntenic, with most of the architectural variation being in the relative size of the large and small single copy regions, due primarily to the expansion and contraction of intergenic regions. By contrast, plastid genomes in the conjugating green algae (Zygnematophyceae) show a low degree of synteny with several genome rearrangements implied when comparing relatively closely related taxa. Most zygnematophytes sampled and *Coleochaete* lack an inverted repeat in the plastid genome. However, the Klebsormidiophyceae have large inverted repeat regions and a relatively short small single copy region. In summary, green algal plastid genomes exhibit significant structural diversity within and between groups that will be of interest to researchers studying evolution of this organelle in green plants.

SIGNALING THE EVOLUTION OF MULTICELLULARITY IN THE CHAROPHYTE LINEAGE.

Delwiche, C.F., University of Maryland – College Park
Chang, C., University of Maryland – College Park

The close relationship between green algae and land plants (embryophytes) is now well established. We have used transcriptomic and genomic methods to investigate the phylogeny and genetic capabilities of green algae. These studies revealed striking similarities in the gene complement of charophyte green algae and land plants, including identifying many genes associated with land plant hormone systems, but left open the question of how these genes function in charophyte algae. Focusing on the plant hormone ethylene in *Spirogyra*, we tested the functional role of several genes known to be involved in the ethylene system. There was substantial conservation of function, to the extent that the *Spirogyra* ETR1 (ethylene receptor) homolog could restore function in a triple mutant of *Arabidopsis* nearly as efficiently as the native gene. Several other components of the ethylene system are also functionally conserved. We measured ethylene emission by *Spirogyra*, and identified a dose-dependent response (cell elongation). Taken together, this evidence shows unambiguously that the ethylene system in *Spirogyra* is homologous to that in *Arabidopsis*, and implies that ethylene signaling predates the origin of land plants.

Brown Algal Tree of Life

USING *ECTOCARPUS* GENOMICS TO INVESTIGATE THE EMERGENCE OF COMPLEX MULTICELLULARITY IN THE BROWN ALGAE

Cock, J. M., CNRS, France, cock@sb-roscoff.fr

The brown algae, which are members of the supergroup chromalveolata, are very distantly related both to animals and to green plants. This group of seaweeds evolved complex multicellularity independently of the plants and animals and is one of only a small number of eukaryotic groups that has acquired this level of developmental complexity. Analysis of the genome sequence of the model brown alga *Ectocarpus* has revealed a number of features that may be linked to the emergence of complex multicellularity in this lineage, including a family of membrane-localised receptor kinases that evolved independently in brown algae but strongly resemble the receptor kinases of green plants and animals. The brown algae are also one of only

a small number of eukaryotic lineages that have evolved microRNAs and these molecules may also have played an important role in the evolution of complexity in this group. Genome analysis has therefore provided some clues about the molecular mechanisms that underlie multicellular development in the brown algae but more meaningful comparisons with other multicellular lineages will only be possible if we can obtain a deeper, experimental understanding of these molecular mechanisms. To address this problem, we have proposed and are developing the filamentous brown alga *Ectocarpus* as a model system for the brown algae and are using this system to investigate the genetic basis of specific developmental processes. This work currently focuses on two key aspects of this organism's reproductive biology: life cycle regulation and sex determination.

MYSTERIES IN FRESHWATER BROWN ALGAL EVOLUTION AND ECOLOGY

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The Phaeophyceae is a diverse class of roughly 300 genera and at least 2000 species. Nearly all occur in marine waters, with less than 1% of this total, about 6 or 7 species, known to colonize freshwater environments. Why there are so few freshwater species? Questions of their presumed rarity, and possible evolution from marine to freshwater habitats have puzzled researchers for more than a century, with discoveries of new populations adding to questions regarding their ecology and biogeographic patterns. This talk will review historical and current data on the distribution, ecology and evolution of the two better-known freshwater taxa, *Heribaudiella* and *Pleurocladia*. Both are known from widely scattered freshwater streams and lakes on several continents, although each has been described as “rare” in many publications. Ecological data indicate that both occur in habitats with similar water chemistry and river conditions, but a few documented populations of *Pleurocladia* from brackish water habitats suggest different possible adaptations to salinity. We also review recent genetic data which indicate contrasting patterns of evolution and speciation in *Heribaudiella* and *Pleurocladia*.

KELP GENOME EVOLUTION

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Kelps (Laminariales) form underwater forests where they serve as nursing habitats for diverse marine organisms. Several kelp species such as *Undaria* and *Saccharina* are extensively cultivated in eastern Asia for food because of their high content of iodine and other nutrients. These species are also used in industry for medicine, cosmetics, and as biofuel feedstock. Despite their economic and ecologic significances, only a handful of organelle genomes have been reported from kelps. To better understand kelp genome evolution, we characterized complete plastid and mitochondrial genomes from several kelp species. We also assembled draft nuclear genome data from *Undaria pinnatifida*. Based on comparative genomic analysis, we report extremely high conservation in genome structure among kelp organelle genomes. We will

discuss the evolutionary history of kelps based on multigene phylogenetics, molecular clock analysis, and inspection of organelle and nuclear genome data.

REVIEWING SPECIES RELATIONSHIPS IN BROWN MACROALGAE (PHAEOPHYCEAE) IN THE MOLECULAR ERA

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Assessing species delimitation in brown algae (Phaeophyceae) has proven to be a dynamic and challenging endeavor. Historically, this task focused primarily on the comparative analysis of morphological characters, while in recent years the use of molecular-based phylogenetic analyses has become the status quo and in most cases is mandatory to clarify species boundaries and relationships. Nevertheless, many inter-and intraspecific clusters still remain taxonomically unclear. Here we review species relationships in the orders Fucales and Dictyotales by focusing on the highly polymorphic and taxonomically complex genus *Sargassum* (Sargassaceae) in the former and the cryptic genus *Lobophora* (Dictyotaceae) in the latter. Comprehensive assessments including significant multi-locus sampling and sequencing of type material is critical to delimit species in brown algae, as well as in other groups.

ENIGMATIC BROWN ALGAE

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At the morphological level, brown crusts present simple morphologies and reduced number of diagnostic characters, but molecular evidence suggests that they have more complex phylogenies and that the species-level diversity have been clearly underappreciated. Levels of divergence among worldwide samples of the cosmopolitan *Ralfsia verrucosa*, using the mitochondrial COI-5P gene and the nuclear ITS region, have been acknowledged. Molecular analyses indicate that are many divergent species under *R. verrucosa* identity. A comprehensive survey extended to other crustose species revealed a total of 31 genetic species groups that were after investigated using rbcL and psbA and combined analysis including COI-5P to access phylogenetic relationships. Of the 31 genetic species groups, 19 are assignable to the Ralfsiales and the remaining 12 showed distinct phylogenetic affinities. On the basis of nuclear, plastid and mitochondrial sequence data, the most comprehensive molecular phylogeny of the crustose brown algae to date is presented. According with our results the traditional classification does not accurately reflect the evolutionary history of the crustose brown algae and morphological evidences are feeble to support some of the new lineages found.

BROWN ALGAL ORGANELLAR GENOMES: OVERALL PATTERNS AND INSIGHTS FROM HETEROKONTS

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Brown algae (Phaeophyceae) are one of the most productive and ecologically important lineages in marine ecosystems and represent one of the last lineages in the Eukaryotic tree of life to shift to multicellularity. Members of these lineages (including other heterokonts) generate approximately half the world's oxygen. However, we are just beginning to understand their organellar genomes and architectural changes that accompany their transition to complexity. This presentation will review what is known about plastid and mitochondrial genomes in brown algae and discuss insights gained from a project in a closely related class (Schizocladiophyceae). This project was initiated to understand the organellar genomes of these important primary producers and the genomic changes accompanying their shift to multicellularity. To assure the isolation of pure genomic DNA cultures were grown with GeO_2 to inhibit diatom growth before DNA extraction. Data from a separate HiSeq and Miseq run were collected and assembled. We report here on the size, structure, and gene content of this heterokont lineage and compare it to members of the brown algae. Lastly, we summarize insights these data provided into the evolutionary patterns in organellar genomes from heterokonts to brown algae.

WHAT MAKES ECTOCARPUS CELLS ROUNDER?

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Brown algae are multicellular organisms sharing no common evolutionary history with metazoans and land plants. While they are photosynthetic organisms like land plants, their environment is totally different, with mainly higher external osmotic pressures, different light spectra and exposition to higher mechanical forces. The factors controlling cell differentiation in brown algae have been scarcely studied so far. Here we decipher the physical and biological mechanisms involved in cell rounding in the model brown alga *Ectocarpus siliculosus* (Ectocarpales). During filament growth, cell rounding occurs simultaneously with cells shifting from the apex to a more centered position within the filament (relative position). By contrast to cylindrical cells which ensure apical growth, spherical cells undertake most of filament branching and seem to display a higher resistance to osmotic shock. However, the mechanisms involved in this cell reshaping are unknown. In an attempt to comprehensively understand cell rounding, we gathered a wealth of physical and biological properties: osmotic pressure, volume and surface parameters, cell wall biophysical features, photosynthetic activity, cytoskeleton dynamics and gene expression patterns. Despite the high level of intrinsic cell plasticity displayed for some of these parameters, these data will ultimately be integrated in a comprehensive model accounting for cell rounding in *E. siliculosus*. Results will be discussed in the light of the data obtained in the *Ectocarpus étoile* and *knacki* mutants impaired respectively in apical tip growth and in cell rounding.

Biofuels and Applied Phycology

MICROALGAE: HARNESSING DIVERSE METABOLISMS FOR ENVIRONMENTAL REMEDIATION AND WASTE STREAM TREATMENT

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Conventional wastewater treatment utilizes activated sludge processes in order to remove organic carbon, while additional denitrification and dephosphatation processes must be carried out to remove additional nutrients in order to prevent eutrophication of influent receiving waters, such as lakes, rivers, and bays. The application of algal-biotechnology may provide an alternative solution for nutrient removal from municipal waste streams while generating an economically viable biomass source for the production of plastics, supplementary dietary proteins, and biofuel feedstock.
A high density bioreactor (HDBR) was operated with varying NH_4^+ and NO_3^- loading rates in order to examine the nitrogen removal performance of a photosynthetic microbial community. While total N and NH_4^+ removal occurred over all reactor influent conditions, NO_3^- was found to generally accumulate in the reactor. NO_3^- removal only occurred at the highest NO_3^-:NH_4^+ loading ratios. Accumulation/production of NO_3^- within the reactor suggests the presence and activity of ammonia- and nitrite-oxidizing bacteria (AOB and NOB respectively). To investigate the metabolic composition and community structure and the effects of nitrogen species loading thereon, metagenomic analysis has been carried out on samples collected from two reciprocal loading rates during the operation of this reactor (30:10 and 10:30 mg –N L^{-1} NO_3^-: NH_4^+).

Submitted talks (please note that presenting authors are underlined)

Bold Talks

SYSTEMATICS, PHYLOGENY AND EVOLUTION OF THE FILAMENTOUS RED ALGAE: GENUS *POLYSPHONIA SENSU LATO*

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The cosmopolitan genus *Polysiphonia sensu lato* has been composed of heterogeneous genera. Our morphological and molecular analyses of *Polysiphonia sensu lato* collected from worldwide have supported the description of 16 new species (eight already published), 15 new combinations, and the segregation of four genera. Especially, *Neosiphonia* species have been segregated based on the three-celled carpogonial branches. Of them, *N. harveyi* complex is composed of six species. We sequenced genes from plastid (*rbc*L) and mitochondrial (*cox1*) genomes to examine the phylogeny, species status, phylogeography, and evolution of specimens belonging to this complex collected worldwide. Our data strongly support two species within this complex: *N. harveyi* and "*P. strictissima*." *Neosiphonia harveyi* is composed of seven genetic taxa described here as subspecies on the basis of DNA-based delimitation models. We also estimated the divergence time of these species using substitution rates of combined *rbc*L and *cox1* data sets. We confirm that the center of diversity and origin is the East Asia (Korea and Japan) and that the evolution of these species may have been due to transoceanic dispersal and subsequent allopatric isolation.

COMPARATIVE PLASTID GENOME ANALYSIS FROM THREE NEMALIOPHYCIDAE RED ALGAE

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Red algae are primarily marine with only 5% being freshwater. One of the florideophyte subclasses, Nemaliophycidae, contains three exclusively freshwater orders, six marine, and one with both freshwater and marine. It is likely that all marine and freshwater species were derived from a common ancestor followed by adaptation in these two environments. Since there are few data from freshwater species, a study of these taxa was initiated to provide insights into potential genomic differences. We sequenced plastid genomes from two freshwater species, *Kumanoa americana* (Batrachospermales) and *Thorea hispida* (Thoreales), and one marine *Palmaria palmata* (Palmariales). From comparative genome analysis of these three taxa, we determined that several plastid genes (pbsA, grx, ycf35, ycf46, ycf34, ycf37) were unique to the marine species. With all available red algal plastid genome data, we found some of the genes (pbsA, ycf35, ycf46, ycf34, ycf37) are in all marine species investigated to date. In this symposium, we will suggest a possible evolutionary scenario for the Nemaliophycidae that adapted in different habitats.

ON THE RED ALGAL GENUS GRATELOUPIA IN THE GULF OF MEXICO, FEATURING THE ORGANELLAR GENOMES OF *GRATELOUPIA TAIWANENSIS* (RHODOPHYTA).

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Red algae (Rhodophyta) are economically useful for their gelling compounds, ecologically critical to marine benthic systems, and evolutionarily poised at the intersection of primary and secondary endosymbiotic lineages. Molecular sequencing has transformed our understanding of red algae, revealing genetic and genomic characteristics that had once been completely unknown.

In *Grateloupia*, a red algal genus that is morphologically simple and notoriously difficult-to-identify, sequencing has greatly assisted in identification of species and phylogenetic placement of troublesome taxonomic groups. However, analysis of DNA has also proven useful for genomic comparisons on a larger scale, in order to resolve deep evolutionary questions in terms of overall genome architecture and gene content. In this study, sequencing-based analyses were applied at both levels, examining species of *Grateloupia* both within the genus and from a greater phylogenetic perspective. Phylogenetic analysis of the *rbc*L marker revealed the previously unknown species *Grateloupia taiwanensis*, first reporting this non-native alga from the Gulf of Mexico, and it showed that the species previously known as *Grateloupia filicina* in the Gulf of Mexico actually includes several species. The organellar genomes of *Grateloupia taiwanensis* were also sequenced and annotated; both the plastid and mitochondrial genome are typical of florideophyte red algae in size, gene content, and structure. Mauve genome alignments demonstrated a pattern of genomic rearrangements expected given the overall phylogeny of

STRIKING A BALANCE BETWEEN PHOTOTROPHY AND HETEROTROPHY IN THE MIXOTROPHIC CHRYSOPHYTE *DINOBRYON* SP.

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Many phytoplankton are known to supplement photosynthetic nutrition with uptake of particulate organic substrates in a nutritional mode known as mixotrophy. *Dinobryon* sp. is an obligate phototroph that has been shown to exhibit substantial rates of bacterivory both in laboratory and field experiments. In this study, we examined the roles of light intensity and temperature on mixotrophic activity in a clone of *Dinobryon*. Replicate cultures were acclimated and incubated at four temperatures and two light intensities with concurrent measurements of bacterial ingestion (tracer particles) and primary production (14C incorporation). To evaluate the relative contributions of bacterivory and photosynthesis to the carbon budget of *Dinobryon* sp., carbon incorporation was calculated for both processes. Our results indicate that under both light regimes, ingestion and primary production rates increased with increasing temperature to a maximum at sixteen degrees, after which rates of both processes declined. *Dinobryon* sp. acquired 60-99% of its carbon from photosynthesis. Although higher proportions of carbon were supplied by photosynthesis at every temperature tested, relatively more of the carbon budget was supplied from bacterivory at the lowest temperature.

PHYLOGENY AND FUNCTION: THE ROLE OF THE EUKARYOTIC INITIATION FACTOR 4E IN CONTROL OF GENE EXPRESSION IN DINOFLAGELLATES

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Dinoflagellates have extremely large genomes, genes held in tandem arrays, and a marked lack of identifiable transcription factors. Multiple studies have shown that these organisms have little control over gene expression at the transcriptional level, but do display changes in their proteome in response to environmental stimuli. Our study focuses on a family of dinoflagellate eIF4E

mRNA cap binding proteins, with the hypothesis that some of these family members may support and some may repress translation of specific mRNA or classes of mRNA. *Amphidinium carterae* possesses eight eIF4E family members that phylogenetically group into three clades. We used mRNA cap column chromatography, yeast knockout complementation, and surface plasmon resonance to characterize their function as either a prototypical cap binding protein or as a regulatory protein involved in gene expression modulation. We found that eIF4E-1 family members may serve as cap-binding translation factors, while the eIF4E-2 family member may serve a non cap-binding regulatory role. However, eIF4E-3a does not appear to be expressed at the protein level, despite high transcript abundance. These data reflect functional predications made based on phylogenetic analysis.

EXAMINING THE MOLECULAR PHYLOGENY AND TAXONOMY OF THE RED ALGAL ORDER HALYMENIALES (FLORIDEOPHYCEAE) IN AUSTRALIA TO BETTER CONCEIVE ITS BIODIVERSITY

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Data presented here represent the culmination of four years of work on members of the red algal order Halymeniales from Australia. Taxonomic perspectives regarding the Australian benthic marine red algal flora suffer from a residual bias towards European species, as European references were used to identify most of the flora in the early days of Australian marine Botany. Using the DNA barcode, molecular phylogenetics and traditional alpha taxonomy, the species diversity of this order was investigated. Cluster analysis of barcode data indicated that our collections expanded the order past the known species diversity as represented in the literature. Molecular and morphological data show that both novel and overlooked species are contributing to this spike in observed biodiversity. Novel diversity has been found within every genus within the Halymeniales represented in Australia that was studied here, with the molecular record uncovering diversity in excess of currently described genera. Among our findings, this study: confirms that Australian species assigned to the genera *Cryptonemia*, *Grateloupia* and *Halymenia* do not themselves form monophyletic lineages, the various lines not remotely associated with generitypes reflecting the need for revision on a global scale; clarifies the currently incorrect assignments of Australian representatives of the genus *Aeodes*; resolves Australian species assigned to the genera *Pachymenia* and *Grateloupia* in a new genus *Macromenia*; and establishes that species diversity within the rare genus *Tsengia* is much richer than previously thought.

EVOLUTION OF RED ALGAL PLASTID GENOMES WITH A WIDE RANGE GENOMIC COMPREHENSION

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Red algae played an important role in the evolutionary history of algae because it occupied as one of primary endosymbiosis groups. The red algae also were the plastid donor in a secondary endosymbiotic event that gave rise to the chlorophyll c containing algae (heterokonts, cryptophytes, haptophytes and alveolates). Despite the significance of those roles, only several plastid genomes have been reported from the more than 6000 red algal species. To our understanding of plastid genome evolution, we characterized complete plastid genomes from twenty red algal species with a broad taxon sampling (Bangiophyceae, Compsopogonophyceae, Florideophyceae, Rhodellophyceae and Stylonematophyceae). The plastid genome sizes are 171,384 ~ 209,669 bp with around two hundreds of coding genes. We discovered several horizontal gene transfer events. We will also discuss evolutionary trends of plastid genomes and their structural evolution patterns. The evidences provided high-resolution of plastid genome evolution in red algae.

MORPHOLOGY AND MOLECULAR STUDIES ON LARGE *NEIDIUM* SPECIES OF NORTH AMERICA, INCLUDING AN EXAMINATION OF EHRENBERG'S TYPES

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The diatom genus *Neidium* contains over 300 species of pennate diatoms found in brackish, freshwater environments with many of the larger taxa first described in the 1800s. There continues to be taxonomic confusion over several of the widely found species including *N. dilatatum* and *N. amphigomphus*. In this study large *Neidium* taxa (>50 µm) from North America were examined using both morphology and single cell based molecular data. Specimens from the original field collection housed in the Museum für Naturkunde were examined under LM and SEM. Single cells were isolated from samples collected in New York USA and Ontario CA and sequenced for rbcL and 18S. Maximum Likelihood and Bayesian phylogenetic analyses were completed and compared against current taxa descriptions. Our results confirmed several of the previously named *Neidium* taxa including: *N. tumescens, N. hitchcockii*, and *N. amphigomphus*. A new species was based from *N. dilatatum*; *N. fossum* sp. nov. is distinguished by its size, longitudinal canal structure, central area and proximal raphe ends. Combining morphological and molecular methods will allow for further delineation of diatom taxa.

DIATOM FRUSTULES AS A MECHANICAL DEFENSE AGAINST PREDATION BY HETEROTROPHIC DINOFLAGELLATES

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Much of the success of diatoms is attributed to their silica frustule, presumed to protect them from predation. The purpose of this study is to determine whether diatom frustules defend against predation by heterotrophic dinoflagellates, including *Gyrodinium spirale* and *Noctiluca scintillans*. Two species of diatoms, *Thalassiosira rotula* and *Coscinodiscus radiatus*, were grown in semi-continuous culture with low (20µM) or high (80µM) silicic acid in order to produce cells with thin versus thick frustules. Differences in frustule thickness were shown for both species, with a significant increase in biogenic silica per cell for cultures grown in high silicic acid. Rates of predation by *G. spirale* were the same on *T. rotula* cells with thick versus thin frustules. However, there was a significant difference in growth rate of *G. spirale* feeding on thin frustuled *T. rotula* compared to thick. Similarly, rates of predation by *N. scintillans* were the same on *C. radiatus* cells with thick versus thin frustules. Results from further studies measuring digestion rate of *N. scintillans* on *C. radiatus* will help further elucidate the defensive capabilities of diatom frustules.

ILLUMINATING CRITICAL FACTORS WHEN CONSIDERING WASTEWATER FOR ULTRA-PRODUCTIVE MICROALGAL CULTURE

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Maximum photosynthetic output of high-density microalgal cultures grown on wastewater media is subject to a host of physical, chemical, and biological considerations, the most noteworthy being the turbidity of the given wastewater and the nutrient content available for algal growth. To study the impact of turbidity and nutrient availability, *Scenedesmus acutus*, a common green microalgae found in wastewater, was mass cultured in flat panel photobioreactors with varying thickness (path length) to access the importance of light penetration into wastewater media on algal growth performance. Serial dilutions of dairy wastewater were used to establish baseline growth data for the organism for comparison with growth on standard artificial culture medium (BG-11 Medium). The wastewater dilution rate was optimized for a given bioreactor path length. Nutrient depletion rates were established for the algae strain growing on different dilutions of the wastewaters with differing bioreactor path lengths. Measurements of total photosynthetically active radiation (PAR) and photochemical efficiency (fv/fm) were obtained to demonstrate the importance of light in algal cultivation in wastewater. Culture conditions, including optimal cell density and nutrient level for a given bioreactor path length, were determined to maximize photosynthetic efficiency of the algal strain on dairy wastewater.

Applied Phycology

DIATOM COMMUNITY STRUCTURE ON IN-SERVICE SHIP HULLS

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Diatoms are an important component of marine biofilms found on ship hulls. However, there are few published studies that describe the presence and abundance of diatoms on ships. This study investigated the diatom community structure on six in-service cruise ships, several with the newer fouling release ship hull coatings. Biofilm samples were collected from representative areas of the ship to provide information on the hull zonation, intact and damaged coating, and the niche areas. Diatom communities were dependent on the cruise cycle, ship zonation, and coating type. Samples collected from damaged areas of the hull coating had a similar community composition to undamaged areas, but with higher diatom abundance. Diatom fouling on the niche areas differed from that of the surrounding ship hull. Additionally, several genera were found that are new to the biofouling literature. The fouling release coatings have a greater diatom richness compared to more traditional copper-based coatings, with new diatom genera that have

the ability to stick to ship hulls and withstand hydrodynamic forces, thus creating the potential for new problematic species in the biofilm.

A FUNGAL ORIGIN FOR THE GROWTH PROMOTING EFFECTS OF EXTRACTS OF *ASCOPHYLLUM NODOSUM*?

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Hundreds of publications in the primary literature have demonstrated the effectiveness of extracts of *Ascophyllum nodosum* in promoting plant growth and development and disease resistance. None of these studies, however, has used appropriate controls that recognize the fact that, in nature, *A. nodosum* is a composite organism with a systemic fungal symbiont of *Mycophycias ascophylli*. Here we used commercially prepared extracts from *Fucus vesiculosus* and *A. nodosum* in a series of bioassays with *Lemna minor* and *Vertebrata lanosa*. We evaluated different aspects of growth and photosynthetic processes following exposure to the two extracts and in non-extract controls. The *Fucus* extract typically gave results similar to non-extract controls, whereas the *A. nodosum* extract resulted in a higher growth rate and larger plants in *L. minor*. Similarly, the extract of *A. nodosum* induced higher quantum yields of Photosystem II and greater electron transport rates (rETR) in *V. lanosa*. These results suggest that the active components in the extracts of *A. nodosum* may be derived from the fungal component of the symbiosis rather than the brown algal component.

FUNCTIONAL EXPRESSION OF FETUIN/ASIALOFETUIN SPECIFIC ALGAL LECTIN DOMAINS IN *ESCHERICHIA COLI*

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Plant lectins have attracted much attention for biomedical applications including targeted drug delivery system and therapy against tumors and microbial infections. The main problem of using lectins as a biomedical tool is a batch-to-batch variation in isoforms content. The production of lectins using recombination tools has the advantage of obtaining high amounts of proteins with more precise properties, but there are only a handful of functional recombinant lectins presently available. A fetuin/asialo-fetuin specific lectin, Rhodobindin, has unique tandem repeats structure which makes it useful in exploiting for recombinant lectin. We developed three functional recombinant lectins using *E. coli* expression system: one from full cDNA sequence and two from fragmentary sequences of Rhodobindin. Hemagglutinating activity and solubility of the recombinant lectins were highest at OD 0.7 cell concentration at 20 °C. The optimized process developed in this study was suitable for the quality-controlled production of high amounts of soluble recombinant lectins.

EFFECTS OF DIFFERENT AMMONIUM SALTS ON MEDIUM PH CHANGE, GROWTH AND LIPID ACCUMULATION OF *ACUTODESMUS BERNARDII* UNDER BATCH AND FE-BATCH CUTURES

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Ammonium is the most common nitrogen source for growth of microalgae. However, different anion of ammonium salts may have variable influences on the growth of microalgae due to the pH change of medium containing different anions following culture time. *Acutodesmus bernardii* is a new isolate of oleaginous green microalga. *A. bernardii* was cultured in BG-11 medium containing NH4HCO3, (NH4)2CO3, NH4NO3, (NH4)2SO4 or NH4Cl with the four nitrogen concentrations(1.0mM, 3.0mM , 6.0mM , 9.0mM , 18mM). The results indicated that NH4HCO3, (NH4)2CO3 and NH4NO3 were suitable nitrogen sources for the growth of *A. bernardii*, but *A. bernardii* could not survive in the rest two ammonium salts due to the high acidity of the medium. The initial pH of media with these five ammonium salts ranged from 7.0 to 9.0, and the ultimate pH of media with NH4HCO3, (NH4)2CO3 and NH4NO3 were about 6.0 while those of media with (NH4)2SO4 and NH4Cl fell between 4.0 and 3.0. The optimum initial nitrogen concentration of NH4HCO3, (NH4)2CO3 and NH4NO3 under batch culturing mode were 9.0 mM, 9.0 mM, 6.0 mM, respectively. Three patterns (day 1-3-6 (type A); day 1-3-8 (type B); day 1-3-6-8-10 (type C)) of feeding NH4HCO3, (NH4)2CO3 and NH4NO3 to medium were designed for adjusting the final nitrogen concentration as same as their original initial optimum concentration. The most applicable feeding pattern of NH4HCO3 was type A, while the two others were type C. The appropriate feeding of NH4HCO3, (NH4)2CO3, NH4NO3 could significantly increase the final biomass concentration from 9.1g L-1, 8.7g L-1, 8.5 g L-1 (batch mode) to 10.1 g L-1, 9.7 g L-1, 9.8 g L-1 (fed-batch), and the lipid productivity also raised from 276.0 mg L-1d-1, 255.0 mg L-1 d-1, 308.0 mg L-1 d-1 (batch mode) to 333.0 mg L-1 d-1, 329.0 mg L-1d-1 and 362.0 mg L-1d-1 (fed-batch), respectively. *A. bernardii* can use suitable ammonium salts as nitrogen sources under fed-batch culture to obtain high productivity of lipids for biofuels production.

A DIATOM-BASED BIOLOGICAL CONDITION GRADIENT (BCG) APPROACH FOR ASSESSING STREAM IMPAIRMENT

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The Biological Condition Gradient (BCG) conceptual model provides a basis for scientifically defensible regulatory guidelines. The six BCG categories represent a range of ecological conditions from natural to highly disturbed. We developed a diatom BCG using diatom counts and environmental data from 95 stream sites in five ecoregions in New Jersey (NJ), USA (most sites in total P range of 15 to 200 ug/L and total N 0.5 to 4 mg/L). A human stressor gradient was defined based on a Principal Components Analysis of disturbance-related chemistry and habitat characteristics; diatom taxa were assigned to one of six BCG attributes. A panel of diatom experts assigned 57 sites to BCG categories based on assemblage composition. Rules were developed to assign new diatom samples to BCG categories (e.g., if % sensitive diatoms is > X and % tolerant < Y...). An independent follow-up study tested these rules by applying them to diatom data collected from an additional 42 sites. Agreement between rule-based BCG scores and expert panel scores was 95% for calibration samples, and 79% for the confirmation samples.

EXAMINING BIOLOGICAL CHALLENGES IN ALGAL BIOFUELS AND BIOPRODUCT GENERATION

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It is widely accepted that microalgae have great potential for use in biofuels and bioproducts generation. Nevertheless, major biological bottlenecks exist in making large-scale algal biomass and/or bioproducts generation profitable. These bottlenecks encountered on the way to development of a sustainable microalgal industry have to be overcome. An emphasis of the presentation will be on how to achieve significant increases in biomass/biomolecule productivities. This productivity improvement challenge is independent of the production platform such as photoautotrophy, chemoheterotrophy, or photomixotrophy. Regardless of decisions for a specific cultivation strategy, in any case the question is that of which species and particular platform strains would be used. Once, the species choice is made, the next question of strain development has to be faced. The term strain development includes a host of different issues to be tackled such as the use of classical genetics and genetic engineering, for example in approaches to overcoming light limitation and photoinhibition in phototrophic cultivation modes. In brief, following identification of a platform species, the major challenge in algal biomass/metabolite production appears to be domestication of algal species.

MICROALGAE: HARNESSING DIVERSE METABOLISMS FOR ENVIRONMENTAL REMEDIATION AND WASTE STREAM TREATMENT

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Conventional wastewater treatment utilizes activated sludge processes in order to remove organic carbon, while additional denitrification and dephosphatation processes must be carried out to remove additional nutrients in order to prevent eutrophication of influent receiving waters, such as lakes, rivers, and bays. The application of algal-biotechnology may provide an alternative solution for nutrient removal from municipal waste streams while generating an economically viable biomass source for the production of plastics, supplementary dietary proteins, and biofuel feedstock.

A high density bioreactor (HDBR) was operated with varying NH_4^+ and NO_3^- loading rates in order to examine the nitrogen removal performance of a photosynthetic microbial community. While total N and NH_4^+ removal occurred over all reactor influent conditions, NO_3^- was found to generally accumulate in the reactor. NO_3^- removal only occurred at the highest NO_3^-:NH_4^+ loading ratios. Accumulation/production of NO_3^- within the reactor suggests the presence and activity of ammonia- and nitrite-oxidizing bacteria (AOB and NOB respectively). To investigate the metabolic composition and community structure and the effects of nitrogen species loading thereon, metagenomic analysis has been carried out on samples collected from two reciprocal loading rates during the operation of this reactor (30:10 and 10:30 mg –N L^{-1} NO_3^-: NH_4^+).

EARLY DETECTION OF A MAJOR ZOOPLANKTON GRAZER IN ALGAE CULTURE

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Contamination and grazing of algae by zooplankton (e.g., rotifers, ciliates, and amoebae) represents one of the most challenging issues for sustainable algal mass culture and a major roadblock for large scale cultivation of algae for production of bioenergy and bioproducts. Zooplankton grazers are responsible for frequent algae culture crashes and can reduce biomass yield from 20-80% annually. Rapid detection of grazers entering algae production systems is highly desirable for diagnosis, mitigation and/or control. A fresh water rotifer specie (*Brachionus calyciflorus*) was selected as a model organism to develop an early detection and monitoring program to sustain algae cultivation systems at our facility. A FlowCAM protocol was optimized to detect and quantify the rotifer population. The newly developed method enabled the detection of 1 rotifer in 10 ml sample of high density *Chlorella* sp. cultures. This is an increase of 200 times the detection sensitivity over traditional hematocytometer methods. Further work is underway for the detection of ciliates and other contaminants by FlowCAM.

CONTROL OF CHITIN AND LIPID PRODUCTION IN THE PHOTOSYNTHETIC DIATOM *CYCLOTELLA* SP BY CO-LIMITATION OF SILICON AND NITRATE IN BATCH AND FED-BATCH CULTIVATION

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Controlling the metabolic pathways that microalgae have in a photobioreactor system to produce high value metabolites and biofuels is achieved by specific feeding strategies. Cell biomass, lipid and chitin productivity by the marine diatom *Cyclotella* sp. was studied in a batch and fed-batch cultivation under sequential co-limitation of two macronutrients, silicon (Si) and nitrate (N) in a bubble column photobioreactor. For the cultivation in the photobioreactors, cell suspension was assayed for cell number density, dissolved silicon and nitrate concentrations in the media. In specific points, biomass samples were analyzed for lipid and chitin content. In batch cultivation, experiments were carried out by co-limitation of Si and N, with initial N concentration varying from 0.5 to 5.0 mM at a constant dissolved Si concentration of 0.8 mM. In fed-batch cultivation, experiments are carried in two stages, stage one for cell synchronization, and stage two for the controlled addition of nutrients. The initial Si to N concentration ratio (Si/N) was 0.7, ratio which is maintained along the fed-batch cultivation. In fed-batch experiments, results show that at low and high medium addition rates, the N that is incorporated into chitin can reach above 30% to 5% of the total N delivered, respectively. Low nutrient medium addition rate shuts down lipid production, and is selective for chitin production, and cell production rate is limited by the addition of Si and N. In high nutrient medium addition rate, lipid production is maintained during cell production, chitin production is maintained, but reduced, and the cell production rate is not limited by the addition of Si and N. This concludes that the rate of addition of Si and N (co-limitation) divert the production of chitin and lipids in *Cyclotella* sp., chitin production is linear during the stage two cultivation of the fed-batch experiments, and the nutrient flow rate changed the pattern of lipid and chitin product formation.

SENSATIONAL SEAWEEDS: A NON-MAJORS INTRODUCTION TO MARINE MACROALGAE

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Marine macroalgae may not be considered as charismatic as other inhabitants of the oceans yet they have been an important part of everyday life for thousands of years. A general studies course called "Sensational Seaweeds" was developed for 58 non-majors as part of a suite of electives used to fulfill a general science requirement at Stockton University. The course explored the past, present and future of the cultural, economic and ecologic roles of marine macroalgae. Students represented all 7 major disciplines offered at Stockton and the majority of students were freshmen or sophomores (85%) with limited high school science experience. Initial surveys established an overall negative or neutral opinion towards seaweed. Course activities were varied and included such activities as ecological debates, blog posts, a scavenger hunt and end of semester juried art festival and phyco-feast. At the end of the course, opinions had shifted towards neutral/positive. Many of the elements of this non-majors course can be introduced at varied levels of intensity for use with traditional marine botany courses as well as these general studies experiences.

METAGENOMIC ANALYSIS ON THE INFECTION PROCESS OF *PYROPIA* (=*PORPHYRA*) DISEASES

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Pyropia seafarms are suffering from various diseases, ranging from spectacular outbreaks in natural populations, down to chronic diseases which cause downgrade of crop quality. Recent estimation on economic loss caused by *Pyropia* diseases showed that sea farmers in Korea lose about 10-15 million dollar because of algal disease every year, mostly due to fungal disease caused by the oomycete pathogens, *Olpidiopsis pyropiae* and *Pythium porphyrae*. The recent development of intensive and dense mariculture practices have made some new diseases spread much easier than before. Transcriptomic study revealed that the causative agents of many *Pyropia* diseases are viruses which could infect broad spectrum of *Pyropia* species. Host plants intensively use RNA binding proteins for defense against viral infections in nature. We isolated 6 RNA-binding proteins which are highly upregulated during infection process. Metagenomic studies on *Pyropia* and its epiphytic bacteria showed that some epiphytic bacteria are involved in fungal infection to *Pyropia*. An elicitor released from epiphytic bacteria facilitated zoosporogenesis of *Pythium porphyrae*. The evolutionary warfare between *Pyropia* and its pathogens left many traces in the genomes of both sides. Therefore, proteomic and transcriptomic studies on *Pyropia* and its pathogens are crucial to develop a disease-resistant *Pyropia* strain.

Cell Biology/Molecular Biology

CELL BIOLOGY OF EPIDERMAL SHEDDING IN THE MARINE BROWN ALGA *ASCOPHYLLUM NODOSUM*

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Ascophyllum nodosum is a brown alga that is a dominant species on rocky shores of eastern Canada. A phenomenon associated with *Ascophyllum* is the intermittent shedding of thin sheets of epidermal material, which removes colonizing epiphytes. Based on reports in the primary literature, it was hypothesized that shedding could involve the release of small epidermal cells or alternatively, this process could be described by an abscission-like separation of only cell wall material from the apical portions of cells. Here we used histochemistry and microscopy to evaluate the two models. We found that epiphyte accumulation was accompanied by the formation of thickened, multilayered outer cell walls. Confocal imaging showed these cell walls stained with a fluorescent dye for cellulose but other evidence suggests that lipophilic and membranous material are incorporated as well. Transmission electron microscopy revealed an amorphous material between the fibrillar cell walls. The outer and anticlinal walls then detached so that the shed layer formed a connected series of cell wall caps. These results warrant further investigation into cell wall composition in addition to factors that trigger this process.

THE FLAGELLAR APPARATUS OF *CYANOPHORA*

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Glaucophytes are one of three lineages known to have primary plastids. Their plastids uniquely retain such cyanobacterial features as peptidoglycan and carboxysome-like bodies. In spite of this, glaucophytes were only recognized as a distinct lineage about twenty years ago, having been previously thought of as aberrant green algae. This has meant that most morphological studies of the group have been cursory, generally only noting deviations from a "standard" green-algal bodyplan. In particular, while microtubular roots have been identified in the flagellated genus *Cyanophora*, a full reconstruction of the flagellar apparatus has never been published. We address this deficit by investigating the ultrastructure of *C. paradoxa* through serial-section transmission electron microscopy, and present a computer-based reconstruction of its flagellar apparatus. We also investigate the slightly larger *C. biloba*. We will discuss our findings in the light of our modern understanding of *Cyanophora* as a member of a distinct lineage of algae.

MOLECULAR CHARACTERIZATION OF SOME CYANOBACTERIAL SPECIES IN A COASTAL LAGOON, SOUTH-WEST, NIGERIA

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Ecological studies of cyanobacteria using traditional method is challenging due to the magnitude of phenotypic plasticity among natural microalgal assemblages. In this study, molecular approach was utilized as a complementary tool to facilitate the identification of cyanobacteria in Lagos Lagoon, south-west, Nigeria where recurring blooms have been observed over the past decades. DNA was extracted from six isolated cyanobacterial species followed by PCR amplification of the 16s ribosomal rRNA genes (16s rRNA) using cyanobacterial specific generic primers. The obtained sequences were analyzed by similarity search (blastn) and phylogenetic analysis (16s rDNA) to differentiate species sharing significantly similar sequences. This study confirmed the presence of some cryptic and ecological important cyanobacterial species such as *Chroococcidiopsis* sp., *Leptolyngbya* sp. and *Limnothrix* sp. and *Synechococcus* sp. The identification of these species are significant finding as some of these cyanobacterial species have not been reported in coastal waters of south-west Nigeria.

PUTATIVE SNP MARKERS FROM TRANSCRIPTOMES FOR POPULATION STRUCTURE IN *PORPHYRA UMBILICALIS* (RHODOPHYTA)

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Porphyra umbilicalis is a marine red alga which is distributed along the rocky shores of the NW and NE Atlantic. The population structure of *P.umbilicalis* in the NW Atlantic is still unclear due to the conflicting results from previous surveys using AFLP and SSRs markers. With next-generation sequencing technology and bioinformatics analysis, putative single nucleotide polymorphisms (SNPs) markers of *P.umbilicalis* have been identified from five-transcriptome libraries. After stringent filtering, there are 851 putative SNPs present in all five libraries and other 6126 putative SNPs are found in at least one library. These putative SNPs are needed to be validated, after which SNPs markers will be used to examine the population structure of six populations *P.umbilicalis* in the NW Atlantic.

DARK SURVIVAL AND RECOVERY OF A FOREIGN ORGANELLE-RETAINING DINOFLAGELLATE AND ITS HAPTOPHYTE PREY AND PLASTID SOURCE FOLLOWING A SIMULATED AUSTRAL WINTER

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The Ross Sea dinoflagellate (RSD), a novel Antarctic kareniaceaen species, retains plastids from its haptophyte prey, *Phaeocystis antarctica*. Experiments with unialgal cultures of the haptophyte and mixed cultures of both species were designed to assess survival during 150 days of darkness, and recovery of abundance and photosynthetic function upon return to the light. The results in both species support overwintering persistence in the dark and a recovery of population growth potential when returned to continuous light for 30 days after 121 days of darkness. P. antarctica in co-culture with the RSD kept in darkness for an additional 34 days declined in

abundance relative to those returned to continuous light. RSD cells exposed to long-term darkness decreased in size with fewer chloroplasts per cell. In addition, the chloroplast size and the intensity of chlorophyll autofluorescence decreased in some RSD cells and the relative frequency of cells lacking fluorescent plastids increased. Unfortunately, conclusions concerning recovery of photosynthetic function for either species, or recovery of RSD abundance over the full austral winter are confounded by a failure of refrigeration equipment at day 137.

SEASONAL PATTERNS OF NITRATE UPTAKE AND EXPRESSION OF NITRATE ASSIMILATING ENZYMES IN *FUCUS VESICULOSUS*.

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The brown macroalgal *Fucus vesiculosus* L. experiences strong seasonal variations in intertidal conditions, including higher dissolved nitrate availability in winter and lower during the growing season. To investigate how these conditions affect nitrogen assimilation, seasonal nitrate uptake rates and expression of nitrogen assimilating enzymes were examined. Nitrate uptake rates varied seasonally and were higher in thalli collected from the high intertidal than the low intertidal. The nitrate reductase (NR) sequence was partially determined and other sequences derived from ESTswere used to develop gene-specific primers. Seasonal patterns in the expression of four key nitrogen assimilating enzymes were examined using nested PCR amplification in thalli collected monthly over a full seasonal cycle. NR transcripts varied seasonally with detection only in thalli collected Aug-Feb. In contrast, NADH-dependent nitrite reductase (NADH-NiR) transcripts were detected in 92% of samples across all seasons. Glutamine synthetase (GSIII) and NADH-dependent glutamate synthase (NADH-GOGAT) were also detected across all seasons, in ~75% of samples. Expression of all genes was not different for high vs low intertidal thalli. While nitrate uptake may be more strongly regulated by intertidal position, the responses of NR expression suggest that this is a key regulation step in seasonal responses in nitrogen assimilation which may be more tightly regulated seasonally than nitrate uptake.

Ecology

A METAGENOMIC ANALYSIS OF SUMMER AND WINTER PROTISTAN PLANKTON IN THE LOWER HUDSON RIVER

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Metagenomic analyses were done using DNA extracted from samples of saline surface water of the lower Hudson River on June 21, 2013 and March 22, 2014. Sample size fractions 80 – 20 um and 20 – 0.2 um, were obtained by sequential filtration of a liter of river water. DNA was extracted and amplified by Polymerase Chain Reaction (PCR) using 2 primer sets for the 18S

small subunit ribosomal gene regions, and then sequenced using the Illumina MiSeq platform. Hydrographic variables were also measured: salinity, temperature, DO, pH, NO3- N, NH3-N, Pi and Secchi depth. For comparison, plankton tows were also done using a 20 micron mesh size net and examined alive by phase microscopy. Taxa were defined based on sequence clusters matching to within 95% similarity. Taxonomic richness was greatest in Winter samples, and greater in the smaller size fraction in both samples. There was comparatively little taxonomic overlap in the two samples. Overall, 22% of clusters could not be matched at the 95% level to known taxa. The Winter sample also contained DNA from terrestrial species, reflecting runoff from rainfall and snowmelt.

STINKING UP THE BEACH: VARIABLE RATES OF DECAY AND DECOMPOSITION OF NATIVE AND INVASIVE SEAWEEDS IN BAYNES SOUND, BRITISH COLUMBIA

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Allocthonous seaweeds that wash up on sandy beaches are an important ephemeral spatial subsidy for the terrestrial invertebrates and microorganisms that inhabit these otherwise nutrient-limited coastal habitats. In turn, these terrestrial organisms play a role in recycling the nutrients trapped in the macroalgae. Invasive seaweeds growing in intertidal and subtidal ecosystems can thus affect the nutrient transport if there is a shift in species washing up during storm systems and the annual winter senescence. To determine how two invasive seaweeds growing in Baynes Sound could be affecting terrestrial organisms, we completed a three-part study to determine: the dominant wrack species, the decomposition and decay rates of those seaweeds, and which seaweed was preferred by herbivores. Overall, the invasive seaweed *Sargassum muticum* showed the highest rate of decomposition and was the preferred seaweed of the gammarid amphipod herbivores. Two native species: *Fucus* sp. and *Ulva* sp., followed closely. Least preferred, though constituting >89% of the wrack composition, was the invasive red seaweed *Mazzaella japonica* which was not significantly different from the native red alga *Chondracanthus* sp.

SHIP HULL TRANSPORT OF MARINE DIATOMS THROUGH FRESHWATER

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Diatoms are a dominant component of marine biofilms that form on nearly all submerged surfaces. Diatoms adhering to ship hulls may be carried thousands of miles to become invasive themselves, or to facilitate invasions of larger macrofouling species by encouraging larval settlement. Freshwater shipping routes are less effective than previously thought at killing macrofoulers traveling between oceans. However, no studies to date have examined how freshwater transport affects the mortality of biofilm organisms such as diatoms. Survivorship and transport of marine diatoms were investigated as biofilms traveled through Florida's Okeechobee Waterway on three modern ship hull coatings: a copper antifouling paint, a silicone fouling-release coating, and an inert epoxy basecoat. Marine biofilms cultivated on both the Gulf of Mexico and Atlantic coasts of Florida were relocated through 244 km of freshwater to the opposite coast on the hull of a specially designed test vessel. Total diatom density was greater on epoxy than the other two coatings. However, all coating types contained diatoms that survived the journey. These results provide further evidence for global biofilm transport and marine bioinvasions through shipping.

A METHODOLOGICAL ASSESSMENT OF EPIPHYTE REMOVAL FROM MARINE SEAGRASSES

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Submersed plants are integral constituents of productive estuaries as the 3-d structural complexity provides colonization area, refugia for sessile and motile organisms, and has primary and secondary productivity orders of magnitude higher than one-dimensional sand/mudlfats. Accurate assessment of seagrass epiphyte biomass is critical to assess anthropogenic stressors and health of this living substrate. Seagrasses tested included *Halodule*, *Thalassia*, and *Syringonium*. An alternative method, using chemical/physical methodology, was compared to the singular published method for removing epiphytes (scraping leaves with a dulled knifeblade or glass slide). MES buffer (0.1M, pH 6.0) was used to dissolve carbonates prior to mechanical agitation for 60 seconds-this treatment did not affect seagrass cell integrity. MES buffer consistently removed more epiphyte pigment (biomass) than scraping (>10%). Epidermal leaf tissue was damaged by scraping procedures; removed seagrass pigment accounted for 30% of epiphyte biomass (using chl b:a ratios), whereas MES extraction had <10% seagrass damage. Processing time with MES buffer was equivalent to the scraping method.

WHAT KILLED DRIFT MACROALGAE PRIOR TO THE SEAGRASS DIE-OFF CAUSED BY THE 2011 SUPERBLOOM IN THE INDIAN RIVER LAGOON, FLORIDA?

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Unprecedented phytoplankton “super blooms” caused catastrophic loss of seagrass in the Indian River Lagoon, Florida, in 2011-2012. Curiously, the drift macroalgae (DMA) community declined precipitously in summer-fall 2010, prior to the seagrass decline. We have begun experiments to determine if one or more environmental extreme in 2010-2011 could have been responsible for the collapse or lack of seasonal resurgence of DMA. Single factor experiments under controlled light, temperature, and salinity conditions in 8-week experiments (1 week of acclimation, 4 weeks of exposure to treatments, 1 week of acclimation back to control levels, 2 weeks of recovery) have determined that: salinity extremes (as low as 12 and as high as 50) were unlikely, at least singly, to have caused the observed DMA decline; that significant DMA losses occurred at temperatures <10 °C, consistent with record-breaking low temperatures in winter 2010; and that low-light levels consistent with sustained low-light stresses present during the superbloom could also have caused significant losses of DMA. We will next examine multi-factor interactions of these stressors and provide estimates of nitrogen and phosphorus release/uptake rates by DMA. This project will contribute to understanding the dynamics and interactions between DMA, phytoplankton, and seagrasses in the IRL.

Evolution

BARCODE GENE EVOLUTION IS OUTPACED BY MORPHOLOGICAL EVOLUTION IN THE FRESHWATER THALASSIOSIRALES: EVIDENCE FOR RECENT, RAPID RADIATIONS

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The prevailing paradigm in protistan systematics and ecology is that many protist species are cryptic, distinguishable by genetic sequences but indistinguishable morphologically. Partly as a consequence of this, there has been increasing interest in developing genetic systems for identification of protists, including diatoms. However, some species, presumably closely related, cannot be resolved by some barcode gene candidates. There has been little formal analysis of the degree of phylogenetic relatedness of diversification versus the success or failure of barcode approaches. We examine 5 proposed barcode regions in freshwater Thalassiosiraceae with a highly resolved fossil record, a highly resolved molecular phylogeny and fine-grained morphometric analyses. The first major finding was that barcode genes consistently underestimate diversity, sometimes by an order of magnitude, even failing to distinguish between established genera. The second major finding was the low resolution is likely due to numerous rapid radiations of freshwater Thalassiosiraceae in the late Pleistocene and early Holocene. Clades which generally inhabit geologically ephemeral habitats (e.g., north temperate lakes) may be more prone to extinction and re-radiation events than clade which inhabit more geologically permanent habitats (e.g., rivers and estuarine environments).

COMPARATIVE DNA SEQUENCE ANALYSIS OF *PYRAMIMONAS PARKEAE* CHLOROPLAST GENOMES

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Next generation sequencing has been widely used in genome sequencing. Due to the higher copy numbers of chloroplast genomes, we normally obtain a tremendous amount of chloroplast data along with the nuclear data from the sequencing step. In this study, we used chloroplast data obtained from Illumina Mi-Seq sequencing and de novo assembly approach to assemble the chloroplast genome of *Pyramimonas parkeae* strain NIES254. We obtained the draft chloroplast genome structurally similar to the published genome of *P. parkeae* CCMP726. The draft genome is quadripartite where the large single copy and the small single copy are partitioned by two copies of inverted repeats. The results of Single Nucleotide Polymorphism (SNPs) analysis of coding sequences of the 3 chloroplastic regions: 1) large single copy region 2) small single copy region and 3) inverted repeat region showed that the coding sequences in the inverted repeat regions contain fewer SNPs than that of the single copy regions. Also, the presence of high number of SNPs between the two algal stains also indicates the ancient divergence of *P. parkeae*

strain NIES254 and CCMP726.

A POLYPHYLETIC ARCHAEPLASTIDA (PLANTAE) BASED ON ANALYSES OF CORE TRANSCRIPTIONAL MACHINERY

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Whether the Viridiplantae, Rhodophyta and Glaucophyta comprise a natural group has been debated for decades. Phylogenomic analyses of large, multi-gene data sets have tended to recover a monophyletic Archaeplastida with strong to moderate support, whereas various studies using individual and/or more slowly evolving genes have found strong support for poly- or paraphyly. Broad scale eukaryotic phylogenetic analyses are known to be complicated by various factors, including lineage sorting of paralogous gene families and sequence biases that cause phylogenetic artifacts. More recently, it has become clear that impacts from non-tree-like inheritance, that is, from endosymbiotic and horizontal gene transfer (EGT and HGT respectively), could have strongly impacted phylogenomics studies that led to widespread acceptance of the Archaeplastida. Attempting to overcome these complications, we have analyzed core functional domains of eukaryotic transcriptional machinery. Based on both theoretical grounds and empirical evidence, these sequences should be among the most immune to factors like EGT and covarions, both of which can be nearly impossible to interpret rigorously without prior knowledge of organismal relationships. Our results provide strong support for a polyphyletic Archaeplastida.

FEATURES OF DINOFLAGELLATE MOLECULAR EVOLUTION

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Dinoflagellates have massive genomes, with high levels of gene duplication. Dinoflagellate molecular phylogeny is poorly resolved, particularly amongst the core dinoflagellates. The distance between a species pair varies dramatically from gene to gene, and between different gene copies. Duplication also makes orthology assessment difficult. Rough clustering of transcriptome data within an individual dinoflagellate can be used to demonstrate the extent of duplication. The degree of conservation was approximately quantified for genes with at different levels of duplication. Characteristics of highly conserved genes include high transcript abundance, massive duplication, and many synonymous nucleotide substitutions between gene copies, which are likely encoded in duplicated tandem arrays. A second category includes genes with lower levels of duplication and more amino acid substitutions between gene copies. However, the amino acid substitutions between gene copies are often of functionally equivalent or similar amino acids. The best example of this second category is the eukaryotic initiation factor 4E gene family. The patterns of dinoflagellate molecular evolution are presently more useful for describing the mode and tempo of gene duplication, than for resolving dinoflagellate phylogeny.

RECENT MOBILITY OF PLASTID ENCODED GROUP II INTRONS AND TWINTRONS IN FIVE STRAINS OF THE UNICELLULAR RED ALGA *PORPHYRIDIUM*

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Group II introns are closely linked to eukaryote evolution as nuclear spliceosomal introns and the small RNAs associated with the spliceosome are thought to trace their ancient origins to these mobile elements. Therefore, elucidating how group II introns move, and how they lose mobility can potentially shed light on fundamental aspects of eukaryote biology. To this end, we studied five strains of the unicellular red alga *Porphyridium purpureum* that surprisingly contain 42 group II introns in their plastid genomes. We focused on a subset of these introns that encode mobility-conferring intron-encoded proteins (IEPs) and found them to be distributed among the strains in a lineage-specific manner. The reverse transcriptase and maturase domains were present in all lineages but the DNA endonuclease domain was deleted in vertically inherited introns, demonstrating a key step in the loss of mobility. *P. purpureum* plastid intron RNAs had a classic group IIB secondary structure despite variability in the DIII and DVI domains. We report for the first time the presence of twintrons (introns-within-introns, derived from the same mobile element) in Rhodophyta. The *P. purpureum* IEPs and their mobile introns provide a valuable model for the study of mobile retroelements in eukaryotes and offer promise for biotechnological applications.

METABOLIC CONNECTIVITY AS A DRIVER OF HOST AND PLASTID ENDOSYMBIONT INTEGRATION

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The origin of oxygenic photosynthesis in the Archaeplastida ancestor laid the foundation for the evolution of multicellular life. We hypothesize that primary plastid endosymbiosis relied critically on the establishment of a metabolic connection between the host cell and captured cyanobacterium. We also posit these connections were dominated by existing host-derived components. To test this latter idea, we used phylogenomic and network analysis to infer the phylogenetic origin and evolutionary history of 37 validated plastid membrane (permeome) transporters from Arabidopsis thaliana. Consistent with our hypothesis, we find that 57% of these genes are of eukaryotic origin and that the captured cyanobacterium made a relatively minor (albeit important) contribution to the process. We also tested the hypothesis that the bacterium-derived hexose-phosphate transporter UhpC might have been the primordial sugar transporter in the Archaeplastida ancestor. The results I will discuss advance understanding of plastid integration and favor a host-centric view of endosymbiosis. Under this view, nuclear

genes of either eukaryotic or bacterial (non-cyanobacterial) origin provided key elements of the toolkit needed for establishing metabolic connections in the primordial Archaeplastida lineage.

EVIDENCE FOR RECENT AND RAPID RADIATION OF THE MODERN FRESHWATER THALASSASIORALES FLORA

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The prevailing paradigm in protistan ecology and evolution is that dispersal, and molecular evolution outpace morphological evolution, contributing to the impression that “everything is everywhere” and that crypticism abounds. Genetic evidence for this comes primarily from analysis of genes that often used as species “barcodes”. However, there has been little formal analysis of the degree of phylogenetic relatedness of diversification versus the success or failure of barcode approaches. We examine 5 proposed barcode regions in freshwater Thalassiosiraceae with a highly resolved fossil record, a highly resolved molecular phylogeny and fine-grained morphometric analyses. The first major finding was that barcode genes consistently underestimate diversity in *Stephanodiscus* Ehrenb., sometimes by an order of magnitude. The second major finding was the low resolution is likely due to numerous rapid radiations of freshwater Thalassiosiraceae in the late Pleistocene and early Holocene. We suggest that clades which generally inhabit geologically ephemeral habitats (e.g., north temperate lakes) may be more prone to extinction and re-radiation events than clade which inhabit more geologically permanent habitats (e.g., rivers and estuarine environments).

ASSESSING THE EVOLUTIONARY HISTORY OF THE CLASS SYNUROPHYCEAE USING FOSSIL REMAINS, MOLECULAR APPROACHES AND MORPHOMETRIC ANALYSES

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An extensive array of fossil specimens from a middle Eocene locality, coupled with a molecular phylogenetic analysis containing over 60 species, and a morphometric examination including 125 taxa, are used to explore the evolutionary history of the heterokont algal group, the Synurophyceae. The group originated in the upper Jurassic, with the two keystone genera, *Mallomonas* and *Synura*, diverging in the Early Cretaceous. *Mallomonas* further splits into two major subclades, signaling the evolution of the V-rib structure believed to aid in the spacing and organization of scales on the cell covering. The genus *Synura* is also comprised of two primary subclades, largely corresponding to species with a forward projecting spine on the scale versus a keel positioned on the scale proper. Our analysis further suggests that the bristle, characteristic of the genus *Mallomonas*, evolved multiple times giving rise to the two common types of

structures present today. A third of the fossil species represent extinct lineages, all of which had gigantic scales coupled with large cells that did not survive the ancient greenhouse climate characteristic of the Eocene.

THE TETRAPYRROLE SYNTHESIS PATHWAY AS A MODEL OF HORIZONTAL GENE TRANSFER IN EUGLENOIDS

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The history of euglenoids may have begun as early as ~2 bya. These early phagotrophs ate cyanobacteria, archaea, and eubacteria. The subsequent appearance of red algae and chromophytes, provided euglenoids with additional food sources. Following the appearance of green algae, euglenoids acquired a chloroplast via a secondary endosymbiotic event with a green algal ancestor. This endosymbiosis also involved a massive transfer of nuclear-encoded genes from the symbiont nucleus to the host. Expecting these genes to have a green algal origin, this research has shown, through the use of DNA-sequences and the analysis of phylogenetic relationships, that many housekeeping genes have a red algal/chromophyte ancestry. This suggests, that many other endosymbiotic/horizontal gene transfers, which brought genes from chromophytes to euglenoids, may have been taking place, long before the acquisition of the chloroplast. The investigation of the origin of the enzymes involved in the tetrapyrrole synthesis pathway provides insights into horizontal gene transfer in euglenoids and demonstrates that the euglenoid nuclear genome is a mosaic comprised of genes from the ancestral lineage plus genes transferred endosymbiotically/horizontally from green, red, and chromophytes lineages.

Genomics

COMPARATIVE GENOMICS OF A BACTERIVOROUS GREEN ALGA REVEALS EVOLUTIONARY CAUSALITIES AND CONSEQUENCES OF PHAGO-MIXOTROPHIC MODES OF NUTRITION

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Cymbomonas tetramitiformis—a marine prasinophyte—is one of only a few green algae that still retain an ancestral particulate-feeding mechanism whilst harvesting energy through photosynthesis. The genome of the alga is estimated to be 850Mbp–1.2Gbp in size—the bulk of which is filled with repetitive sequences—and is annotated with 37,366 protein coding gene models. A number of unusual metabolic pathways (for the Chloroplastida) are predicted for *Cym. tetramitiformis*, including pathways for Lipid-A and peptidoglycan metabolism. Comparative analyses of the predicted peptides of *Cym. tetramitiformis* to sets of other eukaryotes revealed that non-phagocytes are depleted in a number of genes, a proportion of which have known function in feeding. In addition, our analysis suggests that obligatory phagotrophy is associated with the loss of genes that function in biosynthesis of small molecules (e.g. amino acids). Further, *Cym. tetramitiformis* and at least one other phago-mixotrophic alga are thus unique, compared to obligatory heterotrophs and non-phagocytes, in that both feeding and small molecule synthesis related genes are retained in their genomes. These results suggest that early, ancestral host eukaryotes that gave rise to phototrophs had the capacity to assimilate building block molecules from inorganic substances (i.e. prototrophy). The loss of biosynthesis genes, thus, may at least partially explain the apparent lack of instances of permanent incorporation of photosynthetic endosymbionts in later-divergent, auxotrophic eukaryotic lineages, such as metazoans and ciliates.

GENOME REDUCTION DRIVES ALGAL EVOLUTION AND BIODIVERSITY

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Genome reduction is usually associated with loss of functions and the narrowing of prospective habitats. This is exemplified by intracellular symbionts and parasites that often rely on host derived metabolites for survival. The role of genome reduction in potentially promoting the evolution of novel traits and thereby expanding biodiversity of free-living eukaryotes is unexpected. Red algae (Rhodophyta), the sister lineage to green algae and land plants (Viridiplantae) are a monophyletic lineage of widely distributed and highly successful photosynthetic eukaryotes that live both in “normal” environments such as the intertidal zone and deep waters as well as in extreme environments associated with volcanic hot springs. Strikingly, recent studies of genome data suggest that red algae have limited gene inventories when compared to Viridiplantae. This is primarily explained by a phases of massive genome reduction that occurred in the common ancestor of all red algae leading to the loss of one quarter of its conserved core genes. Here, we analyze the recent red algal phylogenomic data that provide further support for the ancient red algal genome reduction. We demonstrate ancient horizontal gene transfers that impacted pathways of stress tolerance, suggesting an extremophilic lifestyle. These results are consistent with the ‘hot start’ hypothesis for red algal evolution and highlight the role of genome reduction in precipitating divergent pathways of evolution between red algae and Viridiplantae. The surprising trajectory of genome diminution followed by recovery in red algae may provide a unique model for understanding taxonomic and morphological diversification under the yoke of a minimal genome.

THE CHLOROPLAST AND MITOCHONDRIAL GENOMES OF THE TUBULAR GREEN MACROALGA *ULVA* SP. (ULVOPHYCEAE, CHLOROPHYTA)

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Sequencing chloroplast and mitochondrial genomes has allowed for a better understanding of the evolution of these organelles as well as green algal phylogenetic histories. Since only limited genomic data was previously available from the Ulvophyceae, we sequenced and annotated the

first organellar genomes of the ecologically and economically important green algal genus *Ulva*. The 99,983 bp chloroplast genome of *Ulva* sp. was highly gene compact and AT-rich. A total of 102 genes (71 protein-coding genes, 28 tRNAs, and three rRNAs) were identified, and five introns were present in four genes: atpA (1), petB (1), psbB (2), and rrl (1). The mitochondrial genome was 73,493 bp, which followed the "expanded" pattern also seen in other ulvophyceans and trebouxiophyceans. Fifty-six genes were annotated (29 protein-coding genes, 25 tRNAs, and two rRNAs), and ten introns were identified in five genes: cox1 (4), atp1 (1), nad3 (1), nad5 (1), and rrs (3). Both genomes continued to reveal the highly rearranged nature of the chlorophytan organellar genomes. Additionally, a phylogenomic analysis of 51 plastid protein-coding genes showed no support for a monophyletic Ulvophyceae *sensu lato*.

ANALYSIS OF *SYMBIODINIUM* GENOMES REVEALS REMARKABLE DIVERGENCE

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Symbiodinium are symbiotic dinoflagellates that commonly reside in cnidarians, including reef-building corals. This symbiotic association is pivotal to reef survival. As part of the Reef Future Genomics (ReFuGe) 2020 Consortium that is established to generate reference genetic data for the Great Barrier Reef and reefs in the Red Sea, we generated draft *de novo* genome assemblies (>30-fold coverage) from two *Symbiodinium* isolates of Clades C (origin: Magnetic Island, Australia) and F (CS-156). Computational estimate of genome size is 1.5Gbp (Clade C) and 1.1Gbp (Clade F). We recovered major phylogenetic markers in the nuclear and organellar genomes, and identified putative plastidal (minicircles) and mitochondrial genomic sequences. We recovered up to 64% (for Clade C) and 58% (for Clade F) of the core conserved proteins across key eukaryote genomes, and our comparative analysis using existing transcriptome data indicates substantial level of inter-clade divergence. Our findings lend support to the established inter-clade relationships of *Symbiodinium*, and interestingly, suggest a trend of genome reduction from the basal lineage (Clade A; size estimate 3Gbp) through to the more recently diverged lineages.

TWINTRONS OF THE EUGLENOPHYTA - A COMPREHENSIVE COMPARATIVE ANALYSIS

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Euglenoid chloroplast genomes contain a unique feature – Twintrons, or, introns within introns. These genome features are comprised of either group II or group III introns that are contained within an external group II or group III intron and are thought to act as mobile genetic elements.

Twintrons were first identified in the chloroplast genome of *Euglena gracilis*, which contains 15 twintrons in total, and a subsequent analysis of the *Monomorphina parapyrum* chloroplast genome was found to contain 6 homologous twintrons. Over the last 3+ years, many new euglenoid chloroplast genomes have been characterized – including at least one representative of each genus, and in some cases, multiple representatives within a genus. These new genomes allowed us to perform a comprehensive comparative analysis with the 15 twintrons identified in *E. gracilis* and elucidate trends throughout the Euglenophyta, including the reliability of the presence of a particular twintron within a species, a genus, or a family. In addition, we have been able to add a significant amount of evidence to previous research that identified the probable ancestral intron within the Euglenophyta.

GENOME EVOLUTION IN RED ALGAE ON THE PATH TO PARASITISM

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Genomic studies have revealed substantial genome evolution in highly derived parasites as they increasingly rely on their host for survival. However, the initial effects of an organism transitioning from a photosynthetic to a parasitic life strategy remain mostly unknown. Parasitism has independently evolved in red algae more than a hundred times, providing a framework for making direct comparisons between a parasitic and a free-living red alga that share a recent common ancestor. Recently we sequenced a highly reduced plastid from the alloparasite *Choreocolax polysiphoniae* that has lost genes involved in photosynthesis. Here we present data from genomic and transcriptomic sequencing of the *C. polysiphoniae* and its free-living host *Vertebrata lanosa*. These data show a reduction in the expression of nuclear-encoded plastid-targeted genes that encode proteins for the phycobilisome and other photosynthesis related functions. Additional comparative data from *V. lanosa* and *C. polysiphoniae* will be presented and the genomic consequences and implications for the evolution of parasitism in red algae will be discussed.

TEMPO AND MODE OF DIATOM PLASTID GENOME EVOLUTION

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Knowledge of genome architecture evolution and nucleotide substitution rates are essential for our understanding of the tempo and mode of molecular sequence evolution. So far, fifteen diatom plastid genomes have been published, and they show variable genome sizes and extensive genome rearrangement. Our recently published research added another seven diatom plastid genomes, revealing conserved gene order and expanded inverted repeats in plastid genomes of the order Thalassiosirales and documenting the first loss of photosynthetic genes in a photoautotrophic diatom (*Rhizosolenia imbricata*). Our 19 newly finished plastid genomes (*Proboscia*, *Guinardia striata*, *Actinocyclus sultilus*, *Rhizosolenia setigera*, *Eunotogramma*, *Plagiogrammopsis*, *Attheya*, *Plagiogramma*, *Pteroncola*, *Licmorphora*, *Acanthoceras*, *Psammoneis*, *Triceratium dubium*, *Discostella*, *Stephanopyxis palmeriana*, *Rhizosolenia fallax*, *Astrosyne radiata*, *Biddulphia biddulphiana*, *Biddulphia tridens*) show extensive genome rearrangements with genome size ranging from 121,011bp to 201,816bp. We will be presenting diatom phylogeny using the total 41 complete plastid genomes, and test the efficacy of genome rearrangement data in resolving phylogenetic relationships. We will also be presenting the first genome-wide evolutionary rate analysis in diatoms, and implications of rate variation for understanding diatom evolution.

CHLOROPLAST GENOMICS OF *TRACHELOMONAS ELLIPSODALIS* (EUGLENACEAE) AND *PHACUS ORBICULARIS* (PHACACEAE)

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The Euglenaceae contains eight genera with seven published chloroplast genomes representing four of those genera: three from *Euglena*, one from *Strombomonas*, one from *Colacium*, one from *Monomorphina*, and *Euglenaformis proxima*. The Phacaceae contains three genera with no published chloroplast genomes. Here, we analyze the synteny of the recently completed chloroplast genomes of *Trachelomonas ellipsoidalis* and *Phacus* orbicularis to *Strombomonas acuminata* and *Eutreptia viridis*, respectively. Our results showed the genomes of *S. acuminata* and *T. ellipsoidalis* varied in size by 42.3Kb, due to introns (147 vs. 98, respectively), and exhibited near perfect synteny for five out of seven homologous gene clusters. In contrast, the genomes of *P. orbicularis* and *Eut. viridis* varied in size by only 895 bp, but with nearly the same difference in introns (66 vs. 23, respectively), and showed extensive rearrangements, i.e. no synteny among 13 homologous gene clusters. This work, combined with previous comparisons indicates that the number of introns has greatly increased in both the Euglenaceae and Phacaceae lineages.

THE UNEXPECTED EXTREMOPHILE: TOLERANCE TO FLUCTUATING SALINITY IN THE GREEN ALGA *PICOCHLORUM*

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Picochlorum SE3, a green alga (Chlorophyta, Trebouxiophyceae), was isolated from a shallow brackish-water lagoon in San Diego County, California. Despite its apparent mesophilic environment, we postulate that environmental fluctuations can act as extreme selective pressures resulting in genomic “footprints” with similarities to the more conspicuous extremophiles. Its small reduced genome (13.5 Mbp), sequenced in our lab in 2013, encodes just 7,367 genes, but is, nonetheless, highly robust in the face of light, temperature, and salinities fluctuating between freshwater and 3x seawater. We challenged *Picochlorum* SE3 with high or low salinity shock to investigate, through transcriptome and biophysical photosynthetic analysis, the molecular mechanisms of salt tolerance. About 50% of the genome is affected by salt shock, forming mostly distinct metabolic responses between high and low salinity shock and between the two time points investigated. This indicates that a large portion of the streamlined genome of *Picochlorum* SE3 is dedicated to combating salinity stress, a major factor in its environment. Cells are less stressed by low salinity than high salinity shock, as is apparent from, the faster recovery of water oxidation cycling efficiency, growth rate, and up-regulation of translation under low salinity stress, as well as the up-regulation of photorespiration under high salinity shock. Interestingly, a significant number of coexpressed genes are colocalized in the genome, forming clusters of 2-10 genes (allowing for a maximum of 2 intervening genes) induced upon stress application, few of which appear to be metabolically related. While the salt stress response in *Picochlorum* SE3 is similar to other salt-tolerant algae, colocalization of coexpressed genes may contribute to its rapid recovery during salinity fluctuations. In this work, we present an analysis of classes of genes responsible for halotolerance with particular regard to effects on photosynthetic activity.

Harmful Algal Blooms/ Algal Bioremediation

MICROPLASTICS AND HARMFUL ALGAL BLOOMS – HOW WOULD THEY INTERACT?

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Microplastics are one of the major emerging pollutants in waters around the world. Direct negative impacts of these microplastics on zooplankton and larger invertebrates have been reported in literature through analyses of field samples and laboratory experiments, while similar data on primary producers are not yet widely available. To help fill in the knowledge gap we firstly attempted to establish an effective protocol to harvest microplastics from six widely marketed face and body wash products and characterized and quantified the harvested particles, to be followed by a series of laboratory experiments where these particles were added to common HAB-forming cyanobacteria, such as *Microcystis* and *Dolichospermum* spp. The most frequent particles sizes across products were 50 to 200 µm in equivalent spherical diameter, with typical concentrations of 1.2 to 1.7 mg microplastics per 1 g of product. Most particles detected were non-spherical with highly variable morphologies, despite being called “microbeads”. Based on these findings we hypothesize that these microplastics have a considerable influence on colony formation and maintenance in HAB-forming cyanobacteria, and this hypothesis is currently being tested.

RELATIONSHIP BETWEEN BACTERIAL COMMUNITY STRUCTURE AND BLOOM DYNAMICS OF *COCHLODINIUM POLYKRIKOIDES* IN KOREAN COASTAL WATERS

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Studies of the correlations between the toxic dinoflagellate, *Cochlodinium polykrikoides* and their associated bacterial community composition has not been explored. To understand this correlation, we investigated changes in bacterial community structure through the evolution of a *C. polykrikoides* bloom in Korean coastal waters via clone library analysis. Alpha-, Gamma-proteobacteria and Flavobacteria were found to be dominant phyletic groups during *C. polykrikoides* blooms. The proportion of Gamma-proteobacteria, which are comprised of multiple algicidal species, was lower (11.8%) during peak of the bloom period compared to the post-bloom period (26.2%). In contrast, Alpha-proteobacteria increased in dominance during blooms. Among the alpha-proteobacteria, members of Rhodobacterales abruptly increased from 38% in alpha-proteobacteria before the bloom to 74% and 56% during the early bloom and peak bloom stages, respectively. Moreover, multiple sites concurrently hosting *C. polykrikoides* blooms also contained high portions of Rhodobacterales and principal component analysis (PCA) demonstrated that Rhodobacterales had a positive, significant correlation with C. polykrikoides abundances ($p \leq 0.01$, Pearson correlation coefficients). Collectively, this study reveals the specific clades of bacteria that increase (Rhodobacterales) and decrease (Gamma-proteobacteria) in abundance with *C. polykrikoides* blooms.

IDENTIFICATION OF THE SPECIES RESPONSIBLE FOR PARALYTIC SHELLFISH POISONING IN ALASKA

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Paralytic shellfish poisoning (PSP) represents a major economic and health threat to coastal communities along the US west coast, particularly in Alaska where PSP is deemed a public health emergency that must be reported to the State's Division of Epidemiology. PSP is caused by consumption of shellfish that have accumulated potent neurotoxins (saxitoxins) produced by dinoflagellate species in the genus *Alexandrium*. Despite the persistent threat posed by PSP, little is known about which *Alexandrium* species occur in Alaska. The objective of this study was to develop species-specific PCR assays for the six *Alexandrium* species likely to occur in Alaskan

coastal waters. To establish which species were present, we used the assays to screen phytoplankton and sediment samples collected from four locations in the Gulf of Alaska ranging from Southeast Alaska to Kodiak Island (>700 km). *Alexandrium* cultures established from these locations were also screened. A molecular approach was adopted because Alexandrium species are difficult to distinguish using light microscopy. This inability to distinguish species is important from a monitoring standpoint because toxic and non-toxic species frequently co-occur, making it difficult to assess PSP risk from cell counts alone. The molecular assays revealed that both *Alexandrium fundyense* and *A. ostenfeldii* occurred over the entire study area, with *A. fundyense* being most abundant. *Alexandrium fundyense* is known to be the dominant saxitoxin producer in the Gulf of Maine and Bay of Fundy, where PSP research has been ongoing since the 1970s. The prevalence of *A. fundyense* in both regions means HAB management techniques used in the Gulf of Maine may be directly applicable to the PSP problem in Alaska. The assays developed in this study can be incorporated into monitoring systems to provide managers with early warning when the onset of toxic blooms pose a heightened risk of PSP.

COMPETITION IN MACROALGAL BLOOMS: THREE SPECIES OF BLADE-FORMING *ULVA* INHIBIT THE GROWTH OF CO-OCCURRING MACROALGAE THROUGH ALLELOPATHY

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Narragansett Bay has experienced macroalgal blooms dominated by blade-forming *Ulva* for over a decade. Evidence from other systems has suggested that *Ulva* can negatively impact other organisms through allelopathy. The objective of this study was to determine whether three species of blade-forming *Ulva* (*U. compressa*, *U. rigida*, and *U. lactuca*) inhibit the growth of co-occurring macroalgae (*Gracilaria* spp., *Cystoclonium purpureum*, *Chondrus crispus*, and *Ceramium virgatum*) through allelopathy. Macroalgae was grown in divided 1 L mesocosms with either *U. compressa*, *U. rigida*, *U. lactuca*, or alone (control) for 8 days at 22°C and 110 μmol photons/m^2/s. The fresh weight was recorded every other day to determine growth rates. All *Ulva* species significantly inhibited the growth of all four co-occurring macroalgae tested, although the effects were dependent on time. There was a striking effect of *Ulva* on the growth of *Chondrus crispus* after only 2 days of co-culture. In the other three trials, a negative effect of *Ulva* on growth was observed after 6-8 days of co-culture. Our results indicate that competition through allelopathy may be important in macroalgal blooms.

OPTIMIZING POLYCULTURE CULTIVATION AND WASTEWATER TREATMENT IN LARGE-SCALE OFFSHORE PHOTOBIOREACTORS

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Algae Systems has researched, patented, and implemented a novel approach to wastewater treatment, in which municipal wastewater is used to cultivate microalgae in modular, offshore photobioreactors (PBRs). Combining algae nutrient uptake, aeration by photosynthetically produced oxygen, and dewatering via suspended air flotation removes >83% of nitrogen, >95% of phosphorus and >93% BOD from influent wastewater. At the Algae Systems plant in Daphne AL, this process treats up to 50,000 gallons per day of incoming wastewater to discharge standards. The dewatered algae biomass is converted to biofuel via hydrothermal liquefaction. Offshore PBRs contain complex polycultures of microalgae and associated heterotrophs, with the composition of the microbial community shifting naturally based on the dynamic external and internal environment. Beginning with system commissioning in May 2014, microalgae composition has shifted from dominance of *Scenedesmus* sp. to a combination of *Chlorella* sp., *Cryptomonas* sp. and *Scenedesmus* sp. “The more, the merrier” approach to species richness has produced stable communities and very limited system crashes. Consistently efficient nutrient and CO2 uptake is achieved due to niche complementarity, with production rates that are predominantly temperature driven.

USING ALGAE TO BIOREMEDIATE DISCHARGE WATERS FROM POWER PLANTS

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Discharge water streams from different industrial processes often contain contaminant levels that may either approach or exceed current water quality standards. In Arizona, contaminant levels entering water resources are monitored and regulated by the Arizona Department of Environment Quality. Consequently, industry continuously seeks innovative or enhanced solutions for treatment of discharge waters prior to their release to the environment. This research focused on identifying, selecting and utilizing algae strains to remove certain chemical elements/contaminants from discharge waters from two power plants. Two algae strains (*Chlorella vulgaris* and *Scenedesmus* sp.) were selected and cultivated in power plant discharge waters in the laboratory. The elemental removal efficiency and the distribution of metals associated with the algae biomass (absorption and adsorption) were also determined. Approximately 40% of the boron and 70% of the hexavalent chromium, as well as high percentages of other elements (e.g., Selenium and Arsenic) were also removed from discharge waters by both algae strains during laboratory cultivation. Preliminary results suggest that the growth stage of the algae strains is an important factor in the elemental binding and removal process. Further research on the characterization of additional algae strains obtained from a discharge storage pond at one of the power plants for their elemental bioremediation potential is underway.

Phylogeny and Systematics

TAXON-SPECIFIC CHARACTER EVALUATION IN DINOPHYSALES (DINOPHYCEAE), TOWARDS IMPROVED TAXONOMY AND SYSTEMATICS

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Dinophysoid dinoflagellates are a diverse group of thecate taxa with a very special thecal plate arrangement with sagittal suture (dinophysoid tabulation). The number and arrangement of the

thecal plates is highly conservative. Even so the morphological diversity is huge. The hypothetical character evolution of dinophysoid taxa based on morphology is now in the process of being evaluated by molecular studies. These studies demonstrated that *Phalacroma* and *Dinophysis* likely are polyphyletic. The morphological characters used to delimit *Phalacroma* and *Dinophysis* are under discussion and their usefulness for taxonomy and systematics is still unclear. We are evaluating these features and try to find clade-specific morphological characters. For that the natural variability needs to be understood. Intra-specific variability for *Ornithocercus* species will be presented. The genus *Sinophysis* is interesting because it is a potentially basal taxon in the dinophysoid lineage. The genus formed a monophyletic lineage but surprisingly did not cluster together with the other dinophysoid lineages in a monophyletic clade. The topology makes no sense in the light of morphology. This discrepancy will be discussed.

DNA BARCODE ASSESSMENT OF THE GENUS *RHODYMENIA* (RHODYMENIACEAE, RHODYMENIALES) FROM AUSTRALIA REVEALS CRYPTIC AND OVERLOOKED SPECIES DIVERSITY

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Previously published DNA barcode surveys of red macroalgae in Australia have revealed significant cryptic and overlooked diversity for the genus *Rhodymenia* with recognition of *R. novahollandica, R. prolificans, R. stenoglossa, R. wilsonis* and an additional four genetic species groups resolved to *Rhodymenia* that were represented by too few specimens for proper characterization. Since that study, robust sampling efforts in Australia have warranted reassessment and reinvestigation of the taxonomic status of species currently included in the genus *Rhodymenia*. Using the DNA barcode (COI-5P) the present study assigned approximately 200 Australian specimens to the genus *Rhodymenia* with these resolved as 12 genetic species groups. Molecular data confirmed the previously recognized *R. novahollandica, R. prolificans, R. stenoglossa* and *R. wilsonis* as distinct entities while some collections from Lord Howe Island, New South Wales were morphologically assigned to *R. novazelandica* Dawson from New Zealand. The remaining seven genetic groups were established as novel species. Morphological features for distinguishing the recognized Australian species of *Rhodymenia*as well as biogeographical distribution patterns will be discussed.

PHYLOGENY OF *NANNOCHLOROPSIS* (EUSTIGMATOPHYCEAE), INCLUDING STRAINS FROM THE AUSTRALIAN NATIONAL ALGAE CULTURE COLLECTION

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Strains of the genus *Nannochloropsis* (Eustigmatophyceae) held in the Australian National Algae Culture Collection (ANACC) were evaluated by DNA sequence analysis. ANACC Strains were first assessed by sequence analysis of a 900 bp region of the plastid rbcL gene (barcode analysis), which allowed us to place proper species names on most of the strains. However, two strains produced a unique rbcL DNA sequence and were shown to be sister to *N. oceanica* in phylogenetic analysis. Complete rbcL sequences and nuclear 18S rDNA sequences were produced for these two strains and other ANACC strains. The results of phylogenetic analyses of an alignment of the concatenated 18S rDNA and rbcL sequences for *Nannochloropsis* taxa revealed that these strains are a new species, *N. australis*. *N. australis* is thus far only known from waters around Tasmania, Australia. Our analyses also provided strong support for erecting a new genus, *Microchloropis*, comprising the species *M. salina* and *M. gaditana*.

SPOROLITHON PTYCHOIDES (SPOROLITHALES, RHODOPHYTA): GENERITYPE SPECIES OF TYPE GENUS OF THE ORDER ASSESSED BY SEQUENCING TYPE AND TOPOTYPE MATERIAL

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Coralline algae were collected from El Tor, Egypt, type locality of *Sporolithon ptychoides* Heydrich and *S. molle* (Heydrich) Heydrich. DNA sequencing revealed three *Sporolithon* species. Partial rbcL sequences from type material of *S. ptychoides* and *S. molle* were distinct from one another, but each sequence was identical to different field-collected El Tor specimens. From these field-collected specimens we obtained psbA, cox1 and LSU sequences to compare with published sequences of *S. ptychoides*. Sequence divergence values showed that none of the published sequences from Hawai'i, New Caledonia or Brazil are *S. ptychoides*. SEM imaging of the three El Tor species showed vegetative characters that when considered together are diagnostic for *Sporolithon*, namely flared epithallial cells, and the presence of both secondary pit connections and cell fusions. In *S. ptychoides* and *S. molle*, fields of trasporangial compartments were observed buried under new vegetative growth, a feature said to be characteristic of these species. Non-geniculate coralline species reported to have widespread distributions based only on morpho-anatomy, particularly across different biogeographic zones and/or in different ocean basins, need to be confirmed with DNA sequencing.

FROM FOSSILS TO DNA: DEFINING THE DIATOM GENUS *BIDDULPHIA* GRAY

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Within the diatom families Biddulphiaceae and Eupodiscaceae, taxonomic revisions and synonymies are extensive across the genera. SEM-assisted studies have significantly helped to sort out these genera, changing the focus from gross valve symmetry to specific characters on the valves themselves, particularly the structure of pore fields on the valve apices. Recent molecular analyses have mostly supported the revised taxonomy based on valve ultrastructure within the Eupodiscaceae, but have not been so clear with the Biddulphiacae, particularly diatoms with pseudocelli (apical pore fields marked by the decrease in size from the pores on the main part of the valve), such as the taxa in the genus *Biddulphia* Gray. While molecular data suggest that there is a "*Biddulphia*" clade (though with limited taxon sampling which cannot include the diverse array of fossil taxa ascribed to this genus), finding a morphological synapomorphy by which to circumscribe the genus has been more difficult. Looking at fossil and extant taxa, we

found 4 morphotypes for which there is evidence for both morphological and molecular synapomoprhy and suggest a new taxonomic scheme based on these criteria.

MOLECULAR 'FISHING' REVEALS *KALLYMENICOLA* GEN. NOV. INCLUDING THREE NEW HOST-SPECIFIC ENDO/EPIPHYTIC SPECIES OF MEIODISCACEAE (PALMARIALES).

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Contaminant sequences generated during routine COI-5P DNA barcoding of British Columbia Kallymeniaceae had affinities to Meiodiscaceae, Palmariales. To further explore the source, frequency and diversity of the species associated with these sequences in west coast Kallymeniaceae, primers to amplify specifically *rbc*L from Meiodiscaceae were developed. Ultimately 284 kallymeniaceaen specimens representing 17 species were screened with 12 specimens from three species yielding positive PCR amplifications, which after sequencing resolved as three distinct host-specific genetic groups. Combined *rbc* L + COI-5P phylogenetic analyses confirmed assignment of the three genetic groups to a novel lineage in the Meiodiscaceae as a relatively distant sister to the genera *Meiodiscus* and *Rubrointrusa* necessitating a distinct genus for these taxa, *Kallymenicola* gen. nov. Anatomical studies of these 12 specimens revealed endo/epiphytic species with palmarialean attributes (notably asexual reproduction from tetrasporangia with regenerative stalk cells) that were assigned to the three species *Kallymenicola invisiblis* sp. nov. (host = *Pugetia fragilissima* Kylin), *K. penetrans* sp. nov. (host = *Erythrophyllum delesserioides* J. Agardh) and *K. superficialis* sp. nov. (host = *Euthora timburtonii* Clarkston & G.W. Saunders).

THE AMANSIEAE (RHODOMELACEAE) REVISITED: A MULTIGENE APPROACH

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The main objective of this study was to evaluate the generic circumscription and the phylogenetic relationships within the tribe Amansieae and between the Amansieae and other rhodomeloid tribes using a multigene approach. Genomic DNA was extracted using the CTAB method. Sequences of the barcode region of the COI gene and the *psb* A, *rbc*L, and LSU genes were obtained for most of the representatives. Phylogenies based on Bayesian and Maximum Likelihood were generated. Additionally, we study the pattern of evolution of 18 morphological characters within the tribe. Our analysis, confirms that the non-winged genus *Protokuetzingia* is probably the most primitive member of the tribe. Furthermore, *Enantiocladia duperreyii* was recovered as basal to the advanced amansioid taxa. Anatomically, *Enantiocladia duperreyii* shares some anatomical features with *Protokuetzingia* and other with the advanced amansioid taxa, such as the presence of wings. The generic separation between *Amansia* and *Melanamansia* is not supported in our analyses. As suggested by Norris (1988), a close relationship between the Amansieae and the Rhodomelae is possible and needs to be evaluated to elucidate any particular affinity between these two tribes.

DECIPHERING *DISTROMIUM* DIVERSITY FROM THE DEEP: UNIQUE MESOPHOTIC SPECIES FROM THE HAWAIIAN ARCHIPELAGO

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Brown-bladed macroalgae belonging to the Dictyotales are a common component of deep, or mesophotic, macroalgal communities world-wide. In the Hawaiian Archipelago, one of the most common mesophotic genera is *Distromium*. Currently, only one species, *D. flabellatum*, is reported from Hawaii based on morphology. Our goal was to use molecular and morphological techniques to characterize the diversity of *Distromium* in Hawaii's mesophotic zone. Technical diving, submersibles, and remotely operated vehicles were used to collect specimens (n = 18) from 11 locations in the Northwestern to Main Hawaiian Islands from 44 – 89 m depths. Analyses (*psbA*, LSU, and *rbcL* marker analyses and morphological comparisons) suggest that mesophotic *Distromium* in Hawaiian waters is not *D. flabellatum*, but three entities clearly distinct at the DNA sequence level and likely new species. However, blade thickness was the only morphological feature separating these clades. This contrasts with the six existing species of *Distromium*, which were described based on unique morphological and anatomical characters. These species have not been described from shallow water, further adding to the depth of macroalgal diversity found in mesophotic ecosystems.

POLYPHYLY IN *SCYTONEMA* (NOSTOCALES, CYANOBACTERA): PHYLOGENETIC SEPARATION OF THE *S. HYALINUM* GROUP FROM THE TYPE SPECIES *S. HOFFMANII*

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Forty strains morphologically similar to *Scytonema hyalinum* were isolated from diverse regions and habitats (soils in California, Utah, New Mexico, Mexico, Portugal, Ethiopia, and China, a hypersaline lake in Chile, tree bark in Hawaii). While we consider this group a species cluster rather than a single species, phylogenetic analyses based on the 16S rRNA gene, *nif* D, *rpo* C1 and *rbc* LX loci clearly indicate that this species cluster is distant from the clade containing the generitype, *S. hoffmanii*. The *S. hyalinum* clade contains *Symphyonema* and is sister to the clade containing *Brasilonema*, *Symphyonemopsis* and *Iphinoe*. *S. hoffmannii* is basal and paraphyletic to most members of the Nostocales. *S. hyalinum* must be placed in a separate genus, possibly *Symphyonema* or a genus new to science, and the Scytonemataceae will likely require more narrow circumscription.

THE MEDITERRANEAN RED ALGAL GENUS *FELICINIA* (HALYMENIALES, RHODOPHYTA) IS NOT AN ENDEMIC TAXON

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On the basis of three molecular markers and morphological evidence, the new monotypic genus *Felicinia* in the Halymeniaceae was proposed by Manghisi et al. 2014 to accommodate the species previously going under the name *Aeodes marginata* (Roussel) Schmitz 1894 (basionym: *Halymenia marginata* Roussel in Montagne 1838). This taxon was reported to be endemic to the Mediterranean Sea. Here we report this species growing on deepwater rhodoliths from collections made at 65-70 m depth in September 2014 in the vicinity of the Dry Tortugas, Florida, SE Gulf of Mexico. Rhodolith collections were brought back live to our lab at UL Lafayette where they are being maintained in running-seawater holding tanks. Multiple foliose species grow on these rhodoliths, including specimens of *F. marginata* whose identity was confirmed by *rbc* L, LSU and COI sequences downloaded from GenBank. The biogeography of this taxon in the Mediterranean Sea and the Gulf of Mexico will be discussed.

NEXT GEN TAXONOMIC DESCRIPTIONS FOR MICROBIAL EUKARYOTES

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Understanding of microbial eukaryotes has changed dramatically as technology progressed from early studies solely using light microscopy to modern ‘omics research. Each type of data can be useful and over the centuries, large amounts of heterogeneous data about algae have been produced. Studies of microbial eukaryote phylogeny and systematics have difficulty taking advantage of all available data, which is necessary because no single data type can resolve all algal lineages and not all lineages have equal coverage in all data types. Unfortunately, only genomic data is in a format that can be easily mined and analyzed on a large scale, making phenomic data a “second class citizen” in data-driven science. Applying semantic technologies to taxon descriptions can transform phenomic data into a computable format that allows large-scale analysis of that data, similar to those performed on genomic data. This presentation will showcase the application of semantic technology to microbial eukaryote species descriptions using members of the *Gymnodinium* genus and demonstrate some of the advantages of using semantics in algal taxonomy.

HOW MANY SPECIES OF *BANGIA* OCCUR ON THE WEST COAST OF NORTH AMERICA?

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Although no species of the freshwater genus *Bangia* have been recorded from the Pacific coast of North America, species with the *Bangia* morphology are common there. Recent collections and sequencing of material from northern Baja California to the westernmost Aleutian Island, Alaska, indicate there are at least ten species with the *Bangia* morphology. These species occur in two or more genera, which have been identified as `*Bangia*′ 2 and `*Bangia*′ 3 by Sutherland et al. in 2011. Only two of the species have specific epithets: `*Bangia*′ *maxima* and `*B.*′ *vermicularis*. Three of the species are represented by single collections, indicating that they are rare or grow in places or at times when phycologists do not collect. Most of the specimens occur in three unnamed species, all of which are widely distributed along the Pacific coast. Each of the ten or more species will be discussed, including their distributions, seasonalities, habitats and other features that distinguish them. No specimens were sequenced that showed conspecificity with a species outside the region (i.e., there do not appear to be any introduced species—yet).

DOLICHOSPERMUM HANII SP. NOV. (CYANOPHYCEAE); A NEW SPECIES FROM HAN RIVER, KOREA.

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Here, we described a new filamentous cyanobacterial species of the genus *Dolichospermum* from the Han river, S. Korea. *Dolichospermum hanii* sp. nov. was characterized using LM and SEM along with sequencing of the SSU ribosomal regions and *rbcLX* region. The new species is morphologically similar to *D. planctonicum* in the form of trichomes and heterocysts. However, *D. hanii* differs from *D. planctonicum* by the distinguishing morphological characteristics: 1) The width of vegetative cell is generally narrower than *D. planctonicum*, 2) Akinetes having thin cylindrical shape is narrower than center toward ends and surface of akinetes is wrinkled, 3) Akinetes in trichomes develop solitary and depart from heterocysts, 4) Mucilaginous envelopes surrounding trichomes are always formed and rounded mucilaginous sheath covers akinete, additionally. Hence, Akinetes of *D. hanii* have double mucilaginous sheath. Phylogenetic analysis of SSU and *rbcLX* regions place *D. hanii* as a separate group to *D. planctonicum*. Genetic distances of 16S rRNA and *rbcLX* gene between two species were each 0.2-0.3 %, 1.4-1.5 %.

MORPHOLOGICAL AND MOLECULAR ASSESSMENT OF *AVRAINVILLEA* (ULVOPHYCEAE, CHLOROPHYTA) AND IMPLICATIONS FOR INVASIVE SPECIES MANAGEMENT

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The green alga *Avrainvillea* was first identified in the Hawaiian Islands in 1981 off the western shore of Oahu. Today *Avrainvillea* persists as a dominant invasive in the shallows, and in meadow-like populations at greater depths, off the western and southern shores of Oahu. Brostoff (1989) identified the alga as *Avrainvillea amadelpha*, but admitted that this identification was disputable as it resembled other species as well. Additionally, a species of *Avrainvillea* has recently invaded the Mediterranean. Thus far systematic treatments of *Avrainvillea* have relied solely on morphological characters. Preliminary morphological and molecular assessments suggest that the identification of the Hawaiian alga as *A. amadelpha* is most likely incorrect. Comparison of deep-water and shallow individuals shows these populations are morphologically and molecularly indistinguishable; thus, *Avrainvillea* may be native to the Hawaiian archipelago, and only recently invaded the shallow environment. Assessment of the Mediterranean alga suggests that it most likely invaded from the Red Sea. Clear species identification of *Avrainvillea* is crucial given that members of the genus are exhibiting invasive behavior in marine ecosystems outside their native range.

Population Biology/ Biogeography / Large-scale Phycology

WHAT IS HAPPENING TO THE LARGE BROWN SEAWEEDS IN THE NORTHEASTERN ATLANTIC IN A RAPIDLY CHANGING ENVIRONMENT?

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The large brown seaweeds are keystone species, forming habitats in intertidal and shallow subtidal marine ecosystems. These habitats have been profoundly affected by human impact in the northeastern Atlantic due to increasing warming and acidification of the environment. Based on available evidence we predict that kelp forests will disappear from their southern ranges. Over the last decade, there have been an increasing number of reports of decline or loss of these habitat-forming organisms, whilst at the same time there is an increasing interest in their wild harvest and aquaculture for a range of products, including food, alginates, bioactives and biofuels. The British Isles is a ‘goldilocks zone’ for most species of large brown seaweed, lying at the centre of the NE Atlantic distribution for most species and not at climatic tolerance limits. The seaweeds of Britain have notably had a long history of study, although the lack or patchy nature of long term datasets presents a particular challenge. In this talk, we will report on a study of large brown seaweeds between 1974 and 2010 in Britain which reveals a north-south divide of gain and loss of abundance and a mixed relationship with temperature. We will also report on the work we are undertaking to try to determine which environmental factors appear to be potential drivers in these changes, including temperature, salinity, nutrient concentrations, turbidity, dissolved oxygen concentrations and storminess. We will also address how we are tackling the problems of the patchy nature of datasets through our work using images to quantify coastal seaweed habitat.

THE IMPORTANCE OF GENOTYPE IN *MACROCYSTIS PYRIFERA* FORM AND FUNCTION

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Plasticity is an ecologically and evolutionary meaningful trait allowing organisms to respond to environmental heterogeneity. Kelps have been shown to have highly plastic morphological, physiological and life history traits. However, there is a restricted understanding of genetic regulation behind plasticity. This study focus on the potential to modify traits through controlled breeding and grown under common environmental conditions, by testing morphological, growth

and chemical differentiation among nine *Macrocystis pyrifera* strains with different genetic background. The results showed striking differences in the holdfast development and growth capacity at early stages under controlled culture conditions and in the field under common abiotic conditions. In addition, carbohydrates, bioactive compound and amino acid composition, showed significant differences between strains. These results highlight the influence of the genetics on phenotypic diversity, suggesting that heritability is relevant. The understanding of how genetics and the environment regulated kelp plasticity remains as an open question and its key for the development of kelp mariculture. Funding: FB-0001, FONDECYT 1150978 and Corfo-INNOVA 09CTEI-6866.

SPATIAL AND TEMPORAL VARIATION IN ULVOID PROPAGULE AVAILABILITY IN SAN FRANCISCO BAY

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Supply-side ecology, as related to marine intertidal communities, has focused primarily on invertebrate recruitment with much less attention given to the role of propagule supply in the establishment of macroalgal populations. Investigations of the dynamics of nuisance green macroalgae have mostly emphasized post-recruitment processes such as herbivory. Water samples (2L) were collected and cultured monthly at Tiburon to estimate temporal variability in propagule supply and seasonally at four additional sites spanning the central San Francisco Bay to determine spatial variability. Sterile resin settling plates (n=10) were simultaneously installed for 4-week periods along intertidal areas near Tiburon to estimate natural recruitment. Water collected from July 2014-April 2015 produced *Ulva* when cultured with samples collected in spring and summer months yielding greater numbers of recruits/cm2; indicating increased propagule supply at this time of year. Although all sites yielded recruits, sites north of the bay mouth yielded more *Ulva* recruits than southern sites. Late summer 2014 recruitment peaks appear to coincide with decreases in propagule supply but may be explained by spring increases in propagule supply.

THE MACROALGAL HERBARIUM DIGITIZATION PROJECT

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Through the NSF Advancing Digitization of Biological Collections (ADBC) program, funding has been provided to digitize all of the macroalgal specimens in U.S. herbaria and to make the information accessible online. Currently over 1 million specimens in 50 collections at universities, botanical gardens, museums, and field stations are being digitized. Images of each specimen are being captured using high resolution photography. Specimen label information is being transcribed, and where locality information is provided, the collection location is being georeferenced to facilitate mapping. Data is accessible through the project's portal http://macroalgae.org. A brief overview of the digitization methodology will be presented along with a demonstration of how the data portal can be used to study changes in species distribution and algal community structure over time. The NSF ADBC program includes a mechanism to apply for funding to include additional collections in the project. Herbarium personnel and phycologists associated with macroalgal collection that are not currently part of the project are encouraged contact the presenter. People interested in using the project data portal for their research are invited to make suggestions on new features that would facilitate data extraction and visualization.

THE DEVELOPMENT OF NUTRIENT CRITERIA USING THE BIOLOGICAL CONDITION GRADIENT (BCG) APROACH

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The U.S. EPA requires that states develop numerical nutrient criteria. A diatom based transfer function for streams in New Jersey has been developed and taxa attributes have been defined. However, transfer functions do not answer the question of what nutrient concentrations are acceptable. In order to develop nutrient criteria for streams in NJ (USA) we used a diatom based BCG approach (see talk by D. Charles et al.). To develop potential nutrient criteria, we explored the relation of BCG scores to nutrient concentrations, other anthropogenic stressors, and possible confounding variables. BCG scores correlated most strongly with TP and the percentage of forest in the watershed, but were independent from pH. The BCG scores showed a sigmoidal relation to TP. A TP concentration of around 50 µg/L corresponded to BCG scores between 5 and 3, and could be considered as a statewide nutrient criterion that could help promote ecological integrity. Because nutrient concentrations vary in different ecoregions in the state, nutrient criteria should account for this. In addition to deriving nutrient criteria from the BCG scores we also looked for significant changes in the diatom communities along the BCG gradient to determine if there were BCG change-points based on diatom assemblages. A numerical zonation procedure and Threshold Indicator Taxa Analysis, both of which included permutation tests, indicated significant diatom changes at a BCG score near, but better than 4. Sites with BCG scores better than 4 were dominated by attached *Achnanthidium* species, while sites with BCG score of 4 or poorer were dominated by motile species such as *Eolimna minima* and *Nitzschia inconspicua*. Sites with a BCG score near 4 can be considered sites in transition and need attention to prevent impairment, while sites with better BCG scores need protection to stay unimpaired. The BCG approach is very promising and is helping to establish ecoregion specific nutrient criteria in New Jersey.

CYANOBACTERIA FROM THE LAPLAND BIOSPHERE RESERVE, RUSSIA

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The Lapland Biosphere Reserve (LBR) is located in northwestern Russia. The region of LBR is especially unique for biodiversity due to a maritime climate, presence of archean metamorphic rocks, and great habitat diversity. Consequently, cyanobacteria are abundant and the flora is rich, containing 140 morphospecies. Representatives of Chroococcales and Synechococcales are dominant. Specifically, epilithic and epiphytic *Chroococcus*-*Gloeocapsa* species are the most abundant species recorded in LBR. Most excitingly I have found some rare taxa such as *Phormidiochaete nordstaedtii* (generitype), *Gloeocapsa tornensis*, *Gloeocapsopsis dvorakii* as

well as uncertain taxa morphologically similar to *Solentia*, *Hyphomorpha*, *Iyengariella*, and many others. Material assigned to *Solentia* has the morphological characteristics of that genus, but is epilithic on gneiss rather than endolithic in limestone. *Hyphomorpha* has uncertain placement in the Hapalosiphonaceae, but appears to be more morphologically similar to several *Stigonema* species. *Iyengariella* is perhaps the most unusual discovery, as it is a tropical genus in the Symphyonemataceae (Nostocales) with true branching and no heterocytes. All of these taxa belong to poorly known genera of cyanobacteria that lack DNA sequence data, which I am now obtaining.

INVESTIGATING SPECIES DIVERSITY WITHIN THE RED ALGAL GENERA *ANTITHAMNIONELLA*, *HOLLENBERGIA* AND *SCAGELIA* (CERAMIALES, RHODOPHYTA) IN CANADA

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The aim of this investigation was to resolve taxonomic, nomenclatural and distributional uncertainty surrounding species of the red algal genera *Antithamnionella*, *Hollenbergia* and *Scagelia* reported for Canadian coasts. Whereas only two species of *Antithamnionella* are currently recognized in the northeast Pacific, *A. pacifica* and *A. spirographidis*, we have confirmed the presence of an additional species, *A. floccosa*. Contrary to published accounts, *A. floccosa* is more widespread on the Canadian west coast than the morphologically similar *A. pacifica*. For the genus *Hollenbergia* in the northeast Pacific, analyses of genetic data are consistent with the two currently reported species (H. subulata and H. nigricans), however, we present genetic evidence that *H. nigricans* is more closely allied to the genus *Scagelia* than the type species of *Hollenbergia*, *H. subulata*. Finally, while *Scagelia occidentale* is currently reported in the Pacific and Scagelia pylaisaei is considered to be present in the Arctic and Atlantic, our analyses of both COI-5P and ITS resolved two closely related genetic groups with mixing of these populations in the Arctic. We argue that the two closely related genetic groups represent a single species, for which *S. pylaisaei* has priority, and that populations of this species have experienced past isolation (putative incipient speciation) followed by a collapse in barriers.

VIEWING RHODOLITHS AS DIVERSITY- RICH HOLOBIONTS

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Rhodolith beds offshore Louisiana in the NW Gulf of Mexico are associated with salt domes, unique deep bank habitats at 55-75m depth on the continental shelf. Seven sampling expeditions following the 2010 Deepwater Horizon (DWH) oil spill to 2 rhodolith bed habitats revealed a drastic macroalgal die-off that has persisted up to this day (last collections from September 2014) in locations that were diversity-rich pre-DWH. Laboratory observations of bare, denuded, and apparently “dead” rhodoliths collected post-DWH and placed in 75-liter microcosms in our lab, have shown macroalgal regeneration within 3 weeks. Metabarcoding of endolithic rhodolith environmental DNAs with newly designed primers for tufA recovered a wide microbiotal diversity of photosynthetic organisms including numerous seaweed species comprising red, green, brown (and other Ochrophyta) algae, as well as other phototrophic lineages (e.g.

Cyanobacteria). Metabarcoding of 16S V4 from the same endolithic rhodolith DNAs used for tufA metabarcoding recovered in-depth microbiotal taxon coverage, including abundant prokaryotic (phototrophic Cyanobacteria, heterotrophic Bacteria and Archaea), and eukaryotic phototrophic diversity. 16S V4 recovered a similar proportion of phototrophs within rhodoliths pre- and post-DWH suggesting that although not visible in the field, seaweeds are still present in the NWGMx in the form of 'resting' microscopic stages (dormant spores and filaments) within the CaCO3 of rhodoliths. Using tufA and 16S metabarcoding we were able to link the taxonomic identity of the "invisible," cryptic (hidden) parts of a macroalga that are part of a rhodolith's CaCO3 microbiota, with their corresponding "visible" macroscopic thalli through Sanger sequencing of plastid tufA and plastid 16S. We are continuing to characterize rhodoliths as holobionts critical for the cycling of macroalgal communities and as seedbank reservoirs and refugia of dormant microscopic stages of macroalgae.

FACTORS SHAPING PHOTOTROPH-DOMINATED MICROBIAL COMMUNITIES ALONG OAHU'S WINWARD COAST

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Subaerial communities along Oahu's windward coast are usually dominated by the alga *Spongiochrysis hawaiiensis* (Cladophorales, Ulvophyceae); however, biofilms dominated by lichens and *Printzina* (Trentepohliales, Ulvophyceae) are present, in addition to surfaces free of visible biofilm. To investigate factors contributing to biofilm abundance, distribution of dominant biofilm members, and their associated microbial communities, biofilm samples were randomly sampled at four sites (Waimanalo, Kailua, Laie, and Malakaehana) within a distance of 200 m from the high-tide shoreline. Additional samples were taken at three inland sites (Hoomaluhia Botanical Garden, Pali Highway Recreational Area, and Kahana State Park). For each sample, soil salinity, host tree species, tree canopy cover, percent visible biofilm cover, aspect, elevation and density of neighboring trees were recorded. For coastal samples, distance from the high-tide shoreline was also recorded. Amplicons were chosen to capture algal and associated microbial diversity (algae/heterotrophic protists and bacteria: 18S and 16S; fungus: ITS1; archaea: archaeal specific 16S) and sequenced on the Illumina MiSeq platform. Inland vs coastal, dominant biofilm species, and distance from the shore were significant in shaping community structure.

EFFECTS OF OCEAN ACIDIFICATION ON PHYTOPLANKTON PHOTOSYNTHESIS

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Rising atmospheric CO2 concentrations are projected to result in a drop in global ocean pH by about 0.3 units by year 2100. Because low pH impedes the biological deposition of calcium carbonate, much research has focused on how calcifying phototrophs such as coccolithophores will fare in the future ocean. However, less effort has been devoted to understanding the effect of pH and elevated C availability on aquatic photosynthesis in non-calcifying taxa. I conducted laboratory experiments as well as a thorough literature review in order to understand i) how photosynthetic growth rates of phytoplankton change between ambient (~ 380 ppm) or year 2100 (~ 750 ppm) CO2 concentrations, ii) how future CO2 conditions might affect competition between phytoplankton functional groups, and iii) what physiological trade-offs are associated

with acclimation and/or adaptation to a high CO2 environment. I found that larger eukaryotic taxa had a roughly equal probability of growing faster or slower under high CO2, but most cyanobacteria and picoeukaryotes were strongly enhanced under year 2100 conditions. *Prochlorococcus* was a stark exception to other cyanobacteria, and was often strongly inhibited by higher CO2. Elevated CO2 also affected cellular stoichiometry, nitrogen fixation, and photosynthetic efficiency, and the magnitude and sign of these effects varied significantly between functional groups. These findings suggest that differential responses to ocean acidification might influence the competitive fitness, and therefore the prevalence, of different functional groups of phytoplankton, with potential ramifications throughout the marine food web.

LIMITS TO THE POSITIVE EFFECT OF OCEAN ACIDIFICATION ON MACROALGAL PRODUCTION

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Many macroalgal species lack any carbon concentrating mechanism (CCM). Species lacking CCM’s should benefit from ocean acidification in terms of primary productivity and growth. The absolute sizes and pattern of those benefits are unknown. We compared the results of a model based on composite published data, to growth experiments using *Plocamium cartilagineum*, a broadly distributed rhodophyte species lacking a CCM and hypothetically carbon limited under current conditions. We grew *P. cartilagineum*, at 15 and 20°C in seawater aerated with a total of 53 different pCO2s (344 to 1053µatm), in 8 multiweek trials over 12 months. We measured growth and photosynthetic rates. A linear mixed model analysis was used to partition the effect sizes of drivers of variation. Growth rates and maximum photosynthetic rates responded nonlinearly to OA, increasing with elevated pCO2 as a decelerating function up to 450µatm, which matched the model. However, the effect of pCO2 on growth was greater than predicted. Growth rates declined at higher pCO2s. These results predict that the benefit of OA for macroalgal growth may disappear as ocean acidification continues through this century.

Posters

P01. A COMPARISON OF PHYLOGENETIC DIVERSITY IN FIVE MAJOR PHYTOPLANKTON LINEAGES FROM REFERENCE STRAINS AND FIELD-BASED SAMPLES

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Diversity measure are both a fundamental in analyzing microbial communities and also challenging measurement to make on these communities given the lack of a traditional species concept. Numerous methods exist to measure diversity, and some are more applicable than

others in a microbial context. To make improvements, continued development of a microbe-centered diversity measurement that can accurately incorporate the simultaneous variability and similarity within these complex communities we analyzed phylogenetic diversity measures in known organisms and from field-based metagenomes. We used Faith's Phylogenetic Diversity (PD) for the 18S SSU sequence to compare with diversity functional genes (COGs), focusing on 5 globally important marine phytoplankton groups. We then analyzed environmental sequences from a range of available metagnomic data sets using phylogenetic based methods (pplacer) to then compare the PD and abundance weighed PD from field based samples for both operational taxonomic genes (18S SSU) and functional genes. The relationship between the known diversity of reference sequences and the observed diversity in the environment and the relationship between taxonomic genes and functional genes can help us understand evolution of community structure in phytoplankton groups.

P02. THE EFFECT OF VISIBLE LIGHT STRESS ON CHEMICAL SIGNALING IN TWO AUTOTROPHIC DINOFLAGELLATES

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Although dinoflagellates are globally influential members of the planktonic community, little is understood about how their physiological and behavioral responses to stress contribute to defining their ecological niche. Since free-living, marine dinoflagellates tend to bloom in stratified waters, they are likely exposed to intense radiation from the sun in the shallow surface mixed layer for relatively long durations. This study aims to investigate the effect of high intensity visible light on production of signaling compounds, including reactive oxygen species (ROS) and dimethylsulfoniopropionate (DMSP), in two autotrophic dinoflagellate species. When exposed to 850-950 µmol photons m^-2 sec^-1, both *Alexandrium fundyense* and *Heterocapsa rotundata* showed a significant, temporary decrease in photosynthetic efficiency (Fv/Fm), followed by recovery. In addition to Fv/Fm, which was used as a proxy for cell stress, changes in intracellular and extracellular ROS were measured using a fluorescent probe and the Amplex Red assay for hydrogen peroxide, respectively. Intracellular and extracellular concentrations of DMSP were measured as well. Significant changes in intracellular ROS and DMSP were observed in *H. rotundata* and *A. fundyense*, but extracellular H2O2 and DMSP concentrations in stressed cells were indistinguishable from the control.

P03. DIATOM-BASED PROXY FOR SEA ICE EXTENT IN THE BERING AND CHUKCHI SEAS

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The current decline in Arctic sea ice extent prompts questions about how productivity responds to sea ice. In the Bering Sea, productivity is among the highest in the world and is due in part to a range of concentrations of seasonal sea ice. In addition, the silica frustules of diatoms are abundant in the sediments, allowing us to reconstruct sea surface environmental conditions of the past. In 70 sediment samples collected in 1969 and 2006–2008 a total of 402 species have been

identified. The assemblages were compared to satellite-derived sea ice concentrations averaged over the 10 years preceding sampling. At least 8 species demonstrate a significant relationship with ice concentration. In the model we used 3 species with different optima: *Fragilariopsis regina-jahniae* peaks at 60% of ice, *Neodenticula seminae* avoids ice, and *Thalassiosira* sp. nov. prefers more than 70% of ice. Distributions of these species were analyzed using the generalized additive model (GAM). Fitting the GAM to the distribution of the species explained almost 90% of the variation and realistically reconstructed past sea ice decline during a previous warming.

P04. INVESTIGATIONS INTO THE SALINITY TOLERANCE AND ADAPTATION OF *PLEUROCLADIA LACUSTRIS* (PHAEOPHYCEAE).

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A small fraction of a percent of all known brown algae are currently recognized as freshwater species. A better understanding of the evolutionary origin and physiological characteristics of this unique group of algae may provide important insights into the evolution of brown algae and their adaptation to new habitats. *Pleurocladia lacustris* A. Braun is a predominantly freshwater species that has been reported in a few brackish and intermittently-marine environments, suggesting moderate salinity tolerance. We are tracking the response of *P. lacustris* A to increases in salinity through the quantitative measurement of quantum yield of photochemistry and growth rate as well as through the use of microscopic analyses and RNA seq. We have collected *P. lacustris* from California streams to evaluate the range of salinity adaptation and tolerance observed among different environmental isolates and are seeking to establish unialgal cultures. *P. lacustris* has shown tolerance in MiEB12 medium of at least 2.0 ppt NaCl and our next step is to investigate the physiological and transcriptional correlates of such tolerance and whether other environmental isolates may demonstrate similar or higher degrees of adaptability or tolerance.

P05. TAXONOMIC STUDY OF SIMPLE FILAMENTOUS CYANOBACTERIA FROM WET ROCK HABITAT IN UTAH

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Wet rock surfaces have been shown to be ideal habitats for diverse and unique cyanobacterial assemblages. However, studies concerning cyanobacterial species diversity in such communities are still limited in the U.S. Presently, accurate species identification requires a polyphasic approach with some combination of morphological, ultrastructural, molecular, physiological, and ecological characterization. We collected, isolated, and morphologically characterized 44 simple filamentous cyanobacteria strains from wet rocks of the Grand Staircase-Escalante National Monument (GSENM) in Utah. Based upon their morphology, all strains were initially identified as either *Leptolyngbya* or *Pseudanabaena*. However, molecular analyses of 13 of these strains indicates that they represent distantly related clades in the Synechococcales, including

Nodosilinea sp., *Oculatella cataractarum*, *Geitlerinema splendidum*, four species in an as-yet undescribed genus sister to *Oculatella*, as well as one or two species in a genus sister to *Phormidesmis*. Analysis of the 16S-23S ITS region is planned in the near future.

P06. STRETCHING RELIEVES STRESS: ELASTICITY AMELIORATES DRAG IN *ASCOPHYLLUM NODOSUM*

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Intertidal organisms are adapted to a variety of environmental conditions including wave action. To evaluate wave action on *Ascophyllum nodosum*, samples were collected from two sites in Nova Scotia: a sheltered environment in Antigonish Harbour (AH) with virtually no wave action, and an exposed site on the Atlantic coast at Tor Bay (TB). Fifty fronds were pulled from the substratum to determine frond stress prior to dislodgement. Twenty fronds (ca 35-70 cm long) from each site were returned to the laboratory to evaluate mechanical properties of three different frond portions in the upper, middle and lower thirds of each frond. Fronds from TB were significantly different in all aspects of strength relative to AH. In addition fronds from TB showed increased stretching prior to breakage relative to AH. Differences between the strength at the different sites likely reflect adaptation to wave action. At both sites the fronds were significantly stronger at the holdfast than at positions along the frond. This allows fronds to break at upper portions of the frond before increased drag can remove the entire frond.

P07. THE UTILITY OF BAR-CODING IN *SARGASSUM* SPECIES

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Sargassum is one of the most ecologically important and widespread brown algal genera. The genus commonly forms either pelagic floating beds or large coastal stands in tropical to subtropical ecosystems. However, there its evolutionary history and phylogeny remains elusive. Progress is hampered by high rates of phenotypic plasticity as well as a lack of in depth studies of Caribbean *Sargassum* species. This is especially true for coastal areas of Panama, where the estimates of diversity suggest that the region has many undiscovered species. The development of DNA barcoding regions for *Sargassum* would solve the problems with morphological identification and enable comprehensive phylogenetic analysis. Unfortunately, some of the most promising mitochondrial gene regions (e.g. COI) amplify poorly with existing primers. The goal of this project is to compare four gene regions for barcoding utility, compare novel and previously developed COI primers, and use this data to contribute to the resolution of *Sargassum's* phylogeny emphasizing section *Sargassum* species. Twenty-one samples from the Caribbean Sea and the Pacific Ocean in areas surrounding Panama were obtained. All 21 samples were successfully extracted for total genomic DNA using a modified CTAB method, whole genome amplified (Genomiphi) with the DNA archived. Primers for CIO were redeveloped and all gene regions were amplified (COI, Z-LSU, rbcLS and ITS-2), and sequenced. Master alignments are in the process of being complied with new and GenBank data.

Phylogenetic analysis using these alignments will establish their barcoding utility as well as provide important insights into the evolutionary history of select *Sargassum* species.

P08. DISTRIBUTION OF *NITELLOPSIS OBTUSA* IN NEW YORK, U.S.A.

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The charophytic green alga *Nitellopsis obtusa* (Characeae: Charophyta) was first reported in the New World in the St. Lawrence River in 1978. Since that time, *N. obtusa* has been reported from inland lakes throughout Michigan, northern Indiana, and western New York and has been listed as an aggressive invasive species by the United States Geological Survey. We studied the distribution of *N. obtusa* by surveying 390 waterbodies throughout New York State, recording Characeae species presence and water chemistry parameters. In total, *N. obtusa* was found in 17 counties at 31 sites, including 16 inland lakes, 7 sites in the St. Lawrence River, and 8 sites in Lake Ontario. This included new reports from five counties (Franklin, Ontario, Seneca, Wayne, and Yates). Much of the distribution pattern of *N. obtusa* in New York was correlated with human activity and water chemistry data. Among sites with Characeae (174), water chemistry parameters differed significantly between sites with *N. obtusa* and those without. Further work is needed to understand how environmental variables and human activities contribute to the current distribution of *N. obtusa* in North America.

P09. STUDIES OF THE SOIL ALGAE IN THE KOLA PENINSULA

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Studies of soil algae began in the Laboratory of Ecology of Microorganisms of the INEP in the 1980s under the guidance of Prof. E.A. Shtina. This research dealt with the biodiversity of algae in Al-Fe-humus podzols, dominating in the Kola Peninsula, in tundra zone and northern taiga subzone. Algae from both unpolluted and polluted territories have been investigated. The main sources of pollution in the Kola Peninsula are heavy metals (e.g. Cu, Ni, and Co) and fluorine compounds, which are released into the air due to industry. Moreover, in our lab have been explored the morphological changes of algae in term of heavy metals, using culturing techniques. At present, the studies of algae of podzol soils of the Kola Peninsula are continuing. 180 species of algae was found. Most abundant algae in the studied soils are Chlorophyta (Chlorophyceae, Trebouxiophyceae), Xanthophyta, Cyanobacteria, less abundant are Charophyta (Klebsormidiophyceae), Bacillariophyta, Eustigmatophyta and Euglenophyta. The following,

common genera are resistant to pollution: *Chlamydomonas, Chlorococcum, Pseudococcomyxa, Stichococcus, Coelastrella, Myrmecia, Klebsormidium, Interfilum, Xanthonema, Eustigmatos, Nostoc*, and *Leptolyngbya*.

P010. EVALUATION OF SUBTIDAL AND DEEP-WATER POPULATIONS OF *EISENIA ARBOREA* ALONG THE CALIFORNIA COAST: SPECIATION OR ADAPTATION?

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Kelp forests are very productive ecosystems in temperate subtidal communities around the world. Past research suggests that water flow and hydrodynamic pressure differences between the shallow subtidal and deep subtidal zones may shape algal morphology. *Eisenia arborea* is an example of a kelp species with populations in the shallow subtidal deep subtidal zones near Catalina Island with distinct morphological differentiations. Whether the morphological differentiation is caused by phenotypic plasticity or genetic differences remains unclear. The goal of this research is to determine whether these populations are still one species adapted to different flow regimes or have diverged into two distinct species. Samples representative of the two populations were collected and total genomic DNA extracted. The Z fragment of the large subunit of ribosomal cistron (LSU) and the mitochondrial COI gene region were amplified and sequenced. Based on the differences in polysaccharide content from the DNA extractions; distinction between these two populations is evident. Both gene regions have sufficient variation to be used to determine population differences in *Eisenia*. Sequencing and phylogenetic analyses of both gene regions for the two populations are in progress with exciting results to follow.

P011. *MICROTHAMNOS* GEN. ET SP. NOV. (TOLYPOTHRICHACEAE): A NEW GENUS OF CYANOBACTERIA ISOALTED FROM SUBAEROPHYTIC HABITATS IN NORTHEAST FLORIDA.

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Cyanobacteria are common components of freshwater and terrestrial ecosystems. Many cyanobacteria are capable of nitrogen fixation, potentially leading to blooms in aquatic habitats and providing nitrogenous compounds in terrestrial environments. While there are many studies of cyanobacteria in aquatic habitats due to their prevalence in cyanobacterial harmful algal blooms, much of their biodiversity in other habitats remains unknown. For example, the biodiversity of epiphytic and subaerial cyanobacteria remains largely unexplored. The purpose of this paper is to typify a new genus of subaerial, nitrogen-fixing cyanobacteria from epilithic habitats of Jacksonville, FL (USA). Our new isolate is filamentous and morphologically

resembles *Hassalia* with copious basal heterocytes, colorless sheaths, false branching, barrel shaped cells and adnate growth. We amplified and sequenced the 16S rDNA gene and the 16S-23S ITS region. Phylogenetic analyses employing the 16S gene revealed our new strains formed a cluster unrelated to *Hassalia sensu stricto* in a monophyletic clade with additional uncultured cyanobacterial clones from Genbank. The ITS secondary folding patterns of the Box-B and D-stem were different than those of related genera (e.g., *Hassalia*, *Tolypothrix*, etc.). Thus, we propose the erection of a new genus *Microthamnos*.

P012.A MORPHOLOGICAL AND MOLECULAR SURVEY OF ULVALES (CHLOROPHYTA) SPECIES IN THE BAY OF FUNDY REGION (NEW BRUNSWICK, CANADA)

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Herbarium collections available at the University of New Brunswick suggest that there are probably 26 genetically unique species of the order Ulvales present in the Bay of Fundy – this in stark contrast to reports in morphology-based floristic surveys. Clearly a full account of the Bay of Fundy ulvalean flora using molecular techniques is overdue. Unfortunately this task is complicated by contradictions within molecular databases regarding the application of names associated with morphospecies relative to genetic groups – unique genetic groups have been granted multiple morphospecies names, while reciprocally individual morphospecies have been linked to many genetic groups. These inconsistencies render molecular identification via sequence comparison to extant records in the various molecular databases unreliable. To alleviate this problem, our study will generate a detailed morphological description of each specimen collected from the Bay of Fundy to augment the standard DNA data. Using morphological descriptions in comparison with corresponding type descriptions, as well as considering the presence of a genetic group in the type locality, we intend to apply meaningful morphospecies names to the genetic groups present in the Bay of Fundy.

P013.7000 GENETIC CROSSTALKS BETWEEN CRYPTOPHYTE PREY AND KLEPTOPLASTIC CILIATE, *MESODINIUM RUBRUM*

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The kleptoplastic photosynthesis of the ciliate, *Mesodinium rubrum* is achieved using a consortium of cryptophyte algal organelles, including numerous plastid-mitochondrial complexes and one or more cryptophyte nuclei which is transcriptionally active (karyoklepty). It is still unknown to what extent the sequestered nuclei regulate plastid activity and organelle division in the ciliate cell. TEM and fluorescent microscopy showed that the sequestered nuclei and plastids could divide 5-6 times in the ciliate cell loosely synchronizing their division to the host cell division. To decipher genetic control of this process, we developed genomic resources from the cryptophyte *Teleaulax amphioxeia* strain CR-MAL01 and *M. rubrum* using 454 pyrosequencing. About 20% of transcripts in ciliate were from the sequestered cryptophyte

nuclei. Most (>98%) cryptophyte genes detected in the ciliate cell showed identical sequences with those of CR-MAL01 strain suggesting that there is no permanent cryptophyte endosymbiont in the ciliate cell. Time-series microarray hybridizations were carried out between mRNAs isolated from the ciliate and an oligochip consist of 15,654 primers designed from *T. amphioxeia* ESTs. The ingested cryptophycean nuclei were transcriptionally active over 13 weeks. Most cryptophyte genes (>93.9%) expressed in free living cryptophyte cell are consistently detected in the ciliate cell. However, about 40% of them showed significant change in the expression level over 2 fold; 22.4% up-regulated and 18.3% down-regulated. The cryptophyte gene regulation in the ciliate cell was not random. Most cryptophyte genes involved in light and dark reaction of photosynthesis as well as chlorophyll assimilation was consistently up-regulated and many genes involved in flagella maintenance and movement were significantly down-regulated. These results suggest that a large epigenetic modification occurred after cryptophyte nuclei sequestered to the ciliate cell.

P014.ISOLATION AND CHARACTERIZATION OF PHYTOCHROME SIGNAL TRANSDUCER FHY1 IN *SPIROGYRA VARIANS*

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The filamentous green algae *Spirogyra varians* shows different photomovement in response to red and blue light, which is mediated by phytochrome and phototropin, respectively. The filament shows typical phototropic movement to the blue light but, in red light, it shows irregular twisting movement. The combination of blue and red light response makes complicated pattern of photomovement of Spirogyra under natural light. The red light movement was reversed by a short exposure (<30s) to far-red light implied. Phytochrome regulate gene expression after it is translocated into the nucleus after conjugation with FHY1 (far-red elongated hypocotyl 1). A homologue of FHY1 gene was isolated and characterized from *Spirogyra varians*. FHY1 homologue of *Spirogyra varians* contained an NLS (nuclear localization signal) at the N-terminus and a phytochrome binding motif at the C-terminus. The phytochrome binding motif sequence showed high homology with land plants. The expression of the FHY1 gene was down regulated soon after exposure to red and far-red light. The speed of photomovement increased according to the nuclear accumulation amount of phytochrome. Our results suggest that FHY1 plays a key role in the phytochrome signal pathway in the photomovement of *Spirogyra varians*.

P015. SYSTEMATICS, PHYLOGENY AND EVOLUTION OF THE FILAMENTOUS RED ALGAE: GENUS *POLYSPHONIA SENSU LATO*

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The cosmopolitan genus *Polysiphonia sensu lato* has been composed of heterogeneous genera. Our morphological and molecular analyses of *Polysiphonia sensu lato* collected from worldwide have supported the description of 16 new species (eight already published), 15 new

combinations, and the segregation of four genera. Especially, *Neosiphonia* species have been segregated based on the three-celled carpogonial branches. Of them, *N. harveyi* complex is composed of six species. We sequenced genes from plastid (*rbc*L) and mitochondrial (*cox1*) genomes to examine the phylogeny, species status, phylogeography, and evolution of specimens belonging to this complex collected worldwide. Our data strongly support two species within this complex: *N. harveyi* and "*P. strictissima*". *Neosiphonia harveyi* is composed of seven genetic taxa described here as subspecies on the basis of DNA-based delimitation models. We also estimated the divergence time of these species using substitution rates of combined *rbc*L and *cox1* data sets. We confirm that the centre of diversity and origin is the East Asia (Korea and Japan) and that the evolution of these species may have been due to transoceanic dispersal and subsequent allopatric isolation. ;

P016. COMPARATIVE PLASTID GENOME ANALYSIS FROM THREE NEMALIOPHYCIDAE RED ALGAE

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Red algae are primarily marine with only 5% being freshwater. One of the florideophyte subclasses, Nemaliophycidae, contains three exclusively freshwater orders, six marine, and one with both freshwater and marine. It is likely that all marine and freshwater species were derived from a common ancestor followed by adaptation in these two environments. Since there are few data from freshwater species, a study of these taxa was initiated to provide insights into potential genomic differences. We sequenced plastid genomes from two freshwater species, *Kumanoa americana* (Batrachospermales) and *Thorea hispida* (Thoreales), and one marine *Palmaria palmata* (Palmariales). From comparative genome analysis of these three taxa, we determined that several plastid genes (pbsA, grx, ycf35, ycf46, ycf34, ycf37) were unique to the marine species. With all available red algal plastid genome data, we found some of the genes (pbsA, ycf35, ycf46, ycf34, ycf37) are in all marine species investigated to date. In this symposium, we will suggest a possible evolutionary scenario for the Nemaliophycidae that adapted in different habitats.

P017. FIELD APPLICATION FEASIBILITY ASSESSMENT OF THE NAPHTHOQUINONE GROUP FOR MITIGATION OF FRESHWATER DIATOM *STEPHANODISCUS* BLOOMS

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Although many algicidal substances have been developed, their field application remains a serious challenge due to their high toxicity in the ecosystem and for economic reasons. Therefore, we evaluated the claim that Naphthoquinone (NQ) derivatives can be used for the efficient mitigation of natural *Stephanodiscus hantzschii* blooms in freshwater. To select the best algicidal NQ compounds, we tested total 85 of for algicidal activity on *S. hantzschii* species. Among them, NQ 4-6 showed the highest algicidal activity (96%, ≥ 0.2 _M). We carried out an acute toxicity assessment of the new algicide and found that NQ 4-6 had advanced solubility and lower toxicity as represented by the survival rates of *Selenastrum capricornutum*, *Daphnia magna*, and *Danio rerio*, which are interconnected components of the freshwater ecosystem. NQ toxicity was not observed at the optimal algicidal-activity concentration (0.2 µM), indicating a lack of significant toxic effects. In the acute toxicity test, we found no significant difference between the NQ 4-6 treatment group at a 0.2 µM concentration and the control group for any of the three organisms. To evaluate the possibility of field application of NQ 4-6, we first performed microcosm tests. In the microcosm test (60 L), *S. hantzschii* was completely eliminated 10 days after inoculation with NQ 4-6 compound (0.2 µM). In microcosm experiments, the dynamics of the biotic (except the phytoplankton) and abiotic factors showed similar trends in the control and treatment groups. These results indicate that the NQ 4-6 compound is promising for use as a selective control for *S. hantzschii* that does not cause negative side effects in the freshwater ecosystem. Therefore, NQ 4-6 compound has potential as an alternative algicidal substance to effectively mitigate natural *S. hantzschii* blooms.

P018. DIGITIZATION AND CATALOGUING OF THE UNIVERSITY OF ALABAMA ALGAL HERBARIUM (UNA)

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The UNA herbarium was founded by Dr. Eugene Allen Smith in 1901 and named after Charles Mohr in honor of his collections. The UNA algal herbarium has been going through a recent process of modernization by databasing vouchers for public access. This database increases accessibility of the herbarium to phycological researchers. All UNA algal herbarium vouchers have been barcoded and entered into an online database for free access. The UNA specimens have been also digitized and publicly accessible through the www.macroalgae.org website. The algal vouchers were re-organized alphabetically by phyla followed by genera and then species names according to AlgaeBase. Currently, the total number of algal specimens is 1608. The number of countries represented at UNA algal herbarium is ten. As a result of our databasing and digitization work, phycologists around the world have now direct access to the UNA algal collections.

P019. MITOCHONDRIAL GENOMES FROM THE GREEN ALGAL FAMILY HYDRODICTYACEAE (SPHAEROPLEALES, CHLOROPHYCEAE)

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Green algal mitochondrial genomes are variable in size, gene content, and gene order. The class Chlorophyceae is represented by mt genomes of the order Volvocales, but the lack of characterized green algal mt genomes at finer taxonomic scales preclude a thorough understanding of green algal genome evolution. This study comprises the first within-family investigation of mt genome diversity, and the first complete genomes sequenced from Hydrodictyaceae (order Sphaeropleales). We present four completely sequenced mitochondrial genomes spanning three taxa and four phylogenetic groups, *Stauridium tetras*, *Pseudopediastrum boryanum*, and *Pediastrum* duplex. The size range of 37,723 bp to 53,560 bp is attributed to intergenic region expansion while intron diversity and gene rearrangements appear to follow phylogenetic patterns. These data provide insight and support for phylogenetic relationships among Hydrodictyaceae, and further taxon sampling could contribute to resolving systematic questions surrounding this family.

P020. MOLECULAR-ASSISTED ESTIMATE OF GREEN ALGAL DIVERSITY IN RHODE ISLAND.

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Understanding the combined threats of global climate change and biological invasions requires a comprehensive understanding of species richness patterns across the diversity of life. For many groups of organisms, molecular validation of species richness is required to account for cryptic diversity, which underestimates richness, and phenotypic plasticity, which overestimates richness. Based on a survey of the literature I project that species richness of marine algae in RI might approach 300 species, but a systematic, molecular-based evaluation of species richness has not been undertaken despite the recognition of important environmental changes occurring throughout region. Based on literature reports 80 species of marine Chlorophyta have a distribution that includes RI, but only 20 species have been specifically documented in RI. Here I present an updated account of green algal diversity in RI based on DNA Barcoding and morphological examination of recently collected specimens. Our molecular-based inventory from tufA data confirms the presence of 24 species, which includes several species that have no close sequence match in public databases and therefore might represent new distributional records. Continued morphological and molecular examination will help to resolve species identities and evaluate whether these species represent floristic changes resulting from anthropogenic stress or simply the elucidation of true patterns of diversity using more sensitive methods.

P021. THE MOLECULAR AND MORPHOLOGICAL DIVERSITY OF THE FRESHWATER GREEN ALGAL GENUS *HYDRODICTYON* (SPHAEROPLEALES, CHLOROPHYCEAE)

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The freshwater green algal genus *Hydrodictyon* comprises six recognized species, of which only three have been studied in the context of a molecular phylogeny. *Hydrodictyon reticulatum* is known for nuisance blooms in many freshwater lakes, ponds, and slow moving streams around the world, including but not limited to Australia, Southeast Asia, and the United States. Recent molecular studies have suggested that *Hydrodictyon* may be more diverse than what is currently recognized. Therefore, samples of *Hydrodictyon* were obtained from collections in the Central New York State area, preserved specimens from The New York Botanical Garden Starr Herbarium (NY), and donations from the phycological community for study. Analysis included morphological characterization and sequencing of the mitochondrial encoded nad2 and the chloroplast encoded rbcL genes. The phylogenetic results have elucidated key information regarding the diversity of *Hydrodictyon* as a whole.

P022. GENE EXPRESSION AND GENE ONTOLOGY IN TWO SPECIES OF MIXOTROPHIC ANTARCTIC PHYTOPLANKTON

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Phagotrophic phytoplankton, which both photosynthesize and consume prey, occur throughout the world's oceans and have potential for significant ecological impacts on marine food webs. We describe transcriptional expression profiles of two polar green algae, *Micromonas* sp. CCMP 2099 and *Pyramimonas tychotreta*, and evaluate differential gene expression in an attempt to identify genes involved in mixotrophy. Replicate cultures of each species were incubated under nutrient conditions that either stimulated or inhibited feeding. Ingestion rates were confirmed experimentally and replicates collected for RNA isolation and RNASeq (Illumina MiSeq). For *Micromonas* and *Pyramimonas*, reduction in nutrients resulted in differential expression (at least a 4-fold change) of 71 and 4504 genes, respectively. Gene Ontology (GO) profiles of expression patterns showed large investment in membrane and intercellular processes as well as biological processes involved in metabolism for both prasinophytes, although many expressed genes lacked well-described ontology. Although GO analysis showed responses to treatment conditions in both algae, response patterns differed between species. This study provides insight into the connection between the ecological impact of feeding and physiological functioning of mixotrophic algae from polar regions.

P023. EVALUATING HETEROTROPHIC GROWTH CAPABILITIES OF CHLAMYDOMONADALEAN ALGAE THAT SYMBIOSE WITH SPOTTED SALAMANDERS

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Chlamydomonadalean algae are well known symbionts of spotted salamanders, *Ambystoma maculatum*. Molecular work has revealed non-monophyly of the symbionts and algae. Previous work from our lab indicates that algae from eggs of a given clutch are genetically more similar than algae among clutches of a single pond, supporting a maternal contribution. We hypothesize that symbionts temporarily live within the mother and are partitioned to embryos before encapsulation. If this occurs, the algae must survive within a female's reproductive tract without photosynthesis. To evaluate this possibility, eight symbiotic strains representing three phylogenetic lineages isolated from salamander eggs of one pond were grown under both phototrophic and heterotrophic conditions. Each strain was cultured from a starting population of 250,000 cells/ml in three different media, containing Bolds Basal Medium (BBM) with and without an additional source of organic carbon, and under two different photoregimes: 16:8 L:D or 0:24 L:D. Each treatment consisted of four replicates and was grown for 16 d. Cultures were agitated every day, and populations quantified every two days using a flurometer. Results from our pilot study of two symbiotic strains indicate highest growth in BBM + 1% glucose media under both photoregimes.

P024. MORPHOLOGICAL, MOLECULAR AND PHYLOGENETIC ASSESSMENT OF *TRENTEPOHLIA ARBORUM* (ULVOPHYCEAE, CHLOROPHYTA) FROM BRAZIL

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Trentepohlia arborum is one of the most widespread algae in tropical terrestrial habitats. The goal of this study was to analyze field collected specimens in order to understand the taxonomic circumscription of this species. Specimens representing several populations from different geographic locations from Brazil were collected. Samples from natural areas located in Southern, Southeastern and Midwestern Brazil were gathered from a variety of substrata and different types of vegetation (Savanna, rainforest, Araucaria forest and seasonal semideciduous forest). Morphological data were compared vis-à-vis molecular information using the rbcL marker. Seventeen *T. arborum* populations resulted in a consistent set of morphological features (habit, shape of vegetative cells number and shape of gametangia and sporangia) and close to those of the original species description. Most Brazilian *T. arborum* strains were clustered in one large clade along with other strains with world wide distribution. Other sequences conforming the morphological description of *T. arborum* are forming a different clade with only neotropical samples. Our results are rendering *T. arboroum* as a non-monophyletic species and represent another example of cryptic speciation among terrestrial algae.

P025. IDENTITY OF THE DOMINANT BLOOM FORMING GREEN SEAWEED, *ULVA COMPRESSA*, IN JAMAICA BAY, NEW YORK

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Nitrogen pollution is a major cause of eutrophication, driving primary production in shallow estuaries such as Jamaica Bay, NY. Marine macroalgae respond to this excessive nutrient availability by enhanced growth rates and significant, often problematic, biomass accumulations. In Jamaica Bay, species of the macroalgal sea lettuce genus, *Ulva* accumulate in significant quantities during summer months. During the summer of 2013 biomass accumulations reached has high as 1 kg dry wt m-2 with an average of 250 dry wt m-2 and is similar to biomass accumulations in other highly nitrogen loaded estuaries such as Waquoit Bay, MA, Venice Lagoon, Italy, and the Yellow Sea in Qingdao, China. We identified the species of *Ulva* by comparing the tufA gene sequences of several specimens collected across a variety of environmental conditions and revealed a single species, *U. compressa*, as the primary green algal constituent of these biomass accumulations. Though identical to tufA sequences labeled as *U. compressa*, Jamaica Bay specimens exhibit a blade morphology that is inconsistent with the original description for a tubular species. While morphological variation is well established for this species, the presence of the blade-forming species *U. rigida*, confirmed by ITS rDNA sequences in another recent study in Jamaica Bay, complicates our understanding of macroalgal responses to coastal eutrophication. In order to better understand *Ulva* species richness of Jamaica Bay accumulations, sequences of the ITS rDNA are being generated from specimens exhibiting blade and tubular morphologies, from environmental samples as well as samples cultured under different laboratory conditions. In this way, we will test the hypothesis that Jamaica Bay *U. compressa* exists as both a tube and a blade, and that environmental features may control morphological expression as has been shown in other studies.

P026. CRYPTIC DIVERSITY OF ALGAL TURF COMMUNITIES IN LONG ISLAND SOUND, CONNECTICUT, USA

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Algal turf communities are highly productive and ecologically important habitats found in tropical and temperate locations. While these communities have been studied extensively in tropical habitats, species composition of algal turfs still remains largely unknown, and there is limited knowledge of algal turf communities in temperate regions. This study examines fine-scale species diversity in algal turf communities from two locations in and adjacent to New Haven Harbor in Long Island Sound, Connecticut, USA. Rarefaction curve analysis suggests that bacterial cloning was only able to partially reveal all of the community diversity within these algal turfs. Variation among algal species was observed both within and between sites, with greater diversity uncovered when using the partial SSU nuclear marker compared to the chloroplast-encoded UPA (23S). Algal species ranged from microscopic diatoms to macroalgal specimens, revealing cryptic diversity resolved by molecular analysis. This study is the first to provide insight into the species composition of temperate turf communities. Results suggest when studying these communities, though not as diverse as tropical communities, there is still much diversity to uncover.

P027. PHYLOGENETIC ANALYSIS OF CAROTENOID BIOSYNTHESIS PATHWAY GENES IN LABYRINTHULOMYCETES

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Labyrinthulomycetes are heterotrophic, basal heterokonts with fungus-like lifestyles that likely play major roles as marine decomposers. Despite their ubiquity and abundance in the oceans, they remain poorly understood. The recent sequencing of three diverse labyrinthulomycete genomes (one aplanochytrid and two thraustochytrids) is providing new insight into their physiology and ecology. Many labyrinthulomycetes synthesize xanthophylls, and we noticed the presence of rhodopsin-like genes (which would require a carotenoid-derived retinal chromophore) in both thraustochytrid genomes, so we have been investigating their potential pathways of carotenoid biosynthesis. It appears that all three labyrinthulomycetes use the mevalonate (MVP) pathway to synthesize geranylgeranyl diphosphate (GGPP). The enzymes converting GGPP to beta-carotene are fused into a unique, single protein in the two thraustochytrids, and the phytoene synthase and lycopene cyclase domains of this fused protein both show strong evidence of being acquired by horizontal gene transfer. In contrast, the squalene synthase found in all three genomes is most closely related to other heterokont genes. Genes potentially involved in converting carotenes to apocarotenoids or xanthophylls have also been identified.

P028. INTEGRATED THE BIOMASS PRODUCTION OF STARCH-RICH, SETTLEABLE GREEN MICROALGA *DESMODESMUS INSIGNIS* AND DAIRY WASTEWATER TREATMENT

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A mutual-beneficial pattern which wastewater treatment coupled with the production of clean, renewable microalgae-based biofuels has received a lot of attention. In this study, the growth, morphology, settling performance, and starch accumulation of *Desmodesmus insignis* were investigated. The removal efficiency of nitrogen and phosphorus by this microalga from dairy wastewater was also analyzed. *D. insignis* was grown in BG-11 media containing four different initial concentrations of NaNO3 (18 mmol/L, 9 mmol/L, 6 mmol/L and 3.6 mmol/L) and dairy wastewater (DWW) diluted into four concentrations (25%, 50%_75% and 100%) with Ø3.0 cm column photobioreactors. The maximum biomass concentration, total carbohydrate and starch contents were obtained in 18 m mol/L NaNO3, which were 6.23 g/L, 50.76% (d.w.) and 40.95% (d.w.), respectively. However, the highest biomass concentration and total carbohydrate content achieved in 100% DWW, which were up to 10.31g/L and 54.44% (d.w.), respectively. The peak starch content of *D. insignis* was gained in 75% of DWW with 50.88% of dry biomass. In BG-11 medium, the highest volumetric starch content (2.55 g/L) and volumetric starch productivity (0.21 g/L/d) of *D. insignis* were obtained in medium containing 9 mmol/L NaNO3. The maximum volumetric starch content and volumetric starch productivity of *D. insignis* grown in 75% of DWW reached 4.86 g/L and 0.41 g/L/d, respectively. *D. insignis* could also effectively remove nitrogen and phosphorus from different dilutions of diary wastewater. The removal efficiency reached 78.05~90.34% (N) and 95.76~98.74% (P). *D. insignish* possesses higher settling ability, and cells cultured in BG-11 medium and 75% of DWW could finish settlement within 60 and 90 minutes, respectively. This research demonstrated that starch-rich, settleable microlga *D. insignis* could be grown in dairy wastewater for feedstock production of bioethanol combined removing nitrogen and phosphorus of DWW.

P029. MORPHOLOGY AND GENOMICS OF A NEW MANTAMONAD

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Mantamonads were first described from the Irish Sea in 2011, and are a deeply branching heterotrophic eukaryote lineage with uncertain phylogenetic position. While phylogenetic analyses place mantamonads sister to either apusomonads or ancyromonads within the putative group Apusozoa, these topologies are only weakly supported. Unfortunately, all cultures of the original strains died within a year of their initial description, limiting the amount of data that could be collected from this lineage. Here we characterize a new strain of mantamonad, collected in Okinawa, using scanning electron microscopy, the first such observations for any mantamonad. Consistent with light-microscopic observations of the Irish Sea strain, the new isolate is a small plastic cell (~3–5 µm long) with a long trailing flagellum and a short, stiff anterior flagellum. We are now gathering draft genome data for the new strain as well. The addition of these new data to phylogenetic studies may clarify the relationships among the eukaryotic supergroups and help resolve the root of the tree of eukaryotes. They will also elucidate the metabolic capacities of mantamonads, and may inform our understanding of the evolution of sex and multicellularity.

P030. *WYNNEOPHYCUS GEMINATUM* GEN. ET COMB. NOV. (DELESSERIACEAE, RHODOPHYTA), BASED ON A RED ALGA PREVIOUSLY KNOWN AS *HYPOGLOSSUM GEMINATUM* OKAMURA

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Wynneophycus gen. nov. is a monotypic genus based on *Hypoglossum geminatum*, a species described by Okamura from Japan. On the basis of comparative morphology, the new species, *Wynneophycus geminatum*, is corresponded to the original description of *H. geminatum*. *Wynneophycus* is characterized by a discoid holdfast; erect or decumbent blades; blades monostromatic with percurrent midribs; branched from the axial cells of midrib; an apical cell division; several orders of lateral cell rows and paired transverse periaxial cells; the lateral cells forming second-order cell rows with all forming third-order rows; midrib becoming corticated and forming a subterete stipe below as the blade wings are lost. Distinctive features for the new genus include tetrasporangia which initiated only from 2nd-order cell rows and both pericentral cells, always situated at second- or third-order blades in 1 layer; branching in pairs on dorsal face. Phylogenetic analyses of the LSU rDNA and rbcL sequence data also support the separation of *Wynneophycus* from *Hypoglossum*. We herein report the first record of the genus, and describe *Wynneophycus geminatum* gen. et comb. nov. within the subfamily Delesserioideae.

P031. THE GENUS *CRYPTONEMIA* (HALYMENIALES, RHODOPHYTA) IN BERMUDA INCLUDING THREE NEW SPECIES AND *C. BERMUDENSIS* (COLLINS ET M. HOWE) COMB. NOV.

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Cryptonemia specimens collected in Bermuda over the past two decades were analyzed using gene sequences of LSU rDNA and rbcL as genetic markers to elucidate their phylogenetic positions. They were additionally subjected to morphological assessment and compared with historical collections from the Bermuda islands. Five species are presently found in the flora including what has traditionally been called *C. luxurians*; three new species, *C. antricola*, *C. lacunicola* and *C. perparva*; and *C. bermudensis* comb. nov. based upon *Halymenia bermudensis*. Of the seven species presently known in the western Atlantic flora, only one has been found in Bermuda. None of the specimens found in the islands could be attributed to *C. crenulata*, a species reported for Bermuda beginning in the late 1800s.

P032. TWO NOVEL CYANOBACTERIAL CONSTITUENTS ISOLATED FROM A TRIPARTITE LICHEN OF MARBLE HEADSTONES

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Cyanolichens, or lichens containing a cyanobacterial member, are common components of epilithic and epiphytic habitats throughout the world. All lichens contain at least a single photobiont, and only ca. 10% of all lichens contain cyanobacteria as their primary photobiont. The majority of tripartite lichens (those with two photosynthetic members) contain a single cyanobacterial photobiont and a green alga. The cyanobacterial member of a lichen is typically filamentous and heterocyte forming (e.g., *Nostoc*, *Calothrix*), putatively contributing carbon and nitrogenous compounds. In this paper, we describe two novel cyanobacteria isolated from a tripartite lichen containing no algal symbionts, inhabiting marble headstones (Jacksonville, FL, USA). The lichen itself is composed of the mycobiont *Fusarium oxysporum*. The first cyanobacterial constituent belongs to the widely distributed subaerial genus Chroococcidiopsis. Based on 16S rDNA gene sequence data, morphological assessments, secondary folding patterns of the ITS region, and ecological characteristics, our strain did not match any currently described taxon, and thus we propose the name *C. epilithica*. The second cyanobacterial member is filamentous and falls within the nitrogen-fixing genus *Tolypothrix*. Based on the same set of parameters, we propose *T. feralis* sp. nov. This tripartite combination of two cyanobionts living in a common layer with the mycobiont, and lacking an algal photobiont, is rare. Because both cyanobionts were also new species, epilithic lichens in subtropical Florida may represent untapped reservoirs of diversity for photooxygenic taxa.

P033. EVOLUTIONARY HISTORY OF THE ENZYMES INVOLVED IN THE CALVIN-BENSON CYCLE IN EUGLENIDS

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Euglenids are an ancient lineage that may have existed as early as two billion years ago. A mere 64 years ago, Melvin Calvin and Andrew A. Benson performed experiments on *Euglena gracilis* and elucidated the series of reactions by which carbon is fixed and reduced during photosynthesis. However, the evolutionary history of this pathway (Calvin-Benson cycle) in euglenids was more complex than Calvin and Benson could have imagined. The chloroplast present today in euglenophytes arose from a secondary endosymbiosis between a phagotrophic euglenid and a prasinophyte green alga. A long period of evolutionary time existed before this secondary endosymbiotic event took place, which allowed for other endosymbiotic events or gene transfers to occur prior to the establishment of the green chloroplast. This research revealed the evolutionary history of the major enzymes of the Calvin-Benson cycle throughout the euglenid lineage and showed that the majority of genes for Calvin-Benson cycle enzymes shared an ancestry with red algae and chromalveolates suggesting they may have been transferred to the nucleus prior to the acquisition of the green chloroplast.

P034. SHALL WE EAT? - A DESERT TARDIGRADE'S QUESTION IN FRONT OF AN ALGAE DISH

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The feeding behavior of tardigrades (water bears) living in desert soil communities is unexplored, particularly with respect to consuming algae. As a first step in investigating invertebrate grazing on desert soil algae, we have begun foraging trials. We hypothesized that algae will be taken up as food. We also hypothesized that not all algae are preferred equally as food sources. Tardigrades (*Macrobiotus* sp.) were extracted alive from biocrusts. We estimated food attractiveness by scoring proximity of grazers to algal patches in laboratory microcosms. In our first experiment, tardigrades were exposed to four eukaryotic and four prokaryotic algae species in separate microcosms. Uptake was scored by determining percent of grazers with green intestinal contents. All algae were eaten, however ANOVA showed differences in attraction scores among the algae species. We also tested whether tardigrades exhibit preference between algal taxa. Tardigrades were presented with three cyanobacteria and three eukaryotic green algae species in pairs yielding 15 taxa combinations. The Bradley-Terry model demonstrated significant differences in food preference. Our data represent first insights into the desert soil food web.

P035. DEFENSE RELATED DECADIENAL ELICITS CHANGES IN FATTY ACID & LIPID CLASS COMPOSITION IN THE DIATOM *PHAEODACTYLUM TRICORNUTUM*

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Diatoms release polyunsaturated aldehydes (PUAs), in defense to inhibit herbivore reproduction. Treatment of *Phaeodacylum tricornutum* (Pt CCMP2561), with 10 µM, decadienal (PUA, DD) altered lipid compositions. At 3hr, significant decline in saturated and unsaturated fatty acids (0.5-0.7 fold) were seen except 18:1. At 6hr, significant decrease in 14:0 (0.81 fold), 18:0 (0.74 fold) & 20:5 (0.82 fold) were reported. Significant increases in fatty acids 18:1 (1.12 fold) and 18:2 (1.46 fold) were seen. The phospholipids, PG (0.69 fold) and PS (0.36 fold) declined significantly whereas PE increased significantly (1.79 fold) at 3hr. At 6hr, significant decline in PI (0.79 fold), PS (0.28 fold) & LPG (0.56 fold) lipid classes and significant increases in PC (1.21 fold) & PE (2.7 fold) were seen. DD had no significant effect on abundant glycolipids (DGDG/MGDG). DD treatment resulted in greater decline in PUFAs than MUFAs or SFAs, which might strengthen membrane against oxidative attack. Non-polar lipids increased by 16% and 38% at 3h & 6h with DD treatment. Our data suggests that DD treatment altered certain membrane phospholipids to change membrane permeability and strengthen membrane against oxidative attack.

P036. CO-OCCURRENCE OF ANABAENOPEPTINS AND OTHER TOXINS IN MARINE AND FRESHWATER CYANOBACTERIA

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Harmful cyanobacterial blooms are causes of human and ecosystem health impacts. Cyanobacteria produce a variety of secondary metabolites, including the well-researched neuro-, hepato-, and cytotoxins. Anabaenopeptins (a group of protease inhibitors) are one of the least known cyanotoxin groups yet co-occur with these better known toxins and may result in synergistic damage to organisms. As the occurrence of this toxin class is poorly documented, freshwater and marine cyanobacterial genera were evaluated for the presence of cyanotoxins using high performance liquid chromatography/time-of-flight and triple quadrupole mass spectrometry. Co-occurrence of cyanotoxins (i.e anabaenopeptins and microcystins) was observed in 11 cyanobacterial genera, including *Microcystis*, *Anabaena*, *Planktothrix*, *Cylindrospermopsis* and *Pseudanabaena*. Six anabaenopeptins found in marine *Synechococcus* sp. were not present in a freshwater *Synechococcus* species. Among freshwater cyanobacteria, the coccoid forms accumulated less anabaenopeptins than filamentous forms. The recognition of co-occurrence of multiple cyanotoxins within single species/blooms is critical in understanding synergistic action of these co-occurring toxins found in marine and freshwater systems.

P037. *HAPTEROSIPHONIA* (CERAMIALES, RHODOMELACEAE): A NEW GENUS OF MARINE RED ALGAE FROM THE PACIFIC OCEAN.

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Polysiphonia sensu lato is one of the largest rhodophyte genera with approximately 200 species and has been composed of heterogeneous genera. This study is segregating *Hapterosiphonia* gen. nov. from *Polysiphonia* sensu lato based on morphological characters and molecular data. The new genus contains the following four new combinations, namely, *Hapterosiphonia confusa*, *H. paniculata* subsp. *paniculata*, *H. paniculata* subsp. *tapinocarpa*, and *H. sabulosia*. These four taxa are distributed in the Pacific Ocean. *Hapterosiphonia* is characterized by having rhizoids cutting off from pericentral cells, multicellular lobed terminations of rhizoids (diagnostic genus character), 8–12 ecorticated pericentral cells, procarps with a four-celled carpogonial branch, spermatangial branches arising on a furcation of the trichoblast, and tetrasporangia arranged in straight or spiral series. The generitype *H. paniculata* subsp. *paniculata* is found along the Pacific coast of South America (Peru and Chile), *H. confusa* along the Pacific coast of North America (California, USA), and *H. paniculata* subsp. *tapinocarpa* and *H. sabulosia* along the Pacific coast of Asia (Japan and Korea). Our rbcL and cox1 phylogenies revealed close relationships of *Hapterosiphonia* with the genus *Lampisiphonia* from Spain.

P038. *PTEROSIPHONIA SPINIFERA* (RHODOMELACEAE, CERAMIALES) KNOWN AS *P. ARENOSA* OR *P. PENNATA* FROM THE PACIFIC OCEAN.

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The polysiphonous genus *Pterosiphoniais* characterized by having thallus bilaterally symmetrical, erect axes with alternately distichous branches of determinate or indeterminate growth, flattened to strongly compressed, and congenital fusions of proximal parts in short laterals with main axes. Twenty one species have been currently described in the genus *Pterosiphonia*. *P. arenosa*, *P. pennata*, and *P. spinifera* have being collected from Pacific coast of South America and the Northwest Pacific region. Although the Korean *P. arenosa* was clearly distinguished in morphology and molecular analyses from the European *P. pennata*, the morphology of *P. arenosa* highly resemble to *P. spinifera* from the Peruvian Coast and did not show any relevant evidence to consider *P. arenosa* and *P. spinifera* as different entities. Our rbcL analyses also confirm the close relationship between them. Thus, based on principle of priority, the Korean *P. arenosa* should be reassigned in synonymy with the Peruvian *P. spinifera*. Our study confirms the wide occurrence of *P. spinifera* in the Pacific Ocean (Chile, Korea, and Peru) and the wide distribution of *P. pennata* in the Atlantic (Europe and Brazil).

P039. FIRST RECORD OF *NEOSIPHONIA ECHINATA* (RHODOMELACEAE, RHODOPHYTA) IN THE SOUTH PACIFIC: AN INVASIVE SPECIES SPANNING SOUTHEAST ASIA.

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Neosiphonia echinata, a well known western Atlantic species, is here reported for the first time from Indonesia and this extends its distribution into Southeast Asia. *Neosiphonia echinata* was collected from Sulawesi, Indonesia as an epiphyte on *Kappaphycus alvarezii* in a culture farm. We also collected this species from Florida, USA, and then compared their morphology and molecular data. *Neosiphonia echinata* is identified by having erect main filaments arising from prostrate filaments, numerous rhizoids cutting off from the proximal end of pericentral cells by a cross wall, four pericentral cells throughout the thallus, ecorticate axes, very long and abundant trichoblasts more than twice forked, abundant adventitious laterals, procarps with four-celled carpogonial branches, and a spiral arrangement of tetrasporangia. Our phylogenetic analyses of rbcL and cox1 indicate that *N. echinata* found in Indonesia was almost identical to material from the Western Atlantic Ocean. *N. echinata* may be categorized on the last phase of the invasion process “persistence”. The shipping trajectory western Atlantic-Mediterranean-Indonesia might be considered as the possible pathway of introduction as a consequence of ballast water and hull fouling.

P040. *POLYSIPHONIA FRESHWATERI* AND *POLYSIPHONIA KOREANA*: TWO NEW SPECIES OF *POLYSIPHONIA* (RHODOMELACEAE, RHODOPHYTA) FROM KOREA.

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Polysiphonia sensu lato comprises approximately 200 species, which are currently assigned to several different genera. To date, one of these genera, namely, *Polysiphonia*, has been reported to have 17 species. Here, we describe for the first time *P. freshwateri* sp. nov. and *P. koreana* sp. nov. from Uljin and Ulleung Island, Korea, based on morphological and molecular evidence. *Polysiphonia freshwateri* sp. nov. and *P. koreana* sp. nov. are characterized by having the typical *Polysiphonia* features. *Polysiphonia freshwateri* sp. nov. is further characterized by having abundant trichoblasts, conspicuous scar cells, and tetrasporangia arranged in spiral series. *Polysiphonia koreana* sp. nov. is further characterized by having very scarce scar cells placed between two pericentral cells, from which cicatrigenous branches arise. The results of our rbcL sequence analyses support the taxonomic placement of *P. freshwateri* sp. nov. and *P. koreana* sp. nov. within *Polysiphonia*.

P041. COLONIZATION AND ABUNDANCE OF *CHARA ZEYLANICA* IN A TROPICAL BRACKISH LAGOON.

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The native green alga *Chara zeylanica* is generally rare in Hawaii, found in freshwater streams and ponds. In 2008, an enclosed, brackish (7.5-8 ppt) 21.8 hectare lagoon with an average depth of 6 m was created in Ewa, Hawaii. *Chara* was first noted in 2011, and rapidly colonized the Lagoon bottom. SCUBA surveys in Jan 2014 revealed the average percent cover of *Chara* over the Lagoon bottom was 55 percent. Monthly surveys of *Chara* since July 2014 found coverage has increased to 89 percent, with canopy heights up to 110 cm. The presence of reproductive *Chara* individuals and its high biomass suggest the lagoon is an ideal habitat for this species. Irradiance at 6 m depth has generally been high, ranging from 136 to 508 microeinsteins per meter squared per second. Overall, the water has become clearer, with light attenuation changing from -0.48 to -0.29 per meter. The high abundance of *Chara* and increasing water clarity suggest this species is important for nutrient dynamics, and likely assists in maintaining a clear water state within the lagoon.

P042. *LYCHNOTHAMNUS BARBATUS* IN THE NEW WORLD.

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The bearded stonewort, *Lychnothamnus barbatus* (L. Meyen) H. von Leonhardi, is an aquatic macro-alga belonging to the Characeae (Charophyceae: Charophyta). This sole extant species of *Lychnothamnus* is considered rare or endangered throughout its scattered range in Europe, Asia, and Australia. In 2012, the first documented extant population of *L. barbatus* in the New World was discovered in Adams County, Wisconsin, U.S.A. Between 2012 and 2014, populations of *L. barbatus* have been confirmed in 14 lakes in Adams, Waushara, and Sauk Counties, Wisconsin. Using point-intercept aquatic plant surveys we present the known distribution and relative abundance of *L. barbatus* in each lake. Morphological and DNA sequence data confirm identification, but have yet shed little light onto the North American origin of this rare species. By continued research we seek to investigate the extent of *L. barbatus* distribution in the Midwest, whether this species is native or exotic, and how long it has occurred there.

P043. *EUGLENA* OSCILLATES BETWEEN PHOTOPHOBIA AND PHOTOPHILIA.

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Euglena are photosythetic, single-celled protists with flagella, eyespots and mouthparts. They are known to actively seek nutrients and light, although a sudden bright flash will cause them to be temporarily photophobic. This study shows a striking new phototactic behavior in euglena -— an oscillation in the preference for light. *Euglena gracilis* were placed in linear and T-shaped tracks where they had a choice of moving into or avoiding light by gathering in track compartments that were bright, dim or dark. After 100 minutes the populations were measured in each compartment. The *Euglena* oscillated between photophilia (light loving) and

photophobia (light fearing) with a period of five days. The effect was stronger in fluorescent light than in incandescent light, suggesting that the spectrum of light matters. This oscillation may be tied to the cell cycle or metabolic rhythm.

P044. A DESCRIPTION OF A NEW SPECIES OF *NODOSILINEA* (CYANOBACTERIA), ISOLATED FROM SPRINGS IN NORTHERN FLORIDA.

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Cyanobacteria are amongst the oldest and most ubiquitous known prokaryotes. Often found in aquatic environments, they may form large aggregate mats that may become planktonic, epiphytic or epipelic. The objective of this study is to characterize a novel, sub-tropical species of the recently erected genus *Nodosilinea* isolated from an epipelic habitat on the sandy bottom of a freshwater spring (Ichetucknee Springs, Florida). Though morphologically similar to members of the commonly encountered genus *Pseudanabaena*, our new taxa exhibited the presence of nodules when grown in low light levels, the apomorphic feature for *Nodosilinea*. This generic affiliation was further confirmed via genetic data (16S rDNA gene sequence) and folding structures of the 16S-23S intergenic spacer (ITS) region. We present two new strains differentiated by slight morphological disjunctions, and propose the species epithet *N. fontis* (spring-dwelling *Nodosilinea*).

P045. A NEW DIATOM SPECIES *HALAMPHORA RAPHEARCUARTA* FROM MARINE COASTAL HABITATS OF THE US ATLANTIC COAST

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The genus *Halamphora* Levkov is abundant and diverse in benthic marine coastal habitats. Species within *H. coffeaeformis* are notoriously difficult to identify because of the high degrees of phenotypic plasticity and semicryptic diversity. Our investigations of diatom communities of the mudflats and vegetated marshes along the mid-Atlantic US coast revealed the presence of at least one previously undescribed species within this complex. This new species *Halamphora raphearcuata* is characterized by arcuate raphe and straight ventral valve margin. It is most similar to *Amphora spartinetensis* Sullivan and Reimer described from the coastal marshes of the state of Delaware. *H. raphearcuata* is smaller in size, areolae and ventral striae are denser compared to those in *A. spartinetensis*. *H. raphearcuata* is also very similar to the iconotype of *A. sancti-martiali* var. *faureli* Amosse described from brackish waters in Algeria, but differs for it by the higher striae density. *H. raphearcuata* also shows similarity with *A. pannucea* Giffen in size and dorsal striae density, but the later has rounded ends while *H. raphearcuata* has slightly protracted, capitate and slightly ventrally bent ends.