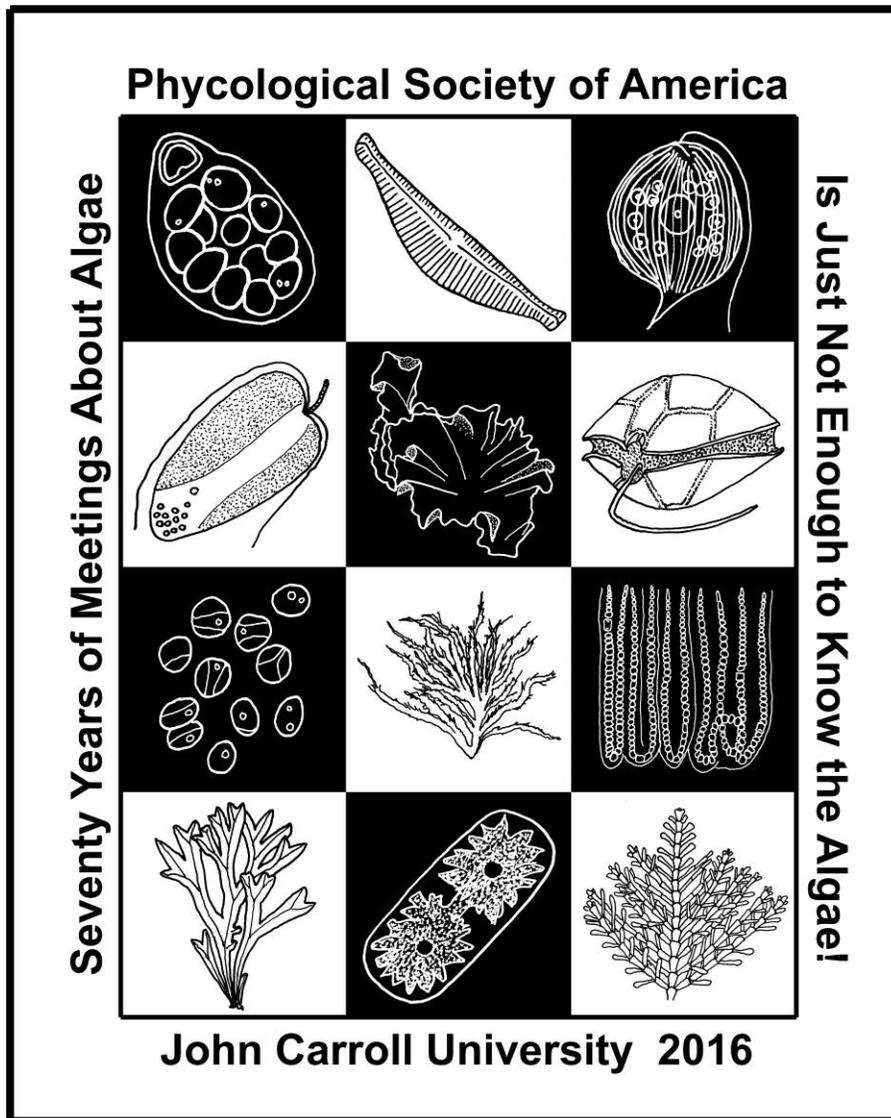


51st Annual Meeting of the Phycological Society of America



July 24-28, 2016 C.E.
John Carroll University
Cleveland Heights, Ohio



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

LOCAL ORGANIZERS FOR THE 2016 PSA ANNUAL MEETING:

Jeffrey R. Johansen, John Carroll University

Morgan L. Vis, Ohio University

PROGRAM DIRECTOR FOR 2016:

Dale Casamatta, University of North Florida

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Mariana Cabral de Oliveira, Department of Botany, Biosciences Institute, University of São Paulo, São Paulo, SP 05508-900 Brazil

Treasurer, *ex officio*

Eric Linton, Department of Biology, Central Michigan University

Meeting acknowledgements

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

Jeff Johansen, Local Organizer and general go-to person extraordinaire

Morgan Vis, Co-Local Organizer, also extraordinaire

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

Julie Wolin for her excellent field trip leading

The excellent staff at John Carroll University

Chelsea Villanueva and Jessica Brown 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:

Great Lakes Algae: Euan D. Reavie

Biofuels and Applied Phycology: Milton Sommerfeld



PSA Presidential Message

Welcome Phycophiles! We complete the Trifecta of memorable and momentous meetings in 2016 in Cleveland: The NBA Finals, The Republican National Convention and the Phycological Society of America Annual Meeting. This is the 70th yearly meeting of our society devoted to the study of algae. Local organizers, Jeff Johansen and Morgan Vis, along with Program Director, Dale Casamatta, have organized a splendid meeting. We look forward to five days of stimulating symposia, workshops, talks and posters focused on these ubiquitous photosynthesizers. We also will recognize the magnanimous gift to the PSA by our late colleague, Dr. Norma J. Lang. We are honored that members of the Lang family will be present with us to celebrate and remember Dr. Lang.

If you have any questions or concerns while at the meeting, please come to the PSA Headquarters' Room or Registration Desk.

I hope that you have a productive and enjoyable meeting.

Be Well,

Paul W. Gabrielson

PSA President 2016

Journal of Phycology

An International Journal of Algal Research



Published on behalf of the
Phycological Society of America

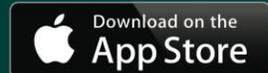


Co-Editors:
Debashish Bhattacharya, Rutgers University, USA
Michael Graham, Moss Landing Marine Laboratories, USA
Arthur Grossman, The Carnegie Institution, USA
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General Cleveland Information

The Meeting Venue

The meeting will take place on the campus of John Carroll University in University Heights, a bedroom community suburb of Cleveland, Ohio. The center for the meeting will be Dolan Center for Science and Technology, which has a large auditorium, smaller meeting rooms, a large atrium for the reception and auction, and quiet seating areas for catching up with colleagues or initiating collaborations. Housing and meals will be available on campus. Parking is plentiful and free. The campus is close to direct public transportation to the airport. The campus is a 15 minute drive to Wade Oval, which features the Cleveland Museum of Art, the Cleveland Museum of Natural History, and the Cleveland Botanical Garden. Further afield, Cleveland offers the Rock and Roll Hall of Fame and numerous restaurants, local breweries, and live music venues.

Housing Options

There is sufficient housing on campus to house all participants. You have a choice of staying in standard double dorm room with two dormitory-style bathrooms per floor (Millor Hall = \$45 per person/per night with double occupancy in the room), or a suite of two double rooms with a shared front seating area and shared bathroom (Bernet Hall = \$60 per person/per night with double occupancy in the room), or a single room within a suite (Bernet Hall = \$75 per person/per night). Prices include linens. Parking by the dorms and everywhere on campus is free. Housing is available for the entire time of the meeting, with the official program starting Sunday night the 24th and ending Friday morning, July 29th. Workshops and field trips are on Sunday before the meeting.

For couples, we recommend staying in a double occupancy room in Bernet Hall. If you wish to share the lobby and bathroom with another couple, those requests will be honored. For couples wishing to bring young children, there is no extra charge for the child/children if a bed is not required (the couple brings sleeping bags for the children). If a bed is needed, then the standard room rate applies to the child.

There are a number of hotels within a 12 minute drive from campus, if that option is preferred. These include: Homewood Suites by Hilton (\$170), Hotel Indigo Cleveland-Beachwood (\$127), Double Tree by Hilton (\$125), Embassy Suites (\$172), Aloft Beachwood (\$169), Extended Stay America (\$76), Courtyard by Marriot (\$142), Fairfield Inn and Suites by Marriott (\$147), and Hampton Inn and Suites (\$130). You will need transportation to and from the meeting venue if you elect to stay in a hotel.

Getting to Campus

The address of the university is 1 John Carroll Boulevard, University Heights, Ohio 44118. If you are coming by car, you can use an online map to learn the best route from your location. Highway 271, Chagrin exit, is the closest freeway entrance to John Carroll. From there it is 12 minutes by car.

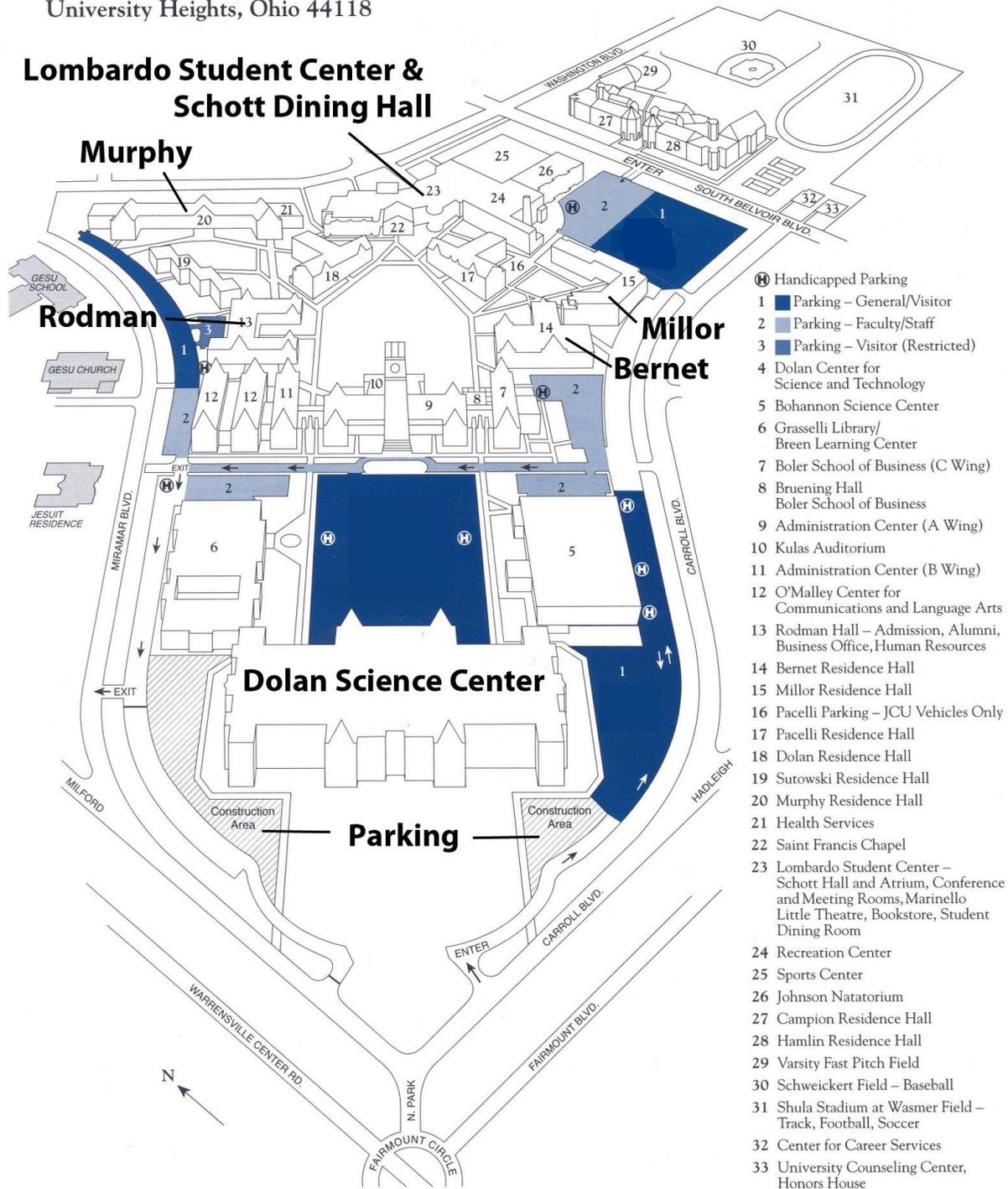
If you plan to fly, the closest airport is Cleveland Hopkins International Airport. It is about a 45 minute drive from campus, 50 minutes by train. If you elect public transportation from the airport, purchase an all-day pass (\$5, validate it there) take the Red Line which leaves from the level below baggage claim in the airport. Get off at Tower City (the only underground stop after the airport), transfer to the Green Line, which you reach by going through the control area, and take the train to the Warrensville Stop. From there, it is a 20 minute walk to campus. For those for whom a 20 minute walk is difficult, contact the local host, Jeff Johansen, and arrangements will be made to pick you up from the RTA stop at Warrensville.



John Carroll University

20700 North Park Boulevard
University Heights, Ohio 44118

Lombardo Student Center & Schott Dining Hall



There is parking all around Dolan Science Center (there are no construction areas - old map).

PSA 2016 Annual Meeting Schedule of Events

Saturday, July 23

- PSA Board of Trustees: 4:00-6:00 pm (Dolan W323)
-

Sunday, July 24

- PSA Executive Committee: 9:00-5:00 pm (Dolan W323)
- Field trip to Punderson State Park and Triangle Bog (Julie Wolin): 9:00-4:00 pm (meet outside Dolan W128)
- Workshop: *Diatom taxonomy* (Matt Julius): 9:00-5:00 p.m. (Dolan W217)
 - Workshop: *Submitting data to the electronic sequence databases: taxonomic dos and dont's* (Sean Turner): 1:00-3:30- **free and open to the public!** (Donohue Auditorium)
 - PSA Opening Reception: 6:00-9:00 (Dolan Atrium)
 - Ceremony in memory of Norma Lang
-

Monday, July 25

- Morning Plenary Lecture: *Algae in the Anthropocene: Studying human impacts using lake sediments* (John Smol, Queen's University) (Donohue Auditorium)
 - Morning Symposium: Bold Award Talks (Donohue Auditorium)
 - Contributed Papers
 - Workshop: Algae as Art- **free and open to the public!** (3:15-4:15) (Donohue Auditorium)
 - PSA Poster Session I (odd numbers) (5:30-7:00)
 - Exciting Auction (7:00-10:00) (Dolan Atrium)
-

Tuesday, July 26

- Morning Plenary Lecture: *Great Lakes: Past and Future Change* (Martin Auer, Great Lakes Research Center, Michigan Technological University) (Donohue Auditorium)
- PSA Presidential Symposium: *Algae and The Great Lakes* (Organized by Euan D. Reavie, CWE Associate Director, University of Minnesota)

- a. *Nearshore vs. Offshore cyanobacterial blooms in Lake Erie* (G.S. Bullerjahn, Bowling Green State University)
 - b. *Long-term remote sensing on Lake Erie using Landsat* (J.C. Ho, Stanford University)
 - c. *Lake Erie's re-eutrophication: degradation, adaptation, and restoration* (D.D. Kane, Defiance College)
 - d. Hypoxia in Lake Erie is mostly driven by diatoms (E.D. Reavie, University of Minnesota, Duluth)
- BBQ luncheon (with vegetarian options, of course) (Lawn in front of Schott Hall)
 - Contributed papers (Donohue Auditorium and A203)
 - Riveting PSA Business Meeting (4:00-5:30 p.m.) (Donohue Auditorium)
 - Inaugural PSA Legacy Reception (7:30-8:30 p.m. -hosted by the legendary Rick McCourt and the PSA Board of Trustees) (Alumni Lounge, Rodman Hall)
 - Evening workshop: How to publish in the *Journal of Phycology* (presented by Arthur Grossman, Kirsten Müller, and Chris Lane and the dedicated *Journal of Phycology* editorial team, 7:00-8:30) ((Dolan A203)
 - Student Social (8:30-10:00) Led by the indomitable Emily Johnston
-

Wednesday, July 27

- Morning Plenary Lecture: *Freshwater Diatom Biogeography: From 'Everything is Everywhere' to Phylogeography* (Pat Kocielek, University of Colorado, Boulder)
 - Contributed Papers
 - *Journal of Phycology* editorial lunch (12:00-2:00) (Dolan W323)
 - An Exploration of the World Class Cleveland Museum District (shuttle services provided *gratis* to Wade Oval, 5:30-9:00 p.m.)
-

Thursday, July 28

- Contributed papers
 - Afternoon workshop: *Scientific Illustration of Algae: tips and issues for preparing publication quality illustrations* (1:00-3:30) (Dolan W213)
 - PSA Poster Session II (even numbers) (3:00-4:30)
 - Luxurious PSA Banquet and Award Ceremony (6:00-10:00 p.m.) (Lombardo Student Center)
-

Monday, July 25

07:00-08:30 Breakfast (Schott Dining Hall)

8:30 Opening Remarks (Paul Gabrielson, PSA President and Jeff Johansen, Local Organizer)
(Donohue Auditorium)

9:00 *Plenary Talk- Algae in the Anthropocene: Studying human impacts using lake sediments*
(John Smol, Queen's University)

10:15-10:45 COFFEE BREAK

Bold Award Competition (Donohue Auditorium)

Session moderator: Patrick Martone, University of British Columbia

10:45 TRACING THE MOVEMENT OF THE INVASIVE ALGA *NITELLOPSIS OBTUSA*
USING GENETIC ANALYSES

Sleith, R. S., The New York Botanical Garden, United States, rsleith@nybg.org

Wehr, J., Fordham University, United States, wehr@fordham.edu

Karol, K. G., The New York Botanical Garden, United States, kkarol@nybg.org

11:00 A METABARCODING FRAMEWORK FOR FACILITATED SURVEY OF
ENDOLITHIC PHOTOTROPHS WITH TUFA

Sauvage, T. M., University of Louisiana at Lafayette, United States, tomsauv@gmail.com

11:15 MOLECULAR SYSTEMATICS AND ORGANELLAR GENOMICS OF
ULVA (ULVOPHYCEAE, CHLOROPHYTA) WITH PHYLOGENOMICS OF THE “CORE
CHLOROPHYTA

Melton III, J. T., The University of Alabama, United States, melto006@crimson.ua.edu

Lopez-Bautista, J. M., The University of Alabama, United States, jlopez@ua.edu

11:30 EXAMINATION OF ANTIBACTERIAL FATTY ACIDS SYNTHESIZED BY
MICROALGAE

Ruffell, S. E., University of Waterloo, Canada, ruffell.sarah@gmail.com

McConkey, B. J., University of Waterloo, Canada, meconkey@uwaterloo.ca

Müller, K. M., University of Waterloo, Canada, kmmuller@sciborg.uwaterloo.ca

11:45 COMPARATIVE IRRADIANCE RESPONSES OF PHOTOSYNTHETIC QUANTUM
YIELD AMONG FRESHWATER PHYTOPLANKTON PIGMENT GROUPS IN CULTURE
AND IN NATURAL COMMUNITIES

Beecraft, L., University of Waterloo, Canada, lnjbeecr@uwaterloo.ca

Watson, S. B., Environment Canada, Canada

Smith, R. E., University of Waterloo, Canada

12:00-1:15 LUNCH BREAK (Schott Dining Hall)

Systematics and Biodiversity I (Donohue Auditorium)

Session moderator: Alison Sherwood, University of Hawaii Manoa

1:15 WHY DID THE OLD GUYS GET IT RIGHT: GENES, MORPHOLOGY, AND THE DIATOM PHYLOGENY

Julius, M. L., St. Cloud State University, United States, mljulius@stcloudstate.edu

Beals, J. M., St. Cloud State University, United States, jmbeals@stcloudstate.edu

1:30 UNSUSPECTED EUKARYOTIC LIFE INHABITS THE ROLLING STONES

Krayesky-Self, S. L., University of Louisiana, Lafayette, United States, slk5014@louisiana.edu

Schmidt, W. E., University of Louisiana, Lafayette, United States,

William.schmidt.algae@gmail.com

Phung, D., University of Louisiana, Lafayette, United States, dhp3591@louisiana.edu

Henery, C., University of Louisiana, Lafayette, United States, ceh0280@louisiana.edu

Sauvage, T.M, University of Louisiana, Lafayette, United States, tomsauv@gmail.com

Camacho, O., University of Louisiana, Lafayette, United States, olgacamacho76@yahoo.com

Felgenhauer, B., University of Louisiana, Lafayette, United States, bef1918@louisiana.edu

Fredericq, S., University of Louisiana, Lafayette, United States, sfredericq@yahoo.com

1:45 ANALYSIS OF RBCL DNA SEQUENCES AND LIGHT MICROSCOPY REVEAL EXTENSIVE DIVERSITY IN CLADE IIA OF THE EUSTIGMATOPHYCEAE

Fawley, K. P., University of Arkansas at Monticello, United States, fawley@uamont.edu

Fawley, M. W., University of Arkansas at Monticello, United States, fawleym@uamont.edu

2:00 A TALE OF KIWIS, KANGAROOS, AND *LIMU*: RESOLVING MESOPHOTIC SPOROCHNALES AND *DICTYOPTERIS* SPECIES (PHAEOPHYCEAE) FROM THE HAWAIIAN ARCHIPELAGO

Spalding, H. L., University of Hawaii Manoa, United States, hspaldin@hawaii.edu

Conklin, K. Y., University of Hawaii Manoa, United States, kyconklin@gmail.com

Cyr, C., University of Hawaii Manoa, United States, ccyr@hawaii.edu

Sherwood, A. R., University of Hawaii Manoa, United States, asherwoo@hawaii.edu

2:15 *CYANOMARGARITA* GEN. NOV.: CONVERGENT EVOLUTION RESULTING IN A CRYPTIC GENUS IN CYANOBACTERIA

Shalygin, S., John Carroll University, United States; Polar-Alpine Botanical Garden-Institute, Russia, sshalygin18@jcu.edu

Shalygina, R., Institute of North Industrial Ecology Problems KSC RAS, Russia, regina_rinat@mail.ru

Johansen, J. R., John Carroll University, United States, johansen@jcu.edu

2:30 TO BE OR NOT TO BE: WILL THE REAL *CHRYSYMENIA* (RHODYMENIACEAE, RHODOPHYTA) PLEASE STAND UP?

Schmidt, W. E., University of Louisiana at Lafayette, United States,

william.schmidt.algae@gmail.com

Arakaki, N., Instituto del Mar del Perú, Callao, Peru, natyarakaki@yahoo.com

Gurgel, C. F., Universidade Federal de Santa Catarina, Brazil, f.gurgel@ufsc.br

Gabriel, D., University of the Azores, Portugal, danielalgabriel@gmail.com
Norris, J. N., Smithsonian Institution, United States, norrisj@si.edu
Ballantine, D., Smithsonian Institution, United States, ballantined@si.edu
Fredericq, S., University of Louisiana at Lafayette, United States, slf9209@louisiana.edu

2:45- 3:15 AFTERNOON COFFEE BREAK

Algae as Art Workshop (3:15-4:15) AN OCEAN GARDEN: SEAWEED AND THE CONVERGENCE OF ART AND SCIENCE. Presented by Josie Iselin, Loving Blind Productions (Donohue Auditorium)

Josie Iselin will discuss her studio techniques for capturing the magnificence of marine algae from California and the Atlantic coasts as well as her process for making her many books on forms in nature and how as an artist she has been drawn into writing the science of seaweed by the intertidal portraits she creates. She will conclude with a brief discussion of the kelp forest situation on the northern coast of California.

Monday Evening

PSA Poster Session (5:30-7:00) (odd numbered posters) Poster set up will be available starting on Sunday, July 24

PSA Auction (7:00-10:00) (Dolan Atrium)

Tuesday, July 26

07:00-08:30 Breakfast (Schott Dining Hall)

8:15 *Plenary Talk: Great Lakes: Past and Future Change* (Auer M., Great Lakes Research Center, Michigan Technological University) (Donohue Auditorium)

PSA Presidential Symposium: Algae and The Great Lakes (Organized by Euan D. Reavie, CWE Associate Director, University of Minnesota) (Donohue Auditorium)

9:15 *Nearshore vs. Offshore cyanobacterial blooms in Lake Erie* (G.S. Bullerjahn, Bowling Green State University)

9:55-10:30 COFFEE BREAK

10:30 *Long-term remote sensing on Lake Erie using Landsat* (J.C. Ho, Stanford University)

11:10 *Lake Erie's re-eutrophication: degradation, adaptation, and restoration* (D.D. Kane, Defiance College)

11:50 *Hypoxia in Lake Erie is mostly driven by diatoms* (E.D. Reavie, University of Minnesota, Duluth)

12:30-1:45 LUNCH BREAK BBQ luncheon (with vegetarian options, of course) (In front of Schott Dining Hall)

Systematics and Biodiversity II (Donohue auditorium)

Session moderator: Heather Spalding, University of Hawai'i at Mānoa

1:45 HAVE MARINE ANIMAL CONSERVATION LAWS CAUSED THE DECLINE OR EXTIRPATION OF MACROALGAL POPULATIONS OVER THE PAST CENTURY IN BERMUDA?

Schneider, C. W., Trinity College, United States, cschneid@trincoll.edu

Flook, C. T., Bermuda Aquarium, Museum & Zoo, Bermuda, Seaflook@gmail.com

2:00 *NOSTOC AND MOJAVIA SPECIES ISOLATED FROM THE SOILS OF THE ATACAMA DESERT, CHILE*

Baldarelli, L. M., John Carroll University, United States, lauren.m.baldarelli@gmail.com

Johansen, J. R., John Carroll University, United States, johansen@jcu.edu

Pietrasiak, N., New Mexico State University, United States, npietras@nmsu.edu

2:15 THERE ARE MORE THAN ONE GENERA OF ZOOXANTHELLAE FROM MARINE INVERTEBRATES

Lee, J. J., CCNY of City University of New York, United States, JLee@ccny.cuny.edu

2:30 PHYLOGENY OF THE POLYPHYLETIC GENUS *CYLINDROCYSTIS*
(ZYGNETOPHYCEAE) AND ITS RELATION TO FILAMENTOUS
ZYGNETATALEANS

McCourt, R. M., Academy of Natural Sciences of Drexel University, United States,
rmccourt@gmail.com

Adair, J. C., Academy of Natural Sciences of Drexel University, United States,
jca57@drexel.edu

Hall, J. D., University of Maryland, United States, jdhall@umd.edu

2:45 *NOSTOC OROMO SP. NOV.* (NOSTOCALES, CYANOBACTERIA) FROM
ETHIOPIA, A NEW SPECIES BASED ON MORPHOLOGICAL AND MOLECULAR
EVIDENCE

Mesfin, M., John Carroll University, United States, melaku.mesfin54@gmail.com

Johansen, J. R., John Carroll University, United States, johansen@jcu.edu

3:00 EXPLORATION OF *PLAKOBRANCHUS SP.* KLEPTOPLAST DIVERSITY IN THE
MAIN HAWAIIAN ISLANDS USING A METABARCODING APPROACH

Wade, R. M., University of Hawaii at Manoa, United States, rmwade@hawaii.edu

Conklin, K. Y., University of Hawaii at Manoa, United States, kyconklin@hawaii.edu

Sherwood, A. R., University of Hawaii at Manoa, United States, asherwoo@hawaii.edu

3:15 MORPHOLOGICAL AND GENETIC DIVERSITY IN THE CARBONATE-BORING
CYANOBACTERIUM *MASTIGOCOLEUS TESTARUM* LAGERHEIM EX BORNET &
FLAHAULT

O'Kelly, C. J., Friday Harbor Laboratories, University of Washington, United States,
cjaokelly@gmail.com

Mottet, G. J., Friday Harbor Laboratories, University of Washington, United States,
gjmottet@gmail.com

Palinska, K. A., University of Oldenburg, Germany, katarzyna.palinska@uni-oldenburg.de

Golubic, S., Boston University, United States, golubic@bu.edu

Tuesday Afternoon/Evening

Riveting PSA Business Meeting (4:00-5:30) (Donohue Auditorium)

Inaugural PSA Legacy Reception (7:30-8:30 p.m. -hosted by the legendary Rick McCourt and the PSA Board of Trustees) (Alumni Lounge, Rodman Hall)

Evening workshop: How to publish in the Journal of Phycology (presented by Arthur Grossman, Kirsten Müller, and Chris Lane and the dedicated *Journal of Phycology* editorial team, 7:00-8:30) (Dolan A203)

PSA Student Social (Emily Johnston) (8:30-10:00) Jake's Speak Easy - Basement of Pizzaz

Wednesday, July 27

07:00-08:30 Breakfast (Schott Dining Hall)

8:30 **Plenary Session: Freshwater Diatom Biogeography: From 'Everything is Everywhere' to Phylogeography** (Pat Kociolek, University of Colorado, Boulder)

Frontiers in Population Biology/Biogeography (Donohue Auditorium)

Session moderator: Suzanne Fredericq, University of Louisiana at Lafayette, United States

9:45 A METABARCODING COMPARISON OF AIRBORNE ALGAE FROM WINDWARD AND LEEWARD OAHU, HAWAII

Sherwood, A. R., University of Hawaii, United States, asherwoo@hawaii.edu

Dittbern, M. N., University of Hawaii, United States, dittbern@hawaii.edu

Johnston, E. T., University of Hawaii, United States, etjohn@hawaii.edu

Conklin, K. Y., University of Hawaii, United States, kyconklin@gmail.com

10:00 BIOGEOGRAPHY OF CORALLINE ALGAE (RHODOPHYTA) BASED ON DNA SEQUENCED TAXA: A FIRST SYNTHESIS

Gabrielson, P. W., University of North Carolina, Chapel Hill, United States,

drseaweed@hotmail.com

Martone, P. T., University of British Columbia, Canada, pmartone@interchange.ubc.ca

Hind, K. R., University of British Columbia, Canada, katy.hind@gmail.com

Hernandez-Kantun, J. J., Smithsonian Institution, United States, jaz1083@gmail.com

Adey, W. H., Smithsonian Institution, United States, adeyw@si.edu

10:15 INTRASPECIFIC SUCCESSION WITHIN *PSEUDO-NITZSCHIA PUNGENS* POPULATIONS IN SOUTHERN KOREAN COASTS VIA USE OF QUANTITATIVE PCR ASSAY

Kim, J. H., Hanyang University, South Korea, diatomist.jin@gmail.com

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Kim, J., Hanyang University, South Korea, ikart00@nate.com

Choi, H., Hanyang University, South Korea, hjchoi426@hanmail.net

Kim, S., Hanyang University, South Korea, brigantia@naver.com

Lee, H., Hanyang University, South Korea, fmfqh@hanmail.net

Han, M., Hanyang University, South Korea, hanms@hanyang.ac.kr

Biofuels (Dolan A204)

Session moderator: Nagwa Mohammady, Alexandria University, Egypt

9:45 ASSESSMENT OF ALTERATIONS IN METABOLOMICS AND LIPIDOMICS OF *NANNOCHLOROPSIS SALINA* IN RESPONSE TO COLD STRESS

Willette, S. M., New Mexico State University, United States, stephwi@nmsu.edu
Gill, S. S., New Mexico State University, United States, sabagill@nmsu.edu
Dungan, B., New Mexico State University, United States, bdungan@nmsu.edu
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St. Hilaire, R., New Mexico State University, United States, rsthilai@nmsu.edu
Holguin, F. O., New Mexico State University, United States, frholgui@nmsu.edu;

10:00 DEVELOPING AN EVOLUTIONARY ROADMAP TO HIGH LIPID
ACCUMULATING DIATOMS: A COMPARITIVE PHYLOGENETIC EVALUATION OF
THE GENUS *HALAMPHORA*

Stepanek, J. G., University of Colorado Boulder, United States, joshua.stepanek@colorado.edu
Kociolek, J. P., University of Colorado Boulder, United States, patrick.kociolek@colorado.edu

10:15 AN ASSESSMENT STUDY ON PILOT SCALE UNIALGAL CULTURE OF
NANNOCHLOROPSIS SP. FOR BIOCHEMICALS AND BIODIESEL PRODUCTION

Mohammady, N. G-E., Alexandria University, Egypt, nagwa_phyco@yahoo.com
ElDiwani, G.; El Khatib K.; Abdel Alim, S.; Kamal, N.; El Arabi, R.

10:30-11:00 COFFEE BREAK

HABS/ Algae and Human Affairs (Donohue Auditorium)

Session moderator: Wayne Litaker, National Oceanic and Atmospheric Administration

11:00 CLADISTIC ASSESSMENT OF CYANOTOXIN PRODUCTION IN MARINE,
FRESHWATER, AND TERRESTRIAL CYANOBACTERIAL ISOLATES

Huang, I., Texas A&M University-Corpus Christi, United States, wade76924@gmail.com
Pietrasiak, N., New Mexico State University, United States, npietras@nmsu.edu
Allen, E., North Carolina State University, United States, ehallen@ncsu.edu
Burkholder, J. M., North Carolina State University, United States, joann_burkholder@ncsu.edu
Gobler, C. J., Stony Brook University, United States, Christopher.Gobler@stonybrook.edu
Casamatta, D. A., University of North Florida, United States, dcasamat@unf.edu
Zimba, P. V., Texas A&M University-Corpus Christi, United States, paul.zimba@tamucc.edu

11:15 EFFECT OF SMALL SCALE TURBULENCE ON THE GROWTH AND
METABOLISM OF *MICROCYSTIS AERUGINOSA*

Wilkinson, A. A., University of Minnesota, United States, ahlve002@umn.edu
Hondzo, M., University of Minnesota, United States, mhondzo@umn.edu
Guala, M., University of Minnesota, United States, mguala@umn.edu

11:30 MODELING *GAMBIERDISCUS* GROWTH IN THE CARIBBEAN AND GULF OF
MEXICO AND POTENTIAL FOR ASSESSING THE RISK OF CIGUATERA FISH
POISONING

Kibler, S. R., NOAA, United States, steve.kibler@noaa.gov
Davenport, E. D., NOAA, United States, Eric.Davenport@noaa.gov
Tester, P. A., OceanTester, Inc., United States, patrica.tester@noaa.gov
Litaker, R. W., University of North Carolina, United States, wayne.litaker@noaa.gov

11:45 CHRONIC DIETARY EXPOSURE TO A CYANOBACTERIAL TOXIN, BMAA, CAUSES HUMAN NEURODEGENERATIVE DISEASE

Metcalf, J. S., Brain Chemistry Labs, The Institute for Ethnomedicine, United States, james@ethnomedicine.org

Mash, D. C., University of Miami, Miller School of Medicine, United States, DMash@med.miami.edu

Davis, D. A., University of Miami, Miller School of Medicine, United States, d.davis12@med.miami.edu

Powell, J. T., Brain Chemistry Labs, the Institute for Ethnomedicine, United States, jpowell@ethnomedicine.org

Bradley, W. G., University of Miami, Miller School of Medicine, United States, Wbradley@med.miami.edu

Banack, S. A., Brain Chemistry Labs, The Institute for Ethnomedicine, United States, sandra@ethnomedicine.org

Cox, P. A., Brain Chemistry Labs, The Institute for Ethnomedicine, United States, paul@ethnomedicine.org

12:00 THE AUDUBON PARK LAGOON NANOSAFARI: INVESTIGATING AN IPAD APP AS A LEARNING TOOL TO LINK MICROSCOPIC ORGANISMS AND PEOPLE VISUALLY

Wee, J.L. Dept. of Biological Sciences, Loyola University New Orleans, New Orleans, LA

Thomas, A.K., Dept. of Biological Sciences, Loyola University New Orleans, New Orleans, LA

Slugher, C.L., Dept. of Biological Sciences, Loyola University New Orleans, New Orleans, LA

Hood, C.S., Dept. of Biological Sciences, Loyola University New Orleans, New Orleans, LA

Underwood, L.E., Dept. of Biological Sciences, Loyola University New Orleans, New Orleans, LA

12:15-1:45 LUNCH BREAK (Schott Dining Hall)

Evolution/Genomics (Donohue Auditorium)

Session moderator: xxxxxx

1:45 GENOMICS SOLVES THE MYSTERY: PALMOPHYLLOPHYCEAE CLASS. NOV. IS THE DEEPEST-BRANCHING LINEAGE OF THE CHLOROPHYTA

Leliaert, F., Ghent University, Belgium, frederik.leliaert@gmail.com

Tronholm, A., Florida International University, USA, ana@tronholm.com

Lemieux, C., Université Laval, Canada, claudelemieux@bcm.ulaval.ca

Turmel, M., Université Laval, Canada, monique.turmel@bcm.ulaval.ca

DePriest, M.S., The University of Alabama, USA, msdepriest@crimson.ua.edu

Bhattacharya, D., Rutgers University, USA, bhattacharya@aesop.rutgers.edu

Karol, K.G., The New York Botanical Garden, USA, kkarol@nybg.org

Fredericq, S., University of Louisiana at Lafayette, slf9209@louisiana.edu

Zechman, F.W., Humboldt State University, USA, fwz1@humboldt.edu

Lopez-Bautista, J.M., The University of Alabama, USA, jlopez@ua.edu

2:00 GOING, GOING, GONE? THE FATE OF PHOTOSYNTHESIS GENES IN A RED ALGAL ALLOPARASITE

Salomaki, E. D., University of Rhode Island, United States, eric.salomaki@gmail.com

Lane, C. E., University of Rhode Island, United States, clane@uri.edu

2:15 REDUCED ALGAL GENOMES REVEAL INSIGHTS INTO THE EVOLUTION OF PRE-MRNA SPLICING

Wong, D., University of British Columbia, Canada, donald.wong@alumni.ubc.ca

Grisdale, C. J., University of British Columbia, Canada

Fast, N. M., University of British Columbia, Canada

2:30 ELUCIDATING RETROGRADE SIGNAL TRANSDUCTION PROCESSES IN THE DIATOM *PHAEODACTYLUM TRICORNUTUM*

Agarwal, A., Rutgers, The State University of New Jersey, United States,

ananya.agarwal@rutgers.edu

Levitan, O., Rutgers, The State University of New Jersey, United States,

levitan@marine.rutgers.edu

Falkowski, P. G., Rutgers, The State University of New Jersey, United States,

falko@marine.rutgers.edu

2:45 CONFLICTING EVIDENCE FOR HORIZONTAL GENE TRANSFER IN *SCYTONEMA HYALINUM*

Johansen, J. R., John Carroll University, United States, johansen@jcu.edu

Mareš, J., Hyrobiology Institute, České Budějovice, Czech Republic, jan.mares@centrum.cz

Pietrasiak, N., New Mexico State University, United States, npietras@nmsu.edu

3:00-3:30 COFFEE BREAK

Systematics and Biodiversity III (Donohue Auditorium)

Session moderator: Maria Oliveira, University of Sao Paulo, Brazil

3:30 EXTRAORDINARY DIVERSIFICATION OF THE ALGA *NANNOCHLOROPSIS* (EUSTIGMATOPHYCEAE) UPON TRANSITION FROM MARINE TO FRESHWATER

Fawley, M. W., University of Arkansas at Monticello, United States, fawleym@uamont.edu

Fawley, K. P., University of Arkansas at Monticello, United States, fawley@uamont.edu

3:45 FIRST REPORT OF AN ENDOLITHIC SPECIES OF *RHODOSORUS* GEITLER GROWING INSIDE LITHOTHAMNION RHODOLITHS FROM LOUISIANA

Phung, D. H., University of Louisiana.edu, United States, dhp3591@louisiana.edu

Krayesky-Self, S. L., University of Louisiana, Lafayette, United States,

sherrykrayself@gmail.com

Schmidt, W. E., University of Louisiana, Lafayette, United States,

william.schmidt.algae@gmail.com

Fredericq, S., University of Louisiana, Lafayette, United States, sfredericq@yahoo.com

4:00 CHARACTERISING THE LIVING PROKARYOTIC MICROBIOME OF THE CALCIFIED RED ALGA *CORALLINA OFFICINALIS*

Brodie, J., Natural History Museum, United Kingdom, j.brodie@nhm.ac.uk

4:15 GENOME BASED PHYLOGENY OF RED ALGAE PROVIDES A ROBUST FRAMEWORK FOR INFERRING EVOLUTION OF KEY CELLULAR TRAITS

Qiu, H., Rutgers University, United States, huan.qiu.bio@gmail.com

Yoon, H. S., Sungkyunkwan University, South Korea

Bhattacharya, D., Rutgers University, United States

4:30 REVISING *CHARA* SUBSECTION WILLDENOWIA

Gottschalk, S. D., Fordham University, United States, sgottschalk@fordham.edu

McCourt, R. M., Academy of Natural Sciences of Drexel University, United States, rmm45@drexel.edu

Karol, K. G., New York Botanical Garden, United States, kkarol@nybg.org

4:45 PHYLOGENETIC POSITION REEVALUATION OF *KYRTUTHRIX* AND DESCRIPTION OF A NEW SPECIES *K. HUATULCENSIS* FROM MÉXICO'S PACIFIC COAST

Leon Tejera, H. P., Departamento de Biología Comparada, Facultad de Ciencias, UNAM, Mexico, hileont@gmail.com

Wednesday Evening

An Exploration of the World Class Cleveland Museum District (shuttle services provided *gratis* to Wade Oval, 5:30-9:00 p.m.)

Wade Oval Wednesday: Live zydeco music, food vendors, the movie *Tomorrowland*

Cleveland Museum of Art: open until 9:00 (free)

Cleveland Botanical Garden: open until 9:00 (\$11 admission)

Cleveland Museum of Natural History: open until 10:00 (\$15 admission)

Barking Spider Tavern: Guitarist Drew Gibson (6:00-7:30 p.m.) (and beers)

Thursday, July 28

07:00-08:30 Breakfast (Schott Dining Hall)

SYMPOSIUM: Applied Phycology. Algae for the 21st Century (Donohue Auditorium)

Coordinator: Milton Sommerfeld

SESSION 1: EDUCATION AND TRAINING: GETTING TO KNOW AND WORK WITH MICROALGAE This session provides a brief overview of the DOE-funded Algae Testbed Public Private Partnership (ATP³), the role of AzCATI and UTEX in education and training of scientists, practitioners, and students in the application of algae to the water-energy-environment-food nexus and brief examples of the types of modules that are part of the quarterly Education and Training Workshops on microalgae that focus on hands-on learning experiences. Session Leader: Thomas Dempster

9:00 OVERVIEW OF ATP³ EDUCATION AND TRAINING WORKSHOPS
Dempster, T. A., Arizona State University, United States, dempster@asu.edu

9:15 INTRODUCTION TO MICROALGAE
Sommerfeld, M., Arizona State University, United States, milton.sommerfeld@asu.edu

9:30 NATURAL PRODUCTS FROM MICROALGAE
Manning, S., University of Texas at Austin, schonna.manning@utexas.edu

9:45 Questions/Discussion

10:00-10:30 COFFEE BREAK

APPLIED PHYCOLOGY SESSION II: METHODS AND SOLUTIONS Session leader:
Schonna Manning

10:30 MOLECULAR AND PHYTOCHEMICAL METHODS FOR THE DETECTION OF THE HARMFUL BLOOM-FORMING ALGA, *PRYMNESIUM PARVUM* CARTER (HAPTOPHYTA)
Sommerfeld, M., Arizona State University, United States, milton.sommerfeld@asu.edu

10:45 USE OF MICROALGAE TO MITIGATE CARBON DIOXIDE EMISSIONS FROM SALT RIVER PROJECTS'S CORONADO GENERATING STATION IN SAINT JOHN'S, ARIZONA
Dempster, T. A., Arizona State University, United States, dempster@asu.edu

11:00 EVALUATION OF NUTRIENT BIOEXTRACTION CAPACITY OF SEAWEED AQUACULTURE IN KOREA
Kim, J. K., Incheon National University, South Korea, jang.kim@inu.ac.kr

Han, T., Incheon National University, South Korea, hanalgae@inu.ac.kr
Seo, E., Incheon National University, South Korea
Jang, S. J., Incheon National University, South Korea
Kim, Y. E., Incheon National University, South Korea
Jung, J. W., Incheon National University, South Korea
Yarish, C., University of Connecticut, United States, charles.yarish@uconn.edu

11:15 CHEMICAL TREATMENT TO CONTROL ZOOPLANKTON CONTAMINANTS FOR SUSTAINABLE ALGAL CULTIVATION

Wang, Y., Arizona State University, United States, ywang187@asu.edu
Eustance, E., Arizona State University, United States, everett.eustance@asu.edu
Sommerfeld, M. R., Arizona State University, United States, milton.sommerfeld@asu.edu

11:30 GLYPHOSATE HERBICIDE TOXICITY TO NATIVE HAWAIIAN MACROALGAL AND SEAGRASS SPECIES

Kittle, R. P., University of Hawaii at Hilo, United States, rkittle@hawaii.edu
McDermid, K. J., University of Hawaii at Hilo, United States, mcdermid@hawaii.edu

11:45 MARINE PLANT AQUACULTURE IN SOUTHEAST ALASKA

Stekoll, M. S., University of Alaska Southeast, United States, msstekoll@alaska.edu
Peeples, T. N., Premium Oceanic, United States, tamsen@premiumoceanic.com

Cell Biology (Dolan W204)

Session Moderator: Martha Cook, Illinois State University, United States

10:30 BUOYANCY MODULATION IN AFLAGELLATE MARINE PHYTOPLANKTON: A BIOENERGETICS ANALYSIS

Lavoie, M., Laval University, Canada, michel.lavoie.4@ulaval.ca
Raven, J. A., University of Dundee, United Kingdom, j.a.raven@dundee.ac.uk
Levasseur, M., Laval University, Canada, maurice.levasseur@bio.ulaval.ca

10:45 SETA STRUCTURE IN MEMBERS OF THE COLEOCHAETALES (STREPTOPHYTA)

Rockwell, T. R., Illinois State University, United States, timr.rockwell@gmail.com
Wilcox, L. W., University of Wisconsin-Madison, United States, lwwilcox@wisc.edu
Cook, M. E., Illinois State University, United States, mecook1@ilstu.edu

11:00 HAVE HOST? WILL GROW: RED ALGAL PARASITE DEVELOPMENT

Freese, J. M., University of Rhode Island, United States, jillian_freese@uri.edu
Lane, C. E., University of Rhode Island, United States, clane@uri.edu

11:15 REMODELING INTERMEDIATE METABOLISM TO ENHANCE LIPID PRODUCTION IN *PHAEODACTYLUM TRICORNUTUM*

Levitan, O., Rutgers University, United States, levitan@marine.rutgers.edu
Agarwal, A., Rutgers University, United States, aa1041@scarletmail.rutgers.edu
Dinamarca, J., Rutgers University, United States, jotadin@gmail.com
Falkowski, P. G., Rutgers University, United States, falko@marine.rutgers.edu

11:30 VIDEO MICROSCOPY OF ZOOSPORANGIAL RELEASE OF THE MULTI-FLAGELLATED ZOOSPORE OF VAUCHERIA SESSILIS: WHY DOES IT SPIN?

Ott, D. W., The University of Akron, United States, dott@uakron.edu

Urzay, J., Center for Turbulence Research, Stanford University, United States, jurzay@stanford.edu

Prakash, M., Department of Bioengineering, Stanford University, United States, manup@stanford.edu

11:45 A NOVEL ANTIFOULING DEFENSE STRATEGY FROM RED SEAWEED: EXOCYTOSIS AND DEPOSITION OF FATTY ACID DERIVATIVES AT THE CELL WALL SURFACE

Paradas, W. C., Instituto de Pesquisas Jardim Botânico Rio de Janeiro, Brazil, wladimirparadas@gmail.com

Salgado, L. T., Instituto de Pesquisas Jardim Botânico Rio de Janeiro, Brazil, lsalgado.jbrj@gmail.com

Pereira, R. C., Universidade Federal Fluminense, Brazil, rcrespo@id.uff.br

Hellio, C., Université de Bretagne Occidentale, France, claire.hellio@gmail.com

Amado-Filho, G. M., Instituto de Pesquisas Jardim Botânico Rio de Janeiro, Brazil, gfilho@jbrj.gov.br

12:00-1:30 LUNCH BREAK (Schott Dining Hall)

Afternoon workshop

Scientific Illustration of Algae: tips and issues for preparing publication quality illustrations (presented by the epic Chris Sheil, 1:00-3:30) (Dolan W213)

Ecology

Session Moderator: Morgan Vis, Ohio University, United States

1:30 DOES PHOSPHORUS LIMITATION AFFECT BIOFILMS IN AMD AND REMEDIATED STREAMS?

Keil, E. J., Ohio University, United States, ek404609@ohio.edu

Drerup, S. A., Ohio University, United States, sd136405@ohio.edu

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

1:45 CORALLINE DIVERSITY ALONG A KELP FOREST DENSITY GRADIENT: HOW BARREN ARE URCHIN BARRENS?

Martone, P. T., University of British Columbia, Canada, pmartone@mail.ubc.ca

Hind, K. R., University of British Columbia, Canada, katharine.hind@botany.ubc.ca

2:00 LIGHT AND ZOOBENTHIC PRODUCTION IN LAKES: TIGHT COUPLING BETWEEN ATTACHED ALGAL PRODUCTION AND THE GENERALIST CONSUMER, *CHIRONOMUS DILUTUS*

Fazekas, H. M., Wright State University, United States, vooss.14@wright.edu

Vadeboncoeur, Y., Wright State University, United States, yvonne.vadeboncoeur@wright.edu

2:15 WHEN ALGAE ARE THE MENU, DIATOMS ARE THE ENTRÉE OF CHOICE FOR *TROPHEUS BRICHARDI* OF LAKE TANGANYIKA

Vadeboncoeur, Y., Wright State University, United States, yvonne.vadeboncoeur@wright.edu

2:30 REDUCED SALINITY AND LOWERED TEMPERATURE AS POTENTIAL BARRIERS FOR THE DISPERSAL OF SARGASSUM HEMIPHYLLUM VAR. CHINENSE ALONG NORTHERN WEST PACIFIC COASTS

Kam, Y. L., Marine Science Laboratory, The Chinese University of Hong Kong, Hong Kong, kambio57@gmail.com

Ang, P., Marine Science Laboratory, The Chinese University of Hong Kong, Hong Kong, putang@cuhk.edu.hk

Thursday Afternoon/ Evening

Workshop: *Scientific Illustration of Algae: tips and issues for preparing publication quality illustrations* (presented by the epic Chris Sheil, 1:00-3:30) (Dolan W213)

PSA Poster Session II, even numbers (3:00-4:30) Poster set up will be available starting on Sunday, July 24

PSA Banquet and Award Ceremony (6:00-10:00 p.m.) (Lombardo Student Center)

2016 PSA Annual Meeting Abstracts

Please note that presenting authors are underlined.

Invited Symposia

Algae and the Great Lake Symposium

NEARSHORE VS. OFFSHORE CYANOBACTERIAL BLOOMS IN LAKE ERIE

Bullerjahn, G. S., Biological Sciences, Bowling Green State University, Bowling Green Ohio, bullerj@bgsu.edu

McKay, R. M., Biological Sciences, Bowling Green State University, Bowling Green Ohio, rmmckay@bgsu.edu

Rozmarynowycz, M., Biological Sciences, Bowling Green State University, Bowling Green Ohio, markjr@bgsu.edu

Davenport, E., Biological Sciences, Bowling Green State University, Bowling Green Ohio

Tuttle, T., Biological Sciences, Bowling Green State University, Bowling Green Ohio

Watson, S. B., Environment and Climate Change Canada, Canadian Centre for Inland Waters, Burlington, Ontario, Sue.Watson@ec.gc.ca

Davis, T., NOAA-GLERL, Ann Arbor, Michigan, Timothy.davis@noaa.gov

Whereas much attention has been devoted to studying the *Microcystis* harmful algal bloom (HAB) events in western Lake Erie, tributary sites are often affected by persistent blooms of *Planktothrix*, a filamentous microcystin-producing cyanobacterium. Our lab is examining the factors allow these organisms to occupy different ecological niches. Regarding *Planktothrix*, HABs are typically of longer duration (May-October), routinely yielding microcystin levels in excess of 20 ppb. In agreement with prior studies on the *Planktothrix* bloom in Grand Lake St. Marys (OH), Sandusky Bay midsummer dissolved inorganic N concentrations often fall below detection, and bottle assays indicate that enhancement of bloom conditions is dependent on N additions, rather than P. Losses of N in Sandusky Bay are attributed in part to high rates of denitrification in the sediments. We hypothesize that N availability is a major driver of *Planktothrix* dominance in the Bay, distinct from open water *Microcystis* HABs in which P is traditionally viewed as the key factor for biomass production. Indeed, work in other labs has shown that *Microcystis* is an effective scavenger for P. The success of *Planktothrix* in an N-limited system is notable given that this genus is not an N fixer, but metagenomic analyses reveal a diverse heterotrophic bacterial community of N fixers contributing new N into the system. Analysis of Sandusky Bay qPCR, metagenomes and 16S iTags also reveals that the bloom is largely populated with nontoxic *Planktothrix* genotypes, and that *Planktothrix* presence and abundance is correlated with N speciation. With respect to offshore *Microcystis* blooms, we are examining diel metatranscriptomes from the 2014 HAB that temporarily shut down the Toledo water supply. Currently, we are analyzing gene expression patterns for functions associated with photosynthetic electron transfer, P scavenging and microcystin synthesis.

LONG-TERM REMOTE SENSING ON LAKE ERIE USING LANDSAT

Ho, J. C., Dept. of Civil & Environmental Engineering, Stanford University, and Dept. of Global Ecology, Carnegie Institution for Science, California, USA, jeffho@stanford.edu

Michalak, A. M., Dept. of Global Ecology, Carnegie Institution for Science, California, michalak@carnegiescience.edu

Stumpf, R. P., National Centers for Coastal Ocean Science, National Oceanic and Atmospheric Administration, Michigan, Richard.stumpf@noaa.gov

Bridgeman, T. B., Department of Environmental Sciences/Lake Erie Center, University of Toledo, Ohio, thomas.bridgeman@utoledo.edu

Information on historical phytoplankton blooms can yield insight that can be used to tackle present-day challenges in inland waters. Thus far, however, attempts to use historical information to understand long-term changes relevant for present-day management have been stymied by a limited historical record in many freshwater systems. For Lake Erie, we augment the existing record based on MERIS imagery that begins in 2002 by generating new information on the spatial extent and timing of blooms from Landsat 5 imagery for 1984-2001. Despite limitations stemming from Landsat's long revisit period and regular cloudiness obscuring scenes, we demonstrate that Landsat is able to generate robust long-term data on Lake Erie and that remotely-sensed historical data add relevant context for addressing current blooms. This new historical record documenting the presence, magnitude, and timing of past blooms expands existing scientific capability to understand the dynamics of bloom occurrence and growth by adding nearly two decades of information to what is known about blooms in Lake Erie.

LAKE ERIE'S RE-EUTROPHICATION: DEGRADATION, ADAPTATION, AND RESTORATION

Kane, D. D., Natural Science, Applied Science, and Mathematics Division, Defiance College, Defiance, Ohio, dkane@defiance.edu

Chaffin, J. D., F.T. Stone Laboratory, Ohio State University, Put-In-Bay, Ohio, justin.chaffin@rockets.utoledo.edu

Conroy, J. D., Inland Fisheries Research Unit, Ohio Department of Natural Resources, Division of Wildlife, Hebron, Ohio, joseph.conroy@dnr.state.oh.us

Culver, D. A., Limnology Laboratory, Department of Evolution, Ecology, and Organismal Biology, The Ohio State University, Columbus, Ohio, culver.3@osu.edu

Total phytoplankton and cyanobacterial biomasses in Lake Erie's western and central basins have been increasing since the mid 1990's, following several decades of declines directly tied to phosphorus abatement. These increases, coupled with hypoxia at a variety of spatial and temporal scales, provide evidence that Lake Erie is currently undergoing re-eutrophication. Both short-term and long-term management actions are necessary to minimize degradation of this resource. Herein, we distinguish between short-term adaptation by the lake's users and long-term restoration of the lake. Short-term adaptation includes monitoring bloom formation and location, toxicity, and if blooms are impacting end users via contaminated water, closed beaches, or other Beneficial Use Impairments (BUIs). Specifically, we provide data related to the efficacy of monitoring buoys as early-warning systems for drinking water treatment plants. Short-term adaptations by Lake Erie's users are necessary and relatively inexpensive compared to what must be done to decrease Cyanobacterial Harmful Algal Blooms (CHABs) and lessen the extent/duration of hypoxia to restore Lake Erie to a more desirable state. Further, long-term

restoration actions must be considered within the context of conditions predicted by climate change scenarios, not current conditions.

HYPOXIA IN LAKE ERIE IS MOSTLY DRIVEN BY DIATOMS

Reavie, E.D., Natural Resources Research Institute, University of Minnesota Duluth, Duluth, MN

Cai, M., Natural Resources Research Institute, University of Minnesota Duluth, Duluth, MN

Twiss, M. R., Department of Biology, Clarkson University, Potsdam, NY

Carrick, H. J., Dept. of Biology & Institute for Great Lakes Research, Central Michigan University, Mount Pleasant, MI

Davis, T. W., National Oceanic and Atmospheric Administration, Great Lakes Environmental Research Laboratory, Ann Arbor, MI

Johengen, T. H., Cooperative Institute for Limnology & Ecosystem Research, Ann Arbor, MI.

Gossiaux, D., National Oceanic and Atmospheric Administration, Great Lakes Environmental Research Laboratory, Ann Arbor, MI

Smith, D.E., Dept. of Biostatistics & Informatics, Colorado School of Public Health, Aurora, CO

Palladino, D., Cooperative Institute for Limnology & Ecosystem Research, Ann Arbor, MI

Burtner, A., Cooperative Institute for Limnology & Ecosystem Research, Ann Arbor, MI

Sgro, G. V., Department of Biology, John Carroll University, OH

Re-eutrophication and harmful algal blooms in Lake Erie have resulted in a renewed call for remedial measures such as reductions of phosphorus loads. Nutrient reductions can have a remedial effect on hypolimnetic anoxia by reducing algal biomass. However, winter-spring blooms of diatoms have not been fully recognized as a source of algal biomass supporting summer hypoxia. We compared spring and summer phytoplankton abundance in central and western Lake Erie based on monitoring data to show that spring phytoplankton biovolume was 1.5- to 6-fold greater than summer biovolume and that most spring biovolume was composed of filamentous diatoms, primarily *Aulacoseira islandica*, that is likely supported by an increasing silica load from Lake Huron. The rise of silica export was attributed to the dreissenid mussel invasion and establishment that reduced diatom abundance in Lake Huron and thereby increased silica availability in the receiving water body of Lake Erie. Winter-spring diatoms, not summer cyanophytes, are likely contributing the majority of the carbon load to the hypolimnion of the central basin of Lake Erie, so remedial measures aimed at reducing hypoxia in Lake Erie must consider these early-year blooms as important contemporary features of the lake that deliver algal biomass to the profundal zone.

Submitted talks (please note that presenting authors are underlined)

Bold Talks

COMPARATIVE IRRADIANCE RESPONSES OF PHOTOSYNTHETIC QUANTUM YIELD AMONG FRESHWATER PHYTOPLANKTON PIGMENT GROUPS IN CULTURE AND IN NATURAL COMMUNITIES

Beecraft, L., University of Waterloo, Canada, lnjbeecr@uwaterloo.ca

Watson, S. B., Environment Canada, Canada

Smith, R. E., University of Waterloo, Canada

Phytoplankton sensitivity to ultraviolet radiation (UVR), and mechanisms to cope with this stress, have been observed for a range of taxa and environments. Bloom-forming cyanobacteria are frequently exposed to high UVR, and some are commonly thought to be more tolerant to sunlight stress. However, interspecific differences in irradiance sensitivity and the implications for natural plankton dynamics are not well resolved. We evaluated this question with a Phyto-PAM fluorometer, which uses variable chlorophyll a fluorescence to measure photosynthetic efficiency, and can discriminate plankton into three major groups: blues, greens and browns. Photosynthetic quantum yield was measured on monoalgal cultures and natural phytoplankton samples exposed to PAR and UVR+PAR, and a model of photoinhibition used to assess irradiance sensitivity among groups and taxa. UVR exposures produced photoinhibition in all phytoplankton groups. Among the cultures, chlorophyte taxa showed the highest tolerance, with average photosynthetic efficiency (yield) reduced by 29% under the UVR+PAR treatment, compared to 46% for chromophytes, and 73% for cyanobacterial taxa, which exhibited the highest sensitivity. A similar degree and ranking of sensitivity by pigment group was observed in samples from a meso-eutrophic embayment. Under the acute exposures applied, differences in UVR sensitivity were explained primarily by varying rates of damage, rather than repair, in the photosynthetic apparatus.

MOLECULAR SYSTEMATICS AND ORGANELLAR GENOMICS OF *ULVA* (ULVOPHYCEAE, CHLOROPHYTA) WITH PHYLOGENOMICS OF THE “CORE CHLOROPHYTA”

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Ulva species are found worldwide in a wide range of salinities and water depths. These algae are known to be taxonomically troublesome due to their simple morphology, cryptic speciation, and morphological plasticity. A molecular investigation based on these algae from Atlantic USA, Panama, and Chile revealed an unexpected diversity consisting of several new reports for each area and up to 12 new species. One new report and likely nonnative species in the Western Atlantic, *Ulva ohnoi* Hiraoka & Shimada, has been forming overgrowths in southern Florida and Texas. Additionally, next generation sequence data of *Ulva* spp. are providing insights into organellar genome evolution and a robust dataset for phylogenomics of the “Core Chlorophyta”. The AT-rich chloroplast genomes of *Ulva* spp. ranged from 92 to 115 kbp and showed interspecific gene rearrangements. Mitochondrial genomes of *Ulva* spp. followed the “expanded-derived” pattern seen in other ulvophyceans, and ranged from 56 to 73 kbp with conserved gene

orders. Variances in organellar genome sizes were mostly due to differences in intron content and intergenic space. Furthermore, phylogenomic analyses using chloroplast and mitochondrial protein-coding genes showed no support for a monophyletic Ulvophyceae *sensu lato*.

EXAMINATION OF ANTIBACTERIAL FATTY ACIDS SYNTHESIZED BY MICROALGAE

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There is a growing effort to combat bacterial resistance, and certain fatty acids have been shown to inhibit bacterial growth. Microalgae can provide a sustainable source of fatty acids, due to their ability to naturally synthesize these lipids. To identify algal fatty acids with antibacterial properties, 29 acids were analyzed using surface zone inhibition assays with *Escherichia coli* and *Staphylococcus aureus*. Of the fatty acids that exhibited antibacterial properties, five representative structures [capric acid, palmitoleic acid, gamma-linolenic acid, arachidonic acid, and docosadienoic acid] were further analyzed. In order to increase the cellular content of these fatty acids within five microalgae, culturing conditions (light, temperature, and nutrients) were manipulated. The microalgae studied included *Rhodella maculata*, *Phaeodactylum tricornutum*, *Boekelovia hooglandii*, *Goniochloris sculpta*, and *Chloridella simplex*. The largest antibacterial fatty acid content, of 206 mg/g dw, was present within *P. tricornutum*. However, due to the low biomass productivity of *P. tricornutum*, *B. hooglandii* had the greatest antibacterial fatty acid productivity in ESP medium, 18°C, 80 $\mu\text{moles/m}^2/\text{s}$, and 17:7h light/dark. This study identified antibacterial fatty acids, which could potentially be used for topical antibacterial applications, and growth conditions that increased algal content of these lipids.

A METABARCODING FRAMEWORK FOR FACILITATED SURVEY OF ENDOLITHIC PHOTOTROPHS WITH TUF A

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In spite of their ecological importance as primary producers and microbioeroders of marine calcium carbonate (CaCO₃) substrata, endolithic phototrophs spanning both prokaryotic (the cyanobacteria) and eukaryotic algae lack established molecular resources for their facilitated survey with high throughput sequencing. Here, the development of a metabarcoding framework for the elongation factor EF-tu (*tufA*) was tested on four Illumina-sequenced marine CaCO₃ microfloras for the characterization of their endolithic phototrophs, especially the abundant bioeroding *Ostreobium* spp. (Ulvophyceae). The framework consists of novel *tufA* degenerate primers and a comprehensive database enabling Operational Taxonomic Unit (OTU) identification at multiple taxonomic ranks with percent identity thresholds determined herein.

TRACING THE MOVEMENT OF THE INVASIVE ALGA *NITELLOPSIS OBTUSA* USING GENETIC ANALYSES

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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 widely reported from inland lakes throughout northern Indiana, Michigan, and western New York, with isolated locations in Minnesota, Vermont, and Wisconsin. The vector(s) by which *N. obtusa* was transported to North America and distributed across the landscape remain unknown. In 2015 and 2016, 740 water bodies were surveyed for *N. obtusa* across New York and New England. Results from this work suggested that *N. obtusa* is primarily moved via recreational boating. However, in other states, birds have been hypothesized to transport *N. obtusa*. Organellar genome sequencing and Genotyping by Sequencing (GBS) methods use next-generation sequencing to identify single nucleotide polymorphisms (SNPs) from across a genome. The quantity and random distribution of SNPs generated by these methods are ideal to address population level questions of movement and distribution. Initial analysis of plastid and mitochondrial genomes has revealed variation between populations in Northern Europe, Central Europe, and North America. Little variation was detected in North American plastid and mitochondrial genomes, indicating that clonal spread of a single introduced population is likely. The results of this research will inform invasive species management and treatment efforts and lead to a better understanding of how invasive species are transported in aquatic ecosystems.

Systematics and Biodiversity I and II

NOSTOC AND MOJAVIA SPECIES ISOLATED FROM THE SOILS OF THE ATACAMA DESERT, CHILE

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Enrichment cultures of 88 different soil collections from the Atacama Desert resulted in the isolation of 31 strains of Nostocaceae from five sites. From these, 14 strains were chosen to represent all distinct morphotypes in each of the five sites for detailed morphological and molecular analyses. Molecular analyses revealed the existence of seven distinct lineages within *Nostoc* and one lineage within *Mojavia*. Two of the *Nostoc* lineages were too close to *N. lichenoides* to justify separation into new species, despite some differences in morphology and ecology. The combined evidence based on morphology, ecology, phylogenetic placement, and secondary structure of the 16S-23S ITS region in the ribosomal operon indicates that the remaining five lineages within *Nostoc* are five separate and diagnosable new species. The *Mojavia* species is also new, being morphologically very distinct from the other described species in the genus.

CHARACTERISING THE LIVING PROKARYOTIC MICROBIOME OF THE CALCIFIED RED ALGA *CORALLINA OFFICINALIS*

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Marine macroalgae host a wide range of microbial organisms of which bacteria are the dominant active group. The living prokaryotic microbiome of the calcified geniculate (articulated) red alga *Corallina officinalis* from the intertidal seashore was characterized based on sequence data of the

V6 hypervariable region of 16S rRNA. An extraordinary diversity of bacteria was revealed: thirty-five prokaryotic phyla were recovered, of which Proteobacteria, Cyanobacteria, Bacteroidetes, Actinobacteria, Planctomycetes, Acidobacteria, Verrucomicrobia, Firmicutes and Chloroflexi made up the core microbiome. Twenty-five per cent of sequences were unclassified, suggesting insufficient sampling of the world's oceans/macroalgae. Diversity in the microbiome varied between the different shore levels over which *C. officinalis* was found, although the community composition did not. The *C. officinalis* core microbiome was similar in composition to those reported in the literature for crustose coralline algae (CCAs) and free-living rhodoliths. Differences in relative abundance of the phyla between the different groups are discussed in relation to the intertidal versus subtidal habit of the taxa and functionality of the microbiome components. The results indicate that considerable work is needed to identify prokaryotic taxa, and to determine the nature of the relationship of the bacteria with the calcified host spatially, temporally and functionally.

EXTRAORDINARY DIVERSIFICATION OF THE ALGA *NANNOCHLOROPSIS* (EUSTIGMATOPHYCEAE) UPON TRANSITION FROM MARINE TO FRESHWATER
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The Eustigmatophyceae is a poorly studied class of stramenopile algae that are primarily freshwater organisms. Some species of the genus *Nannochloropsis* and its sister genus, *Microchloropsis*, are the only Eustigmatophyceae known to inhabit marine environments. The Eustigmatophyceae clearly had freshwater origins, so these two genera likely evolved from an ancestral form that transitioned from freshwater to marine. However, one lineage within *Nannochloropsis* has apparently transitioned back to freshwater from the marine environment. Previous studies using sequences of the plastid *rbcL* gene have shown that the freshwater forms are somewhat more taxon rich than the marine members of the genus. In this study, we examined the diversity of freshwater *Nannochloropsis* using additional strains and additional loci. For all strains, we sequenced the plastid loci *rbcL* and *ccsA*. We also sequenced the additional plastid locus *ccs1* for exemplar strains. Our results show that both *ccsA* and *ccs1* have approximately twice as many substitutions as *rbcL*. Analyses of these data indicate that *Nannochloropsis* has rapidly diversified upon transition to freshwater, whereas marine taxa show a pattern consistent with slow phyletic diversification. To our knowledge, this is the first algal example of either extraordinary diversification or adaptive radiation upon transition from marine to freshwater.

ANALYSIS OF RBCL DNA SEQUENCES AND LIGHT MICROSCOPY REVEAL EXTENSIVE DIVERSITY IN CLADE IIA OF THE EUSTIGMATOPHYCEAE
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The algal class Eustigmatophyceae is distinguished from other stramenopile algae by fine structural features and pigment composition. Eustigmatophyceae are found in freshwater, terrestrial, and soil habitats. Until very recently this unique group of coccoid microalgae was considered to have low diversity; however, we recently demonstrated the presence of a new ordinal-level lineage, the clade Goniochloridales. There are well supported lineages in the

Goniochloridales that we referred to as Clade IIa, Clade IIb and Clade IIc. In this study, we examined the diversity of Clade IIa. New strains were isolated from sites in Arkansas, Michigan, Minnesota and the Czech Republic. We examined 36 strains using analysis of plastid *rbcl* sequences and light microscopy. Phylogenetic analysis of the sequence data indicated 19 phylotypes among the 31 strains that are members of Clade IIa. Most of these strains do not match any existing genera and species in the Eustigmatophyceae or Xanthophyceae. The exception is a strain that we identified as *Tetraëdriella subglobosa*, which had previously been placed in the Xanthophyceae. Our results indicate the presence of multiple lineages within Clade IIa that probably represent new genera.

REVISING CHARA SUBSECTION *WILLDENOWIA*

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In their 1964 revision of the Characeae, R. D. Wood and K. Imahori acknowledge 81 species, a number revised down from a previous estimate of 314 species in the family. This has resulted in the aggregation of numerous morphologically, taxonomically, and ecologically diverse *Chara* into just 19 species with previously recognized species relegated to varietal and formal synonymy. An example of this is *Chara* subsection *Willdenowia*, whose sole representative in Wood and Imahori's treatment is *Chara zeylanica*. In this treatment, *C. zeylanica* exhibits a diverse range of morphologies and traits including plants that are monoecious or dioecious, gametangia that are conjoined or sejoined, different structural and developmental characteristics of gametangia and zygotes, different chromosome numbers, and reproductive isolation. These differences are bolstered by molecular analysis of this geographically widespread taxon, an analysis that reveals that *C. zeylanica sensu* Wood and Imahori represents many distinct, sometimes cryptic, species. Presented here is an overview of the historical treatments of this group, and the current data that support a wholesale revision of *Chara* subsection *Willdenowia*.

UNSUSPECTED EUKARYOTIC LIFE INHABITS THE ROLLING STONES

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We demonstrate unequivocally with SEM, FESM, TEM, epifluorescence and light microscopy, cell cultures, whole genome amplification using REPLI-g on single cells, Sanger sequencing (*cob1*, *tufA*, 18S), *tufA* metabarcoding and sequence analyses, that hitherto unknown benthic life history stages of marine bloom-forming microalgae are associated endolithically within calcium carbonate-lined inner cells of rhodolith-forming crustose coralline algae (rolling stones) for part of their life cycles; such endolithic stages were previously mistaken for chloroplasts, bacteria, starch granules or vesicles. We were able to link the taxonomic identity of endolithic stages of

dinoflagellates (*Prorocentrum lima*) and haptophytes (*Ochrosphaera verrucosa*) growing inside *Lithothamnion* rhodoliths collected offshore the NW and SE Gulf of Mexico at depths of 60-65m, and maintained in closed 75 liter laboratory microcosms in the laboratory, with their corresponding free-living stages through exact DNA sequence matches. The present study opens the door to further explore and assess the universality of endolithic stages within bloom-forming microalgae spanning multiple phyla in marine ecosystems worldwide. As calcium carbonate substrata, rhodoliths may function as temporary reservoirs of microalgae that allows for their seasonal or irregular bloom formation and survival during or following drastic environmental and ecological shifts, such as oil spills. The research will have important implications in predicting the onset of phytoplankton blooms, including those forming HABs (*Prorocentrum*).

WHY DID THE OLD GUYS GET IT RIGHT: GENES, MORPHOLOGY, AND THE DIATOM PHYLOGENY

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A great deal of effort has occurred creating phylogenetic estimates for the diatoms. In virtually all of these estimates, higher level diatom taxonomic groups remain intact as well supported (high bootstrap values) subgroups within the phylogeny. These higher level taxonomic categories were all established prior to the development of molecular tools and were largely based upon frustular morphology. In contrast, higher level taxonomic categories in non-diatom algal lineages were not generally corroborated with phylogenetic hypotheses created using molecular data. These results suggest that morphology in diatoms, as historically treated, is a reliable indicator of past evolutionary history. In this study, we present a morphologically based phylogeny for the diatom subgroups which largely corroborates molecular topologies. Morphological features are identified that facilitate diagnosis of major subgroups within the diatoms. Further it demonstrates that the “controversy” concerning molecules vs. morphology is largely overstated, at least for diatoms.

THERE ARE MORE THAN ONE GENERA OF ZOOXANTHELLAE FROM MARINE INVERTEBRATES

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Symbiotic dinoflagellates can be separated into genera and species on collective characteristics. One major feature is the possession of perinuclear membraneous vacuoles or not. The plastids are either finger-like or mitten-like. Some symbionts have nucleoli (a rare character for dinoflagellates) others do not. In the SEM some cultured zooxanthellae have smooth envelopes others are tufted. There are varied behavioral responses of symbionts to light and surface area.

PHYLOGENETIC POSITION REEVALUATION OF *KYRTUTHRIX* AND DESCRIPTION OF A NEW SPECIES *K. HUATULCENSIS* FROM MÉXICO'S PACIFIC COAST

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Benthic marine heterocytous cyanoprokaryotes of Mexico's tropical coast are being recognized as an important and conspicuous component of the supralittoral and intertidal zones usually

described as an extreme and low diversity biotope. Although *Kyrtuthrix* has been reported from different coasts worldwide, its complex morphology has led to differing taxonomic interpretations and positioning. Ten marine supra and intertidal populations of *Kyrtuthrix* were analyzed using a detailed morphological approach, complemented with ecological and geographical information as well as DNA sequence data of the 16S rRNA gene and associated 16S–23S ITS. *Kyrtuthrix huatulcensis* is described as a new species, different from *K. dalmatica* Ercegovic and *K. maculans* (Gomont) Umezaki based primarily on morphological data. Our material has smaller dimensions in thalli, filaments, trichomes and cells, and possesses differences in qualitative characters as well. Our material is epilithic as in *K. maculans* but not endolithic as in *K. dalmatica*. The analysis of molecular data, mainly 16S rRNA gene sequence, show that this genus is closer to the Rivulariaceae clade than to the Scytonemataceae clade. ITS secondary structure comparison with some of the closer representatives of Rivulariaceae also shows considerable differences, and inclusion of *Kyrtuthrix* within this family may need reconsideration.

PHYLOGENY OF THE POLYPHYLETIC GENUS *CYLINDROCYSTIS*
(ZYGNEMATOPHYCEAE) AND ITS RELATION TO FILAMENTOUS
ZYGNEMATALEANS

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Sampling of 24 strains of *Cylindrocystis* and phylogenetic analysis of these and other Zygnematophyceae using two plastid genes confirms the hypothesis of Hall et al. (2008) that the genus is not monophyletic and needs taxonomic reevaluation that will very likely require the description of additional genera comprising these coccoid, smooth-walled desmids. Conjugation tests for all pairwise combinations of 24 strains of *Cylindrocystis* resulted in three instances of homothallic conjugation and no successful heterothallic conjugation. Based on zygospore structure and sequence differences and the placement of homothallic taxa on the 2-gene phylogeny, we describe two new species. A strain of *Cylindrocystis* sp. UTEX 1925 was revealed through molecular analysis to be *Zygnemopsis desmidioides*. Further molecular sampling of *Cylindrocystis* and other zygnematophytes is expected to reveal species-level differences among morphologically homogeneous grades of algae that will be identifiable based on DNA sequence differences. The partitioning of the zygnematophytes into several ordinal clades is warranted by molecular phylogenetic analysis. An early diverging branch consisting of a single *Debarya*-like strain is sister to several distinct clades comprising: (1) *Spirogyra* plus *Sirogonium*, (2) *Zygnema-Mougeotia-Mesotaenium* and a several clades of *Cylindrocystis*, and a (3) clade comprising those taxa conventionally assigned to the placoderm desmids.

NOSTOC OROMO SP. NOVA. (NOSTOCALES, CYANOBACTERIA) FROM ETHIOPIA, A
NEW SPECIES BASED ON MORPHOLOGICAL AND MOLECULAR EVIDENCE

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In the course of study of the cyanobacterial flora of Ethiopian soil crusts, we isolated a distinctive strain most closely resembling *Chroococcidiopsis kashayi*, and at first considered it to be a new *Chroococcidiopsis* species. However, when placed in nitrogen-free medium this strain developed heterocytes, and consequently was placed in the genus *Nostoc*. It is morphologically distinct from all other *Nostoc* species due to its consistent formation of microscopic few-celled colonies lacking clear filamentous organization, which release smaller colonies from the mother colony, leaving behind a persistent thin firm sheath which resembles cell wall material in the light microscope. Analysis of 16S rRNA and 16S-23S ITS sequence data confirmed its uniqueness among numerous strains of soil *Nostoc*. We are describing it as *Nostoc oromo*, named for the nationality of the people from the region of its origin.

MORPHOLOGICAL AND GENETIC DIVERSITY IN THE CARBONATE-BORING
CYANOBACTERIUM *MASTIGOCOLEUS TESTARUM* LAGERHEIM EX BORNET &
FLAHAULT

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The heterocystous cyanobacterium *Mastigocoleus testarum* is one of the more prominent and widespread carbonate-boring phototrophs. A cultured strain (BC-008) has been used to investigate the mechanism of carbonate boring by microorganisms. Three strains from the Hawaiian Islands were cultured, and their identities established via partial 16s rRNA gene sequences and the morphology of traces formed in *Venerupis* bivalve shells in culture. In addition, partial 16s rRNA gene sequences were obtained from single-cell isolates of two populations in the northeastern Adriatic Sea (Croatia). One of the three Hawaiian strains (FHL205) was identical, in its 16s rRNA gene sequence, to BC-008. The other two Hawaiian strains (FHL400, FHL401), plus each of the two Croatian specimens, differed from BC-008, and from all other published sequences. Moreover, borehole diameters in cast preparations of F205 were consistently smaller than those for genetically-identical strains F400 and F401. Similar variations were observed in literature values for borehole dimensions of *Eurygonum nodosum* (the ichnospecies produced by *Mastigocoleus*). All of the Hawaiian strains grew in culture at 23 °C but not at 15 °C. The morphospecies represents a biological species complex, more closely related to false-branching taxa ("*Calothrix*") than to true-branching taxa. Retypification of *M. testarum* with BC-008 seems inappropriate; the type locality (Kristineberg, Sweden) is cold-temperate, and FHL205 did not grow at non-tropical temperatures.

FIRST REPORT OF AN ENDOLITHIC SPECIES OF *RHODOSORUS* GEITLER GROWING
INSIDE LITHOTHAMNION RHODOLITHS FROM LOUISIANA

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Rhodoliths collected offshore the NW Gulf of Mexico at ~65m have been maintained in closed microcosms. Non-flagellated unicells were captured from the rhodoliths' interior with a micromanipulator and microscope and used to establish cultures following their isolation. These endolithic non-flagellated cells subsequently developed into free-living, flagellated *Ochrosphaera verrucosa* haptophytes, but also into amorphous blobs of palmelloid cell colonies. Each cell has a prominent central pyrenoid, parietal chloroplasts, and a thin or thick cell wall; scattered floridean starch granules were visible in older cells. Single cells, or cell clusters (in pairs, tetrads, or up to 12) were embedded inside an extracellular matrix whose boundaries remain closely appressed to neighboring clusters. Cell division by concavo-convex division resulted in hemispherical cells subsequently expanding in size. Plastid tufA sequence analysis confirmed that the colonies are a new sp. of *Rhodosorus* distinct from the generitype *R. marinus* and *R. magnei*. The 3 spp. can be separated on the basis of color, number and degree of chloroplast lobes, and number of cells grouped in a communal gelatinous envelope. The tufA sequence of the NW Gulf of Mexico *Rhodosorus* is a perfect match to that retrieved by tufA metabarcoding from calcareous coral reef substrata from Okinawa, Japan. This is the first report indicating that a *Rhodosorus* sp. spends part of its life history endolithically inside deepwater rhodoliths, co-habiting with *Ochrosphaera*.

GENOME BASED PHYLOGENY OF RED ALGAE PROVIDES A ROBUST FRAMEWORK FOR INFERRING EVOLUTION OF KEY CELLULAR TRAITS

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Red algae comprise an anciently diverged, species-rich phylum with forms that span unicells to large seaweeds. Here, leveraging a rich red algal genome and transcriptome dataset, we used 298 single-copy orthologous nuclear genes from 15 red algal species to erect a robust multi-gene phylogeny of Rhodophyta. This tree places red seaweeds (Bangiophyceae and Florideophyceae) at the base of the mesophilic red algae with the remaining non-seaweed mesophilic lineages forming a well-supported sister group. The early divergence of seaweeds contrasts with the evolution of multicellular land plants and brown algae that are nested among multiple, unicellular or filamentous sister lineages. Using this novel perspective on red algal evolution, we studied the evolution of the pathways for isoprenoid biosynthesis. This analysis revealed losses of the mevalonate pathway on at least three separate occasions in lineages that contain *Cyanidioschyzon*, *Porphyridium*, and *Chondrus*. Our results establish a framework for in-depth studies of the origin and evolution of metabolic pathways in Rhodophyta.

TO BE OR NOT TO BE: WILL THE REAL *CHRYSYMENIA* (RHODYMENIACEAE, RHODOPHYTA) PLEASE STAND UP?

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The genera in the Rhodymeniaceae that have a hollow thallus lacking diaphragms comprise *Chrysomenia* J. Agardh (including *Gloiosaccion* Harvey), *Botryocladia* (Agardh) Kylin and *Irvinea* Guiry. *Chrysomenia* has traditionally been defined by a lack of internal rhizoids and with the only solid portion of the thallus limited to the stipe, and *Botryocladia* is characterized by the presence of larger, solid axes. Our new revision of *Chrysomenia* indicates that on the basis of vegetative characters alone, the true *Chrysomenia* clade contains taxa that exclusively produce gland cells directly on unmodified medullary cells, and that *Botryocladia* species may or may not cut off gland cells from modified glandiferous medullary cells. Based on phylogenetic sequence analysis (*rbcL*, UPA, LSU sequences) and morphological data, the hollow, gelatinous species *Chrysomenia enteromorpha* Harvey from the Gulf of Mexico and the Caribbean Sea, and *C. wrightii* Harvey from the Northeast Pacific, are newly transferred to the genus *Botryocladia*. Two new species of *Chrysomenia* are reported for the Gulf of Mexico from 60-68 m depth: a broad, foliose species growing attached to rhodoliths offshore Louisiana and the vicinity of the Dry Tortugas, FL, and a slender branched species from the vicinity of the Florida Middle Grounds, Florida. A revised concept of a monophyletic *Chrysomenia* will be discussed in the context of the Rhodymeniaceae.

HAVE MARINE ANIMAL CONSERVATION LAWS CAUSED THE DECLINE OR EXTIRPATION OF MACROALGAL POPULATIONS OVER THE PAST CENTURY IN BERMUDA?

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Unlike the difficulties associated with estimating the diminution of animal size over time in marine megafauna, early seaweed collectors left an extensive archival record of herbarium specimens from locations throughout the world useful for comparative purposes with recent populations of the same species collected today. Using collections in the 1912-1917 Bermuda fascicles of the algal exsiccata *Phycotheca-Boreali Americana*, as well as the extensive Bermuda collections compiled by W.R. Taylor and his students in the University of Michigan Herbarium, we are able to compare the presence and absence of macroalgae from a century ago and today in locations around the islands. Several marine herbivorous fishes, especially parrotfish (*Scarus* spp., *Sparisoma* spp.), have seen increased population sizes since Bermuda enacted the 1978 Protected Species Order. By 1990, when the Bermuda fish trap ban was put into effect, several species of grouper (*Mycteroperca* spp., *Epinephelus* spp.) and Mutton hamlet (*Alphistes*), the main predators of parrotfish and other herbivorous fish, were rarely seen in surrounding waters. Furthermore, in 1982, intertidal grazing West Indian top shells (*Cittarium pica*) were reintroduced to the islands, and since then, along with the rise in parrotfish populations, inshore populations of many algal species have declined or disappeared. We will discuss several large and abundant Bermuda macroalgal species of the early 20th century that today are diminished in size and abundance, and how increased parrotfish and top shell populations over the past 40 years may have caused these changes.

CYANOMARGARITA GEN. NOV.: CONVERGENT EVOLUTION RESULTING IN A CRYPTIC GENUS IN CYANOBACTERIA

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On the genus level, a new cryptic genus, *Pinocchia*, was described by Dvorak et al. (2015) which is morphologically indistinguishable from *Pseudanabaena*. Moreover, quite a few species in genera from diverse orders appear to be cryptic. For example, several cryptic species of *Oculatella* have been found (Synechococcales), as well as cryptic species of *Gloeocapsa* (Chroococcales), and finally, a number of similar species in *Microcoleus* (Oscillatoriales) are known. In our research, we have found a cryptic genus of cyanobacterium which has morphology corresponding to *Rivularia*, but additional information from culture and 16S rRNA gene phylogeny shows that it is representative of a cryptic genus outside of the Rivulariaceae. It appears to be sister to *Scytonema crispum* and Aphanizomenonaceae clades. This new genus, *Cyanomargarita*, contains two species: type species - *Cyanomargarita melechinii*, was collected from a clean subarctic spring on the territory of Kola peninsula (Russia), under the water, where it formed spherical blue-green colonies. Another species - *Cyanomargarita calcarea*, was found from a wet limestone wall in the Sheep Creek Drainage, Utah (USA). Importantly, both species possess clearly distinguishable characteristics, including morphology, preference for different cultural conditions, ecology, molecular data, and p-distance of the 16S-23S ITS region.

A TALE OF KIWIS, KANGAROOS, AND *LIMU*: RESOLVING MESOPHOTIC SPOROCHNALES AND *DICTYOPTERIS* SPECIES (PHAEOPHYCEAE) FROM THE HAWAIIAN ARCHIPELAGO

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Brown macroalgae belonging to the Sporochnales and genus *Dictyopteris* are common components of deep, or mesophotic, macroalgal communities in Hawaii. *Dictyopteris* is called *limu lipoa*, or “gathered from the deep”, in Hawaiian, and is highly prized for the spicy flavor and pungent smell of the two meadow-forming species, *D. plagiogramma* and *D. australis*. Two species of *Sporochnus* are currently reported from Hawaii, but are typically found in low abundance. Our goal was to use molecular and morphological techniques to characterize the diversity of Sporochnales and *Dictyopteris* in Hawaii’s mesophotic zone. Technical diving, submersibles, and remotely operated vehicles were used to collect specimens (n = 32) from 21 locations in the Northwestern (NWHI) to Main Hawaiian Islands (MHI) from 35 – 125 m depths. Analyses (*psaA*, LSU, and *rbcL* marker analyses and morphological comparisons) suggest that mesophotic *Dictyopteris* species are different between the NWHI and MHI regions, with the NWHI species lacking the characteristic venation of MHI samples. The Sporochnales also appear to be more diverse, with specimens morphologically similar to *Carpomitra* and *Bellotia*. Most of these species have strong biogeographic affinities with Australia and New Zealand, and have not been described from shallow water in Hawaii, further adding to the breadth of macroalgal diversity found in mesophotic ecosystems.

EXPLORATION OF *PLAKOBRANCHUS* SP. KLEPTOPLAST DIVERSITY IN THE MAIN HAWAIIAN ISLANDS USING A METABARCODING APPROACH

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Plakobranchnus sp. is a common algivorous sea slug found throughout the tropical Pacific Ocean. It is known for kleptoplasty, or the stealing and retention of chloroplasts, from its algal food sources. *Plakobranchnus* exclusively sequesters chloroplasts from the highly diverse acellular, siphonous green algal orders Bryopsidales and Dasycladales, and therefore can be used as a sampling tool in addition to traditional surveying techniques to assess their diversity. Studies thus far have focused on the kleptoplasty of *Plakobranchnus* in the Western Pacific, and only one site has been assessed in its easternmost populations in the Main Hawaiian Islands. The goal of this study was to assess *Plakobranchnus* kleptoplast diversity as a proxy for siphonous green algal diversity across the Main Hawaiian Islands. Slugs were collected from 10 sites in winter and spring to capture archipelago-wide diversity and account for seasonal variability in both the slug and algae. A portion of the *rbcL* marker was amplified, multiplexed, and sequenced for each slug on an Illumina MiSeq platform. Molecular analyses of *Plakobranchnus* kleptoplasts suggest that despite being collected from highly variable ecosystems, comparable algal source diversity is found across sites. These communities have gone unnoticed in the past due to their size and cryptic morphology. This study illustrates that investigation of plant-herbivore interactions can provide a richer understanding of ecosystem composition and dynamics.

Cell Biology

HAVE HOST? WILL GROW: RED ALGAL PARASITE DEVELOPMENT

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Red algal parasites have independently evolved hundreds of times within the Florideophyceae. Red algal parasites are highly host specific, morphologically reduced, lack pigmentation, and penetrate and establish cellular connections with their host. The relationship between host and parasite has informed the delineation of red algal parasites into adelphoparasites and alloparasites. Adelphoparasites evolved from their current or closely related host and typically only infect one to two closely related species. Alloparasites are capable of infecting multiple hosts that are often distantly related. Fundamental questions regarding parasite infection mechanisms, parasite development, or its repercussions on the host remain incompletely answered for nearly every red algal parasite described. Maintaining host-parasite pairs in culture and manipulating their environment to stimulate the release of spores and control parasite reinfection has allowed for the development of the parasite from spore to mature pustule to be monitored. The application of further microscopy techniques and single cell transcriptomics will give a greater glimpse into the experiences of host and parasite cells during infection.

BUOYANCY MODULATION IN AFLAGELLATE MARINE PHYTOPLANKTON: A BIOENERGETICS ANALYSIS

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Many marine aflagellate phytoplankton regulate cell density, which affects their sinking or rising rate in the water column. For instance, giant diatoms perform vertical migration to benefit from the nutrient-rich deep reservoir at night and the well illuminated surface water during the day. Moreover, several small phytoplanktonic species tend to be denser in the presence of low nitrate concentration at the cell surface, and sink more rapidly toward nutrient-rich patches in the euphotic zone of the ocean. In the present study, we calculated the photon energy cost of three cell mechanisms (cell wall synthesis, polysaccharide synthesis, and replacement of organic solutes of different densities) modulating the rising or sinking speed of cells in a few selected phytoplanktonic species. We found that the three physiological mechanisms could act as ballast in the three species tested in conditions of low nitrate availability at an energy cost (less than 12%) of the total photon energy cost for growth. The replacement of putative low- and high-density organic solutes allowing vertical migration in a giant diatom was more costly than the strategy involving storage/mobilization of dense polysaccharides. This study brings new insights into potential selective advantages of several strategies modulating the buoyancy of aflagellate marine phytoplankton.

REMODELING INTERMEDIATE METABOLISM TO ENHANCE LIPID PRODUCTION IN *PHAEODACTYLUM TRICORNUTUM*

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In the diatom *Phaeodactylum tricornutum*, intermediate metabolism responds to nitrogen stress, leading to cellular lipid accumulation. To understand the underlying regulatory phenomenon of this accumulation, we took an integrative approach and identified major regulatory branch points under nitrogen starvation condition. Our analysis pointed to several biochemical pathways that could be used as genetic targets. We started with examining two distant pathways: nitrogen assimilation and triacylglycerol synthesis. Using an RNAi silencing approach, we obtained a stable nitrate reductase (NR) knock-down transformant, NR21. This transformant exhibited ~50% lower expression and activity of the enzyme, yet simultaneously accumulated >40% more fatty acids, and was characterized by only a ~25% reduction in growth relative to the wild type. Additionally, we overexpressed a specific type II DGAT gene, *DGAT2D*. The resulting transformants had higher *DGAT2D* mRNA and protein levels, and twice as much lipid production. While the two transformations led to increased lipid accumulation by utilizing different cellular strategies, both phenotypes exhibited a decreased investment in the photons required for incorporation of carbon into lipids. In addition, our biophysical data suggest that the redirection of carbon intermediates may be triggered by a retrograde signal transduction pathway (RST), possibly via a redox sensor coupled to the plastoquinone (PQ) pool.

VIDEO MICROSCOPY OF ZOOSPORANGIAL RELEASE OF THE MULTI-FLAGELLATED ZOOSPORE OF *VAUCHERIA SESSILIS*: WHY DOES IT SPIN?

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Video microscopy was employed to document the release and activity of the multi-flagellated zoospores formed from the apical end of *Vaucheria sessilis* filaments. The first indication that a vegetative filament is about to undergo zoospore differentiation begins with the gradual darkening of the tip as cytoplasmic organelles displace the large central vacuole, causing the tip of the filament to enlarge. After several hours, septation of the zoosporangium from the filament occurs and an hour or so later, a “gelatinisation” of the zoosporangial tip occurs, allowing the zoospore to escape from a small opening. The multi-flagellated zoospore begins rotating in a clock-wise direction (as one looks from the tip down) as it slowly squeezes out of the sporangium, taking as long as 15-20 minutes. Mistakes can happen as the zoospore emerges from the sporangium; usually because of some physical disturbance, the outer exposed portion of the zoospore may cease to rotate while the inner portion continues to rotate or the opposite may occur, both resulting in the large zoospore pinching into two functional multinucleate zoospores. After release, the spore continues to slowly swim in a clockwise rotation for around 15 minutes before encysting. By 24 hours the encysted zoospore has formed a small vegetative filament which may form another small zoospore by the next day.

A NOVEL ANTIFOULING DEFENSE STRATEGY FROM RED SEAWEED: EXOCYTOSIS AND DEPOSITION OF FATTY ACID DERIVATIVES AT THE CELL WALL SURFACE

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We investigated the organelles involved in the biosynthesis of fatty acid (FA) derivatives in the cortical cells of *Laurencia translucida* and the effect of these compounds as antifouling (AF) agents by using microscopy and biochemistry techniques. A hexanic extract (HE) from *L. translucida* was split into two isolated fractions called hydrocarbon (HC) and lipid (LI); mainly composed by docosane (HC) and hexadecanoic acid/cholesterol trimethylsilyl ether (LI). Nile red (NR) labeling (lipid fluorochrome) presented a similar cellular localization to that of the autofluorescent molecules (LI). Transmission and scanning electron microscopy revealed vesicle transport processes involving small electron-lucent vesicles, from vacuoles to the inner cell wall. Both fractions (HC and LI) inhibited marine microfouling. The results suggested that *L. translucida* cortical cells can produce FA derivatives and secrete them to the thallus surface, providing a unique and novel protective mechanism against microfouling colonization in red algae.

SETA STRUCTURE IN MEMBERS OF THE COLEOCHAETALES (STREPTOPHYTA)

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The charophycean green algae, which include the Coleochaetales, together with land plants form a monophyletic group, the streptophytes. The order Coleochaetales is distinguished by setae (hairs) encompassed at the base by cell wall material known as a collar or sheath. Previous reports on the structure and growth of setae in *Coleochaete scutata* are in conflict, while details of setae in *Chaetosphaeridium* and other *Coleochaete* species have not been reported. We have demonstrated with calcofluor staining that, in agreement with one report on *Coleochaete scutata*, the hairs of *C. orbicularis*, *C. soluta*, *C. pulvinata*, *C. irregularis*, and *Chaetosphaeridium globosum* are composed of cellulose, and grow from the base. While the whole collar of *Chaetosphaeridium* tested positive for cellulose as indicated by calcofluor staining, only the basal region of the collar in *Coleochaete* species stained with calcofluor. Aniline blue staining revealed regions of callose in setae of all taxa studied. In the *Coleochaete* species examined, but not in *Chaetosphaeridium*, callose was associated with conspicuous internal structures. This association is consistent with a previous report on *Coleochaete scutata*. The width of hairs in members of the *Coleochaete scutata* group (all species of *Coleochaete* studied here except *C. irregularis*) is approximately 1.5 times those of *C. irregularis* and *Chaetosphaeridium globosum*. These results are consistent with a hypothesis that wider hairs are a synapomorphy of the *C. scutata* clade, with narrower hairs representing the ancestral condition.

Ecology

LIGHT AND ZOOBENTHIC PRODUCTION IN LAKES: TIGHT COUPLING BETWEEN ATTACHED ALGAL PRODUCTION AND THE GENERALIST CONSUMER, *CHIRONOMUS DILUTUS*

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Phytoplankton, terrestrially derived particulate and dissolved organic carbon (DOC), and attached algae together form the energetic base of lake food webs. Of these, attached algal production is rarely measured because of a perceived minor role in food web energetics. The widely observed decline in zoobenthic production with depth is usually attributed to temperature rather than resource gradients. We quantified the contribution of attached algal production to a generalist zoobenthic consumer, *Chironomus dilutes* in 9 aquaria linked by a flow-through system. Temperature and phytoplankton biomass were similar across treatments, but we imposed a light gradient to vary attached algal production. Attached algal production was linearly related to light availability and secondary production was a positive linear function of attached algal production. Field measurements in four northern temperate lakes showed a similar tight correlation between light, attached algal production and zoobenthic production. Our research suggests that both eutrophication and increases in DOC loading may cause declines in zoobenthic production by reducing light availability to attached algae on lake sediments.

REDUCED SALINITY AND LOWERED TEMPERATURE AS POTENTIAL BARRIERS FOR THE DISPERSAL OF *SARGASSUM HEMIPHYLLUM* VAR. *CHINENSE* ALONG NORTHERN WEST PACIFIC COASTS

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The brown alga *Sargassum hemiphyllum* has a disjunct distribution pattern in northern west Pacific. This pattern coincides with the distribution of the two varieties, with *S. h. var. hemiphyllum* being found mainly along Japan and Korea and *S. h. var. chinense* mainly found along the south-eastern and southern Chinese coasts. We hypothesized that a temperature gradient along NW Pacific and the presence of large outflow from the two major rivers in China significantly reducing salinity in coastal waters likely served as the barriers for this disjunct distribution pattern observed. We have now experimentally evaluated the thermal and salinity tolerances of different life history stages of *S. h. var. chinense* from Hong Kong in southern China in an attempt to test our hypothesis. Our results indicated that different stages of *S. h. var. chinense* were growing under suboptimal conditions in Hong Kong, with south-eastern Chinese coast being likely the optimal places for their growth. Retarded growth and lower photosynthetic performances of all the vegetative stages were recorded at salinities lower than the ambient (33psu). Receptacles exposed to 15psu rarely released their oogonia/zygotes and none was released at salinity of 5psu. The low tolerances of this species to lowered temperature and reduced salinities appear to support these two factors as barriers to their dispersal. Reduced salinity should continue to serve as a barrier even with increase in sea temperature in the future due to global climate change. This research was supported by Hong Kong RGC GRF 460010.

DOES PHOSPHORUS LIMITATION AFFECT BIOFILMS IN AMD AND REMEDIATED STREAMS?

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Acid mine drainage (AMD) affects streams in the Appalachian region and other mining regions worldwide. Streams impacted by AMD were acidic as well as having high levels of iron and aluminum. To ameliorate water chemistry, treatment systems are employed to raise the pH and precipitate metals leaving downstream the water quality greatly improved. However, after water quality improvement, the biological community of some streams does not recover as expected. It is hypothesized that the biofilm in AMD and AMD recovering streams is limited by phosphorus. To study nutrient limitations, we employed nutrient diffusing substrates containing phosphorus, nitrogen, phosphorus and nitrogen or agar alone. Three streams unimpacted by AMD, four transitional streams showing little improvement, four recovered streams having marked improvement, and three AMD impacted streams were sampled. Extracellular enzyme activity, chlorophyll a, and total lipid profiles were analyzed. Significant differences were observed among stream categories for important variables. However, there were few interactive effects of nutrient treatment and stream category. In most stream categories there was a significant increase in chl. a in the nutrient treatments. As well, phosphorus acquiring enzyme activity decreased with the addition of phosphorus, but was not significantly different among categories. Many of the results corroborate previous studies of phosphorus limitation in AMD and AMD recovering streams.

CORALLINE DIVERSITY ALONG A KELP FOREST DENSITY GRADIENT: HOW BARREN ARE URCHIN BARRENS?

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According to the classic otter-urchin-kelp trophic cascade, when sea otters are removed from kelp forests, urchins increase in abundance, grazing down the kelps and ultimately creating “urchin barrens.” These denuded habitats represent an alternative state dominated by coralline algae, whose calcified thalli resist urchin grazing, and generally lead to declines in species diversity across all trophic levels. However, changes in coralline diversity have never been characterized. Morphological species concepts of coralline algae are deeply flawed and we are underestimating coralline diversity worldwide. For the first time, we use DNA sequencing to describe the diversity of corallines at four sites along the coast of British Columbia, representing a gradient of otter occupation, urchin abundance, and kelp forest density. As expected, coralline abundance increased as kelp forests thinned. Coralline communities were surprisingly rich with 10-12 species identified in kelp forests, 8-9 species in urchin barrens, and several new species that require taxonomic attention. Coralline communities within urchin barrens showed reduced Shannon-Wiener diversity and evenness: a few coralline species, also present in kelp forests, increased in abundance when kelps were removed, and other coralline species were lost altogether. This mismatch between increased abundance and decreased diversity likely reflects grazer-mediated shifts in space or light competition, revising the final chapter of the otter-urchin-kelp paradigm: in urchin barrens, even coralline algal diversity declines.

WHEN ALGAE ARE THE MENU, DIATOMS ARE THE ENTRÉE OF CHOICE FOR *TROPHEUS BRICHARDI* OF LAKE TANGANYIKA

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Lake Tanganyika, East Africa, is the world's second largest freshwater lake and is home to a diverse assemblage of fishes that provide people of the region with both food and income. *Tropheus brichardi* is a common algivorous cichlid that lives in near-shore rocky littoral zone. The growth and distribution of *T. brichardi* is closely correlated with algal nutrient content and eicosapentaenoic acid (EPA) content. We collected *T. brichardi* from 8 rocky sites in the northern basin of Lake Tanganyika to test the hypothesis that they selectively feed on bacillariophyceae (diatoms) because diatoms meet the criteria for a quality algal diet. We compared the relative abundance and biovolume of cyanobacteria, bacillariophyceae and chlorophyta within the environment and in the stomachs of at least two fish from each site. We calculated biovolume using a modified Hillebrand method. We used an alpha electivity index to compare stomach contents and samples from the environment. *Tropheus brichardi* strongly selects for diatoms and avoids ingesting cyanobacteria, and especially chlorophyta. Increased sedimentation at deforested sites was associated with higher algal biomass, but also a higher proportion of chlorophytes in the algal community.

Applied Phycology

USE OF MICROALGAE TO MITIGATE CARBON DIOXIDE EMISSIONS FROM SALT RIVER PROJECT'S CORONADO GENERATING STATION IN SAINT JOHN'S, ARIZONA
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The Federal government plans to impose regulations forcing coal fired power plants to reduce their carbon dioxide emissions by 50% by the year 2030. There is currently no single technology available to achieve such a drastic reduction. Current collaborative research with SRP's Coronado Generating Station has yielded very promising results. We have characterized all available source waters at CGS and have identified two abundant source waters, C Reservoir and CGS Evaporation Pond, that support microalgae growth (one freshwater and one saltwater, respectively). Several naturally occurring microalgae were isolated and screened for rapid growth and oil production from these source waters. One strain, AK-1, a unicellular green alga, appears to be a very promising isolate due to its rapid growth and ability to grow across a broad range of environmental conditions. Rapid growth and high biomass production translates into higher carbon capture. AK-1 is also a prime candidate due to the production of potential revenue generating products and co-products including biofuels and α -linolenic acid. We are concluding this year's research with large scale cultivation trials at AzCATI in 1000 liter open raceway ponds. The AK-1 strain exhibited exceptional growth in the outdoor open raceway ponds and some degree of resistance to external contamination. An overview of the establishment of an open raceway pond algae cultivation and carbon dioxide capturing pilot facility at the Orlando Utility Commission's Stanton Energy Center outside of Orlando, FL will also be presented.

EVALUATION OF NUTRIENT BIOEXTRACTION CAPACITY OF SEAWEED
AQUACULTURE IN KOREA

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Seaweed aquaculture provides ecosystem services, which is improving conditions of the coastal environments by removing nutrients. These ecosystem services are now referred as nutrient bioextraction. Korea is one of the leading countries in seaweed aquaculture. Koreans have harvested nearly 1.1 million tons of seaweed in 2014. Three genera, including brown seaweed, *Saccharina* and *Undaria*, and red seaweed *Pyropia* (formally known as *Porphyra*), occupies nearly 98% of entire seaweed production in Korea. The objective of this study is to evaluate the nutrient bioextraction capacity of seaweed aquaculture in Korea. Three major seaweed species are collected from major seaweed farm areas in Korea, including Wando (Jeon-nam), Kijang (Busan) and Seosan (Chung-nam) during the harvest periods. The productivity of each species in each area are obtained from the Ministry of Oceans and Fisheries of Korea. Tissue nitrogen and carbon concentrations are analyzed after the tissues are dried and ground from many culture areas. Combining the biomass yield, with the tissue nitrogen and carbon concentration of each species, the nutrient bioextraction capacity of each species will be presented.

GLYPHOSATE HERBICIDE TOXICITY TO NATIVE HAWAIIAN MACROALGAL AND SEAGRASS SPECIES

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Glyphosate-based herbicides are commonly used to combat weeds and unwanted grasses in many habitats in the Hawaiian Islands, including near freshwater, marine, and anchialine pond shorelines. Glyphosate is reported to degrade within a few days of application and to break down rapidly in soil, which suggests that it is safe for use near aquatic environments. However, glyphosate can be transported to coastal waters, especially during run-off events. Five native macroalgal and seagrass species and one introduced aquatic vascular plant found in coastal anchialine ponds or in the adjacent intertidal zone were exposed to freshly mixed solutions of a glyphosate-based herbicide in lab experiments. Chlorophyll absorbance and photosystem II (PSII) efficiency were measured after 5 to 7 days of incubation. At herbicide concentrations (0.225 to 1.8 g L⁻¹ glyphosate) below the manufacturer's lowest recommended concentration (3.6 g L⁻¹ glyphosate), chlorophyll absorbance and PSII efficiency differed significantly from the control (0.0 g L⁻¹ glyphosate). Native macroalgae and seagrasses in marine and anchialine aquatic habitats may be negatively affected by use of glyphosate herbicides to control shoreline weeds.

MOLECULAR AND PHYTOCHEMICAL METHODS FOR THE DETECTION OF THE HARMFUL BLOOM-FORMING ALGA, *PRYMNESIUM PARVUM* CARTER (HAPTOPHYTA)

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Prymnesium parvum is a global ichthyotoxic alga that causes harmful blooms, killing many different species of fish and gill-breathing organisms. The toxins formed by “golden algae” are potent at nanomolar concentrations, although many of these compounds have not been characterized and no chemical standards are available. To aid in the rapid detection of *P. parvum*, molecular methods were developed to detect whole cells or extracted DNA using conventional multiplex PCR and real-time quantitative PCR. With conventional PCR, samples positive for *P. parvum* had diagnostic banding patterns in electrophoresis gels consisting of 4 species-specific and gene-specific amplicons. Multiplex RT qPCR allowed quantitative detection of *P. parvum* from as little as 1 cell in samples using the PCR primers with 4 amplicon-specific molecular beacons. Thus far, these PCR-based methods have been capable of positively identifying more than 6 geographically-distant strains of *P. parvum*. Phytochemical methods were also developed for the detection of their toxins, polyketide “prymnesins”, prym1- and prym-2. Streamlined extraction procedures coupled with LCMS permitted the metabolic fingerprinting of these toxins, and allowed for the sensitive detection of prymnesins from modest quantities of culture. Chemifluorimetric methods were also developed for the semi-quantitation of prymnesins using spectrophotometry to measure exotoxins and endotoxins under various conditions. Such tools should broaden our understanding of *P. parvum* and bloom formation.

MARINE PLANT AQUACULTURE IN SOUTHEAST ALASKA

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Although mariculture operations in Alaska have existed for over 100 years, no successful effort has been made to create a viable commercial seaweed venture in the state. Due to recent interest in growing seaweeds as a source of nutrition, we have initiated research on the culture of several species of seaweeds that have commercial potential. In addition, in cooperation with private industry, we are working with state agencies to create a pathway for the permitting commercial seaweed hatcheries and farms. Research involves using various kelp species from SE Alaska to produce cloned male and female gametophytes. These clones can be kept indefinitely by omitting chelated iron from the culture media. Iron at about 2 micromolar will cause initiation of egg production from cloned females. Cremona strings seeded with *Saccharina latissimi*, *Alaria marginata* and *Nereocystis luetkeana* have been placed on longlines and outplanted in the nearshore in Juneau and Sitka, Alaska. Growth of these kelps was measured as function of time, depth and the location of the outplantings. Substantial growth occurs throughout the winter and spring with daily growth rates as high as 5 percent. Light appears to be limiting for growth during the winter months. Quantity and quality of the produced kelps is currently under assessment.

CHEMICAL TREATMENT TO CONTROL ZOOPLANKTON CONTAMINANTS FOR SUSTAINABLE ALGAL CULTIVATION

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Major obstacles for sustainable or long term algal cultivation are the diverse zooplankton contaminants that feed on algae and routinely cause demise of the algal culture, often described as culture crash. The broad taxonomic spectrum of invading zooplankton contaminants creates a major problem for their treatment and control. Key steps in the treatment and control process is the early detection and identification of the contaminant, quantification of the contaminants, and subsequent culture management to control the contaminants. This work focuses on the evaluation of a variety of chemicals used to control components of the complex zooplankton community that invades algae cultures while not noticeably affecting algal growth. Sodium hypochlorite (bleach), quinine sulfate, copper sulfate, Deltamethrin, λ - Cypermethrin were evaluated and the effectiveness was found to differ with respect to taxonomic groups. Our study shows that bleach and copper sulfate were effective in controlling ciliates and rotifers, and copper sulfate was effective in controlling *Poteroiochromonas* sp. Quinine sulfate inhibited the growth of ciliates, whereas Deltamethrin and λ - Cypermethrin were limited in their effectiveness on the contaminants tested.

Biofuels

AN ASSESSMENT STUDY ON PILOT SCALE UNIALGAL CULTURE OF *NANNOCHLOROPSIS* SP. FOR BIOCHEMICALS AND BIODIESEL PRODUCTION

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Unialgal culture of *Nannochloropsis sp.* was batch grown in 200L for each six raceway ponds - at the faculty of Science, Alexandria University - in the spring season of 2015. The aim was to determine the growth characterization and the biochemical composition of algal biomass, as to evaluate the biodiesel processed according to the international standards.

Results showed that the maximum cell population ($40.6 \times 10^6/\text{ml}$) was recorded at the day 14, with a biomass productivity of $1.2 \text{ g L}^{-1}\text{d}^{-1}$. Cell harvesting for all running cultures was yielded 10 kilo algae paste, which on dryness gave 1.05 kilo dry algae powder.

Lipid productivity was $0.46 \text{ g L}^{-1}\text{d}^{-1}$, while the amounts of the following biochemicals were: Total lipids/biomass %, 38; neutral lipids/biomass %, 34; carbohydrate, 14.5 g L^{-1} ; protein, 38.51 g L^{-1} ; Chl a, 6.26 mg L^{-1} ; and total carotenoids, 14.25 mg L^{-1} .

Analysis of FAMES pool demonstrated the presence of 15 fractions; with carbon chain lengths ranged from C6 to C22. Most of the important fatty esters for biodiesel quality are present. Furthermore, the proportion of saturated fatty esters to unsaturated ones was 1.8 approximately. The purity of FAMES comprising biodiesel was 82%. To evaluate the pretend biodiesel according to the European standards (EN14214), detailed chemical analyses were carried out on. In addition, a brief economic evaluation and the fundamental aspects for constructing a commercial scale of algae cultivation system in Egypt were also postulated.

DEVELOPING AN EVOLUTIONARY ROADMAP TO HIGH LIPID ACCUMULATING DIATOMS: A COMPARITIVE PHYLOGENETIC EVALUATION OF THE GENUS *HALAMPHORA*

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Commercial products derived from algal lipids have long been touted as a promising alternative to the petroleum, plant and animal based options currently in production. Although promising, commercial algal lipid production has not reached predicted levels and current screening efforts may not be meeting the needs of a new generation of algal biomass research. An alternative to the broad based screening efforts that characterized early research is a systematic phylogenetic approach. This method uses a known phylogeny to create an evolutionarily representative taxa subsample for further investigation. Lipid content values can then be compared through a meaningful evolutionary context and predictive conclusions can be drawn. In this investigation, 32 taxa from the diatom genus *Halamphora* where investigated for growth and lipid accumulation under nutrient replete and silica deplete conditions. These measured values were evaluated within the context of evolutionary relationships, based on a four marker molecular phylogeny of the genus. Results presented here indicate that there is significant variation within habitat conductivity and lipid accumulation between *Halamphora* taxa and that this variation exhibits a significant phylogenetic signal, in that more closely related taxa resemble each other more than randomly assembled taxa. Because significant signal exists, the *Halamphora* phylogeny can be used as a predictive roadmap for the selection of high lipid accumulating taxa that can be grown under specific conditions.

ASSESSMENT OF ALTERATIONS IN METABOLOMICS AND LIPIDOMICS OF *NANNOCHLOROPSIS SALINA* IN RESPONSE TO COLD STRESS

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Many species of oleaginous microalgae are being researched for the production of different classes of metabolites. Polyunsaturated fatty acids (PUFAs) such as n-3 docosahexanoic acid (DHA) and n-3 eicosapentaenoic acid (EPA) are of particular clinical and health interest for their benefits in preventing cardiovascular disease and Alzheimer's. The species *Nannochloropsis salina* is a well-researched candidate as a commercial source of EPA. PUFAs are often stored in polar lipid pools found in the membrane, where they contribute to fluidity and maintain the structure of the cell. Reduced temperature ("cold stress") is known to increase lipid production, specifically the desaturation and incorporation of PUFAs into the membrane lipid pools. Here we assess the metabolic response of *N. salina* under the following temperature conditions: 5°C, 10°C, 15°C, and 25°C. Initial stress response was determined by photosynthetic activity and oxygen measurements. Decreasing temperatures induce reductions in photosynthetic activity and the proliferation of cells. Alterations in metabolite profiles were quantified with GC-TOF MS to determine metabolic response. Metabolic analysis suggests that a decrease in anaplerosis and depletions in TCA cycle intermediate pools occur in cultures under cold stress. This response indicates cellular metabolic imbalance between treatments in favor of biosynthetic pathways, such as PUFA synthesis and remodeling of the membrane lipid pool. Lipidome profiles were also quantified to determine PUFA and EPA content by fatty acid methyl ester (FAME) analysis.

Frontiers in Population Biology/Biogeography

BIOGEOGRAPHY OF CORALLINE ALGAE (RHODOPHYTA) BASED ON DNA SEQUENCED TAXA: A FIRST SYNTHESIS

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Our understanding of coralline algal biogeography has been hindered by the failure of morpho-anatomical studies to provide characters useful in identifying species and delineating monophyletic genera. Only in the last five years, by applying DNA sequencing to field-collected and type specimens, have biogeographic patterns begun to emerge. Many coralline species are reported to be widespread in different biogeographic provinces and even in different ocean basins based on morpho-anatomy. These distributions have not been supported by DNA sequence data, except for a few tropical Indo-West Pacific/Caribbean Sea species. In the best documented example, *Lithophyllum kaiseri*, *psbA* sequences show little to no variation in specimens in the Western Pacific Ocean, Red Sea and Caribbean Sea. However, most coralline

algae have more restricted distributions. In Hapalidiales, *Clathromorphum* and *Neopolyporolithon* are subarctic and boreal genera, whereas *Callilithophytum* is known only from the boreal Northeast Pacific, and all have been rendered monophyletic. All southern hemisphere *Clathromorphum* species belong in other genera. The Northeast Pacific is revealed as a center of coralline endemism, with six endemic genera. As we further clarify species and resolve monophyletic genera, coralline distribution patterns will play an increasingly important role in understanding marine biogeography.

INTRASPECIFIC SUCCESSION WITHIN *PSEUDO-NITZSCHIA PUNGENS* POPULATIONS IN SOUTHERN KOREAN COASTS VIA USE OF QUANTITATIVE PCR ASSAY

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Three genetic sub-populations (clade I, II and III) of *Pseudo-nitzschia pungens*, potential toxic marine diatom, were known as having different physiological characteristics and distinct distribution. But, due to lack of the method to quantify the each clade of *P. pungens*, there is no study how their different physiologies affect on distribution and dynamics in fields. Thus, we developed the quantitative PCR (qPCR) assay to detect and quantify the *P. pungens* cells of each clade. Two specific primer sets which targeted on clade I and II (Pcla12F/R) and clade III Pcla3F/R were designed. Significant linear correlation (0.998 R^2) were established between Ct and the log of the copy number for qPCR assay of each clade. Interestingly, different fluctuation patterns between clades I and III were revealed in Korean southern coasts during 2009 - 2010. Clade I populations were detected from spring to early winter including lower seawater temperature, whilst, clade III were only prospered during summer to autumn when the higher temperature seasons. These dynamic patterns relating to temperature were coincided in previous physiological experiments for each clade. Especially, clade III abundances were strongly correlated with temperature in redundancy analysis. These results implicate that our qPCR assay is a powerful technique to estimate the cell abundances of each clade of *P. pungens* and could be expected to track different ecological niches and origins of three clades in natural system.

A METABARCODING COMPARISON OF AIRBORNE ALGAE FROM WINDWARD AND LEEWARD OAHU, HAWAII

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Airborne algae are important as colonists of new substrata, sources of inhalant allergens, contaminants of drinking water, and as contributors to the deterioration of architectural

structures, yet little is known about their diversity, abundance, and seasonal patterns in most areas of the world. The Hawaiian Islands are an ideal location for the study of airborne algae due to their distance from continental landmasses, predictable weather patterns, and the ongoing systematic characterization of the algal flora. We investigated airborne algal diversity collected during a 16-day period at six sites on the island of Oahu (three each on the windward and leeward side of the Koolau Mountain range) using a metabarcoding approach with the UPA amplicon and the Illumina MiSeq sequencing platform. Back trajectories of air masses arriving at each site during the study were determined using NOAA's HYSPLIT model. 3,023 OTUs were identified from the sequencing run, of which 1,238 were algal (including cyanobacteria). Proportions of sequences representing broad taxonomic categories of algae varied within and between sites, but a greater number of OTUs was detected from windward than leeward Oahu samples, which is consistent with the arrival of airborne propagules on the prevailing NE trade winds. Back trajectories of air masses indicated a large degree of variation in air mass source during the sampling period such that a single extra-Hawaiian source could not be identified.

HABS/ Algae and Human Affairs

CLADISTIC ASSESSMENT OF CYANOTOXIN PRODUCTION IN MARINE, FRESHWATER, AND TERRESTRIAL CYANOBACTERIAL ISOLATES

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There has been no systematic assessment of toxin occurrence across the Cyanophyceae, even though cyanobacteria produce a variety of secondary metabolites known to cause significant human health and environmental concerns. This study measured microcystin, cylindrospermopsin, anatoxin-a, saxitoxins, anabaenopeptins, antillatoxins, and BMAA accumulation in 33 genera of terrestrial, freshwater and marine cyanobacteria. The presence of cyanotoxins was confirmed using ultra performance liquid chromatography/triple-quadruple and time-of-flight mass spectrometry. Phylogenetic trees were built, according to genera and habitats, to help interpret cladistic relationships of the toxin producers. Aeruginosins, a group of protease inhibitors, were produced by all cyanobacterial genera. The second most common cyanotoxin identified were the anabaenopeptins, a group of carboxypeptidase A and phosphatase 1 inhibitors. Co-production of multiple cyanotoxins was determined in over 50% of the isolates. The terrestrial cyanobacterium, *Capsosira lowie* (Capsosiraceae) is the first species known that produced both epoxy-anatoxin-a and microcystin-LA. This study is the first systematic assessment of cyanobacterial toxins and the diversity of toxin occurrence in different habitats is critical for recognition of toxic cyanobacteria and their management.

MODELING *GAMBIERDISCUS* GROWTH IN THE CARIBBEAN AND GULF OF MEXICO AND POTENTIAL FOR ASSESSING THE RISK OF CIGUATERA FISH POISONING

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Benthic dinoflagellates in the genus *Gambierdiscus* produce potent neurotoxins known as ciguatoxins. These large lipophilic polyether toxins bioaccumulate in the food chain, reaching their highest concentrations in fish. Consumption of fish containing sufficient ciguatoxin causes ciguatera fish poisoning, the largest cause of non-bacterial seafood poisoning associated with eating fish. Because measuring ciguatoxins is expensive and analytically complex, assessing CFP risk through a direct monitoring program is challenging. A possible alternative approach to identify when and where CFP risk is greatest is to develop an ecologically based risk assessment model. Laboratory studies demonstrated that *Gambierdiscus* growth is strongly dependent on water temperature, and much less so on light or salinity. Field studies further indicate that nutrient limitation is not a controlling factor in the benthic habitats occupied by *Gambierdiscus*. This talk presents the results from the first phase of the ecological risk assessment model development which predicts monthly growth rates for five *Gambierdiscus* species throughout the Caribbean and Gulf of Mexico from 2003 to 2013. The hypothesis being tested is that the highest predicted growth rates will correspond with regions where CFP is most commonly reported. The modeling results showed little interannual variation in growth, but that predicted growth rates were highest in the central and eastern Caribbean where reported CFP cases are highest. Differences in local, seasonal and annual growth predicted by the model will be discussed.

CHRONIC DIETARY EXPOSURE TO A CYANOBACTERIAL TOXIN, BMAA, CAUSES HUMAN NEURODEGENERATIVE DISEASE

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The neurotoxic amino acid, β -N-methylamino-L-alanine (BMAA) has been linked to human disease, particularly with the neurodegenerative disease Amyotrophic Lateral Sclerosis/Parkinsonism Dementia Complex (ALS/PDC) among the Chamorro villagers on Guam. The finding of BMAA within the brains of Alzheimer's and ALS patients outside of Guam indicated a cosmopolitan source of production, later found to be cyanobacteria. Recent papers suggest that the toxin may also be produced by diatoms and even dinoflagellates. In order to understand the role of BMAA in neurodegenerative disease, vervets were fed BMAA dosed into fruit at two doses, with the lower dose more closely resembling a lifetime Chamorro BMAA dose. In addition to a control vervet cohort, a further cohort was dosed with BMAA and L-serine. Brain tissues of all vervets fed BMAA contained this neurotoxic amino acid, whereas BMAA was not

detected in the control cohort. Neuropathology consistent with Chamorro villagers who died of ALS/PDC, was evidenced by the presence of neurofibrillary tangles and amyloid plaques in BMAA-dosed vervets. However, no tangles or amyloid deposits were found in brain tissues from control vervets. Co-administration of L-serine, previously shown to block the incorporation of BMAA into proteins, significantly reduced the density of these neuropathological hallmarks of neurodegenerative disease. These findings raise serious concerns about exposure to BMAA through a variety of exposure routes and their effect on human health.

THE AUDUBON PARK LAGOON NANOSAFARI: INVESTIGATING AN IPAD APP AS A LEARNING TOOL TO LINK MICROSCOPIC ORGANISMS AND PEOPLE VISUALLY

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We hypothesized that most people do not understand the critical role microbes play in the Earth's natural systems because they cannot see them. The objective here was to increase understanding of microbial biodiversity and ecological roles by using an iPad application to link learners and microalgal images in a natural setting. Students participated in a "NanoSafari" nature walk with an iPad containing microalgal images and other information from a pond in New Orleans, LA. Images, via photomicrography, and related data on the algal flora were obtained during biweekly sampling January–June 2014 to develop the Audubon Park Lagoon NanoSafari menu line in the "GO to Lake Thoreau" iPad application. The opening screen addressed three questions, "Where is the Audubon Park Lagoon?", "What is a NanoSafari?" and "What are algae?". Next, participants explored three theme-based stations, "Algal Diversity", "Algal Communities" and "Ecological Interactions". The effectiveness of the NanoSafari as a learning tool was tested in a college-level, introductory laboratory course. Ten objective, content questions were administered to three course sections before and after the NanoSafari experience and one control section that did not experience the NanoSafari. There was no difference in the pre-assessment scores between the control and NanoSafari groups. Although pre- versus post-assessment scores increased for both groups, the NanoSafari group increases were larger than the control ($p \leq 0.05$).

EFFECT OF SMALL SCALE TURBULENCE ON THE GROWTH AND METABOLISM OF *MICROCYSTIS AERUGINOSA*

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Harmful algal blooms (HAB) are a ubiquitous water quality, ecological and public health concern. HAB not only increase turbidity and deplete nutrients in lacustrine surface waters; they also can be toxic. *Microcystis aeruginosa* is a widely studied and competitive toxic cyanobacteria species responsible for HAB worldwide. In addition to temperature, light and nutrient abundance, fluid motion is an abiotic environmental factor affecting *Microcystis* physiology. We investigated the effect of small-scale turbulence on the growth and metabolism of *Microcystis aeruginosa* using field measurements, midscale outdoor mesocosms and laboratory bioreactor investigations. Laboratory bioreactor experiments were paired with field measurements in the lacustrine photic zone from Lake Minnetonka (MN) to ensure that turbulent kinetic energy dissipation levels, Reynolds numbers, water temperature, dissolved oxygen and pH were reproduced under laboratory conditions. Our results show that small-scale turbulence affected the metabolic photosynthesis of *Microcystis* without majorly affecting the population growth rate (-5% and 11% for $Re\lambda=33$ and $Re\lambda=15$, respectively, as compared to stagnant conditions, see Wilkinson et al, “Cyanobacteria Research”[Special Issue] *Advances in Microbiology*, 2016). The above experiments were performed using lab cultured unicellular *Microcystis*, our current investigations explore potential differences in growth and metabolic responses between lab cultured unicellular and colonial, actively buoyant, *Microcystis* samples under the same experimental conditions.

Evolution/Genomics

ELUCIDATING RETROGRADE SIGNAL TRANSDUCTION PROCESSES IN THE DIATOM *PHAEODACTYLUM TRICORNUTUM*

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The ability of diatoms to rapidly and reversibly respond to changes in environmental cues (e.g., light, nutrients, temperature) is reflected in physiological plasticity. This has allowed them to rise to ecological prominence over the past 30 million years. However, the mechanisms underlying perception and transduction of these signals remain enigmatic. We postulate that the redox state of the photosynthetic electron transfer chain is a major factor in controlling the expression of nuclear genes. Consequently, we hypothesize that in diatoms, environmental cues are communicated via a retrograde signal transduction (RST) pathways emanating from the plastid. Using our experimental data and the most recent annotation of the *P. tricorutum* genome, we conducted a bioinformatic analysis to identify homologs of proteins that have been identified in signal transduction pathways in higher plants and green algae. Our bioinformatics survey suggests that RST pathways in *P. tricorutum* comprise a simpler, trimmed-down version of those found in the green lineage. However, we suggest that the RST pathway(s) found in extant diatoms are a relic “starter set” of core molecules that were later elaborated upon in other taxa. Currently, we are systematically genetically modifying all of our target genes in *P. tricorutum* to find “environmentally-numb” strains.

CONFLICTING EVIDENCE FOR HORIZONTAL GENE TRANSFER IN *SCYTONEMA HYALINUM*

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16S rRNA gene sequence data have become critical for understanding microbial evolution, definition of taxa (particularly genera, but species as well), estimating metagenomic diversity in localized environments, and estimating total microbial species diversity on the planet. We have recently discovered a highly divergent ribosomal operon in *Scytonema hylainum* that is only 92% identical to the other four operons in the genome, which are all >99.5% similar to each other. If bacterial and archaeal taxa with truncated operons or large insertions and deletions are eliminated, this represents the highest divergence among intraspecific ribosomal operons that has been documented in prokaryotic strains. We have documented the presence of this operon in 14 different strains of *S. hylainum*, which based upon ITS sequences represent at least five cryptic species. This means that the event leading to the production of this unusual operon preceded the evolution of a number of species in this lineage. The differences are localized, but present in all four domains of the 16S rRNA molecule. This could be considered evidence for HGT of an entire 16S rRNA gene, but several inconsistencies contradict this conclusion. For an evolutionarily ancient event such as this (preceding speciation of a number of taxa), one would expect gene conversion, which has not occurred. Furthermore, more divergence among orthologous operons would be expected given the evolutionary time frame. *S. hylainum* presents an evolutionary puzzle that calls into question the assumption that HGT can be used as a ready explanation for the presence of divergent ribosomal genes.

GOING, GOING, GONE? THE FATE OF PHOTOSYNTHESIS GENES IN A RED ALGAL ALLOPARASITE

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Genomic data from highly derived, formerly photosynthetic eukaryotic parasites has revealed fascinating innovations that evolved over hundreds of millions of years, enabling parasites to infect and evade their hosts. However, little is known about the early consequences of an organism transitioning from a photosynthetic life strategy to parasitism. Recent counts identify more than 100 different parasitic red algal species found across eight orders of the Florideophyceae, all of which solely infect other red algal species. These parasitic red algae are classified based on their relationship to their hosts as either adelphoparasites, which infect close relatives, or alloparasites, which infect more distantly related species. This evolutionary gradient of parasite-host relationships provides framework for investigating the early stages of genome evolution as an organism gives up autotrophy in favor of parasitism. Recently we sequenced a reduced plastid genome from the unpigmented alloparasite *Choreocolax polysiphoniae*, which has lost all photosynthesis genes. Here we present transcriptomic data from *C. polysiphoniae* and its free-living host *Vertebrata lanosa*. These data, in combination with genomic DNA sequence data for these taxa was compared with published data for photosynthetic members of the Florideophyceae. *Choreocolax polysiphoniae* appears to have lost almost all nuclear-encoded

genes involved in plastid maintenance and photosynthesis. Investigation of these data and their implications for the evolution of parasitism is ongoing.

GENOMICS SOLVES THE MYSTERY: PALMOPHYLLOPHYCEAE CLASS. NOV. IS THE DEEPEST-BRANCHING LINEAGE OF THE CHLOROPHYTA

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Recent molecular data have revealed an unrecognized early-diverging lineage of green plants, the Palmophyllales, which occur in marine deep water and other dimly lit environments, and shows a unique form of multicellularity (palmelloid organization). The phylogenetic position of this enigmatic group, however, remained uncertain. Here we elucidate the evolutionary affinity of the Palmophyllales using chloroplast genomic and nuclear rDNA data. Phylogenomic analyses firmly placed the palmophyllalean *Verdigellas peltata* along with species of Prasinococcales in the deepest-branching clade of the Chlorophyta. The circular chloroplast genome of *Verdigellas peltata* is 79,444 bp long, which is smaller than most chloroplast genomes (cpDNAs) of free-living green algae, but in the range of published prasinophyte cpDNAs. We identified 113 unique genes, including 85 protein-coding genes, 25 tRNA genes, and three rRNA genes. The small, compact and intronless cpDNA of *V. peltata* showed striking similarities in gene content and organization with the cpDNAs of Prasinococcales and the streptophyte *Mesostigma viride*, indicating that cpDNA architecture has been extremely well conserved in these deep-branching lineages of green plants. The phylogenetic distinctness of the Palmophyllales-Prasinococcales clade, characterized by unique ultrastructural features, warrants recognition of a new class of green plants, Palmophyllophyceae class. nov.

REDUCED ALGAL GENOMES REVEAL INSIGHTS INTO THE EVOLUTION OF PRE-MRNA SPLICING

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Pre-mRNA splicing is a highly conserved eukaryotic process. However, in some protists, under the pressures of genome reduction, the splicing process and machinery can deviate. Our studies extend this assessment to reduced algal genomes, especially those from red algae. Transcriptomic data from the red algal extremophile *Cyanidioschyzon merolae* showed unusually high levels of intron retention, similar to observations in highly reduced microsporidia. We then used the nucleomorphs of secondary endosymbionts as models of genome reduction. Strand-specific transcriptomic data were generated from the cryptophyte *Guillardia theta* and the chlorarachniophyte *Bigelowiella natans*, whose plastids derive from red and green algae, respectively. While the few introns of the *G. theta* nucleomorph are often not spliced and

retained in mature transcripts, the many short introns of the *B. natans* nucleomorph are spliced at typical eukaryotic levels (>90%), which raises the question of whether this difference indicates two independent evolutionary outcomes of genome reduction, or if this reflects the ancestry of the respective plastids. As further sampling of red algae is required to tease apart these alternatives, strand-specific transcriptomes of the mesophilic *Porphyridium purpureum* and extremophilic *Galdieria sulphuraria* were sequenced and analyzed. This not only gives us further insight into red algal genome evolution, but also impacts our broader understanding of the effects of genome reduction on pre-mRNA splicing.

Posters

P01. EXPLORATION OF *SPIRULINA PLATENSIS* AGAINST THE BIOFILM OF NOSCOMIAL PATHOGEN *PSEUDOMONAS AERUGINOSA*

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Multidrug resistant bacterial infections have increased the rate of morbidity and mortality all over the world. Bacteria secrete strong polymeric substances leading to the formation of a complex structure called biofilm, which provides resistance towards antimicrobial agents. *Pseudomonas aeruginosa* are one of the widely studied biofilm forming Gram negative bacteria known to cause nosocomial infection. Quorum sensing (QS), Cell surface hydrophobicity (CSH) and Extracellular polysaccharides (EPS) are the factors influencing biofilm formation of *P. aeruginosa*. To address these problems natural compounds has been targeted. Utilization of *Spirulina platensis* as antibiofilm agent could be a beneficial report due to its utilization as food, feed, and fodder. Based on this background *Spirulina platensis* methanolic extract (SME) was selected against *P. aeruginosa* biofilm. Initially SME at a concentration of 100 ng mL⁻¹ inhibited a maximum of 85% of biofilm, 94% of Cell Surface Hydrophobicity and 95% of Extracellular polymeric substances. Therefore the result confirmed *Spirulina platensis* as a suitable candidate for the elimination of *P. aeruginosa* biofilm.

P02. MORPHOLOGICAL DIVERSITY OF BENTHIC CYANOPROKARYOTA FROM A ROCKY SHORE OF "LOS TUXTLAS" REGION, VERACRUZ, MEXICO

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Studying the diversity tropical marine cyanoprokaryotes is challenging due to the little knowledge there is for this group, as most identification manuals and specialized studies deal mostly with temperate and/or continental European and North American species. Our study analyses samples from "Playa Hermosa", a rocky beach within "Los Tuxtlas" region collected along three seasons. Fifteen cyanoprokaryote taxa from the supra and intertidal fringes are described morphologically and ecologically. Nostocales with eight species, have the most conspicuous growths, in which the four Chroococcales, one Pleurocapsales and one

Oscillatoriales are included. *Lyngbya* sp. grows as a *Bostrychia* sp. epiphyte. Four of our taxa are new reports for the Mexican coasts (*Asterocapsa* sp., *Calothrix* cf. *nodulosa*, *Scytonema* cf. *tolypothrichoides* and *Siphononema* sp.). *Kyrtuthrix* cf. *maculans* is a new report for the Mexican coast of the Gulf of Mexico, *Arthrospira* sp. and *Rivularia* cf. *atra* are new records for the state, and eight extend their known distribution in the state (*Calothrix* sp.1 and sp.2, *Chroococcus* sp., *Lyngbya* sp., *Oscillatoria* sp., *Petalonema* cf. *incrusters*, *Pleurocapsa* sp. and *Scytonematopsis* cf. *crustacea*). Most species were found within the upper intertidal and the supratidal zones than in the lower and middle intertidal.

P03. NUNDUVA A NEW MARINE GENUS OF RIVULARIACEAE FROM MEXICO'S PACIFIC COAST

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We describe a new heterocytous, fasciculated morphotype slightly tapered and with geminate false branching. Four populations were collected and isolated from the supra and intertidal fringe of two localities in the Mexican Pacific Coast. Their morphology was analyzed and their 16S rRNA gene sequence was compared with Genbank available sequences, mainly from order Nostocales. Our populations have morphological features such as geminate branching and hormogonia development similar to some Scytonemataceae members, however phylogenetic analyses revealed that, the strains obtained in this work fall within the Rivulariaceae clade and is closely related to marine taxon *Microchaete grisea* that has recently been assigned to this family. Considering that these strains form a strongly supported clade separated from other strains that are morphologically and phylogenetically similar, we decided to describe a new genus *Nunduva* gen. nov. with *N. fasciculate* as the type species.

P04. INVESTIGATING THE PHYLOGEOGRAPHY OF THE YELLOW SPOTTED SALAMANDER, *AMBYSTOMA MACULATUM*, AND TAXONOMIC IDENTITY OF ITS ALGAL SYMBIONT, *OOPHILA AMBLYSTOMATIS*

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The decline of global amphibian populations is a concern for biologists, as amphibians are often indicators of ecosystem stress. The North American yellow spotted salamander, *Ambystoma maculatum*, is a unique species that shares a mutualistic relationship with a unicellular green alga commonly described as *Oophila amblystomatis*. Though *O. amblystomatis* has been accepted as a "green alga" grouping with the *Chlamydomonas* genus, it lacks any formal taxonomic designation. The objective of this study was to resolve the taxonomic identity of *O. amblystomatis*, as well as to investigate the phylogeographic variability of both alga and its salamander symbiont, and to determine whether potential biogeographic variation reflects theorized patterns of post glacial expansion of North American taxa. Salamander eggs and their

inhabiting algae were sampled from ponds in four southern Ontario locations. Algae were extracted and sequenced using the 18S rRNA marker. Salamanders were sequenced using the Nad4 and D-Loop mitochondrial regions. Preliminary phylogenetic analysis has indicated genetic similarity between salamanders sampled in southern Ontario, but increased variability in comparison with samples from interior and the east coast of North America. These data may suggest the mixing of two divergent salamander populations (coastal and interior clades) in our sample region. Increased sampling across a larger range of these organisms is necessary however, to further support these findings.

P06. SODIUM EXPORT GENES: THEIR EXPRESSION AND ROLE IN SALT ADAPTATION FOR *CHARA LONGIFOLIA* (R. BR.) AND *CHARA AUSTRALIS* (R. BR.)

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Many species within the genus *Chara* have a range of tolerance when exposed to or cultured in varying salinities. We examine four potential genes (SOS1, ACA4, AHA9, PpENA) related to sodium export that have been previously established in embryophytes to determine their potential role in the export of Na⁺ in salt tolerant *C. longifolia* and salt sensitive *C. australis*. Since *Chara* being more closely related to embryophytes than Chlorophytes, we infer that similar genes will likely be the mechanism behind sodium export in *Chara*. Both *C. longifolia* and *C. australis* were exposed to a range of saline treatments: freshwater, saltwater, or during adaptation from freshwater to saltwater. We will examine sequences of genes homologous to these four genes in the unpublished genome of *Chara braunii*. RNA extractions for the treatments have been analyzed through next generation Illumina sequencing to create transcriptome libraries for each of the examined species. These data will be used to determine the gene expression and sequence for the specified genes. Primers will be generated from these sequences for quantitative-PCR to determine expression levels in the salt-sensitive *C. australis* and the salt-tolerant species *C. longifolia*. We hypothesize that the expression of these genes would be greater in the *C. longifolia* than in *C. australis* for all treatments, in higher salinities, and during adaptation to higher salt.

P07. DIVERSITY OF HALYMENIALES (RHODOPHYTA) ON THE BRAZILIAN COAST

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The taxonomic history of Halymeniales (Rhodophyta) is quite problematic, with reports of misidentifications and nomenclatural changes. This study aimed to investigate the diversity of Halymeniales along the Brazilian coast through molecular and morphological techniques. Three molecular markers were sequenced, UPA, COI-5P and rbcL, whose data were allied to morphological characters and resulted in 26 delimited species. A high incidence of cryptic diversity and morphological plasticity was found, as well as a total of 11 new scientific species and putative new genera. Data showed that *Cryptonemia bengryi*, *C. crenulata*, *C. delicatula*, Halymeniales sp. 1 and Halymeniales sp. 1 correspond to five new genera. The invasive

Grateloupia turuturu was detected for the first time on the Brazilian coast. *G. orientalis* and *G. yangjiangensis* constituted new records for Brazil, and this was the first time they were registered outside their type localities. Taxa previously attributed to *Corynomorpha clavata*, *C. seminervis*, *Halymenia floresii*, *H. pseudofloresii* and *G. filicina* refer to entities different from the authentic species and therefore were removed from Brazilian flora. Records of *H. elongata*, *H. floridana* and *G. filiformis* remain to be confirmed, once they could not be molecularly compared to authentic species sequences due to the lack of the latter. Nine taxa previously recorded to Brazilian coast were not found. This study contributed to the knowledge of Brazilian marine flora.

P08. NUTRIENT STATUS DETERMINES THE INTER CELLULAR ORGANIZATION AND DESICCATION TOLERANCE OF *GLOEOCAPSOPSIS* SP.

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We studied growth and desiccation tolerance of *Gloeocapsopsis* sp. isolated from the Atacama Desert. This cyanobacterium belongs to the poorly studied family of Chroococcaceae, and normally develops an organized and multilayered extracellular envelope within which colonies of several cells are formed. We studied the pattern of growth and colony development by using flow cytometry combined with microscopy. During active growth, the percentages of single cells and larger colonies both increased, with growth arrest in stationary phase principally in intermediate colonies. Two different chromatic single cell stages were found, with very distinct autofluorescence emissions – deep red vs. yellow/orange – but with similar light scattering properties. Population distributions between alternate chromatic single cell types and the colony types changed greatly under phosphate limitation, with the disappearance of yellow/orange-fluorescent single cells and a lower portion of large colonies during active growth. Tests of membrane integrity and metabolic activity revealed that cells entered into anhydrobiosis once desiccated under nitrate-limited or replete conditions. However, most cells maintained their metabolisms active when desiccation occurred under phosphate-deprivation, as well as they developed a thicker extracellular envelope with a different structure and permeability. Nutrients appear to play a central role in the intercellular organization of *Gloeocapsopsis* sp. and prior nutrient status could determine the balance between alternative strategies to tolerate desiccation.

P09. POTENTIAL FOR GROUNDWATER CONTAMINATION BY SURFACE WATER SOURCES OF CYANOBACTERIAL TOXINS

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The risks associated with exposure to cyanobacterial toxins are well known, largely from surface water sources. However, much less is known about the risk of exposure to cyanobacterial toxins from ground water sources. Preliminary studies suggest that cyanotoxins can contaminate groundwaters via direct contact or through infiltration. This study employed sediment columns to determine whether cyanobacterial cells or two cyanotoxins, microcystin-LR, a known hepatotoxin and BMAA a neurotoxin implicated in neurodegeneration, can move through Lake Michigan sediment to contaminate groundwaters. Columns 90 cm long were filled with sand, as a control, or Lake Michigan sediment, corresponding to the lake sediment profile. Deionized water flowed through the column at a rate of 150 ml per hour for a total of 70 hours. Samples were collected from different heights of the column every 5 hours. After 24 hours, the separate columns were spiked with either BMAA, microcystin-LR or cyanobacterial cells of known concentration and their migration was monitored for the remaining 46 hours. Samples were analyzed using UPLC-EMD for BMAA, ELISA for microcystin-LR and chlorophyll a for cyanobacterial cells. Results showed that cyanobacterial cells can migrate through sediment and that the flow of cyanotoxins through sediment varies, suggesting that groundwater quality in the Great Lakes region is unequally at risk from cyanotoxin contamination.

P10. A DOPAMINE-PABA ADDUCT ASSAY ENABLES SPECTROPHOTOMETRIC QUANTIFICATION OF DOPAMINE RELEASE BY THE MARINE ALGA, *ULVARIA OBSCURA*

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Dopamine (DA) released by the green macroalga *Ulvaria obscura* undergoes a series of oxidation-reduction reactions. In the first reaction, DA is oxidized to a highly reactive derivative, dopamine-o-quinone (DQ) that then undergoes rapid intramolecular cyclization that is the key event on the route to melanin formation. However, in DA oxidation reactions carried out in acidic conditions (pH 4) in the presence of p-aminobenzoic acid (PABA), the cyclization step does not occur due to the formation of a DQ-PABA adduct. This adduct appears as a stable, reddish chromophore having an absorbance peak (λ_{\max}) at ~450 nm. We have confirmed the usefulness of using DQ-PABA adduct formation as an assay in UV-Vis spectrophotometry experiments to quantify DA concentration in the range of 0.5 – 18 mg/L. We were able to apply the assay to DA released by 1 cm diameter disks cut from field-collected thallus samples of *Ulvaria*. The amount of DA released per disk (~7.8 mg/L) using the assay is equivalent to ~16 $\mu\text{g}/\text{mg}$ wet weight (or ~1.6% of fresh mass) and is in the range of estimates published using other methods (e.g., HPLC). The DQ-PABA adduct assay should thus be useful in testing conditions that affect DA release from *Ulvaria*. As expected, DQ-PABA adduct formation is inhibited by strong antioxidants, such as ascorbic acid and sodium meta-bisulfite.

P11. RESOLVING THE *GRACILARIA DOMINGENSIS* SPECIES COMPLEX (GRACILARIACEAE, RHODOPHYTA) USING MOLECULAR AND MORPHOLOGICAL DATA

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Species in the genus *Gracilaria* that display conspicuously flattened vegetative morphologies are among the most taxonomically challenging groups of marine benthic red algae. This conundrum is a result of the large number of species involved, widespread morphological similarities, and rampant phenotypic plasticity. Within this group, the *Gracilaria domingensis* complex is one of the most common, conspicuous, and morphologically variable species along the tropical Western Atlantic Ocean. Our study assessed the species diversity within this notoriously difficult complex using morphological, phylogenetic, and seven single-marker species delimitation methods (SDM: mBGD, ABGD, GMYCs, GMYCm, SPN, bPTP and PTP) applied to three genetic markers (cox1, UPA and rbcL). Among the markers, rbcL produced the most well resolved phylogeny and achieved the greatest agreement among our SDM analyses. These results, combined with our analysis of morphology, collectively suggest that the *G. dominensis* complex best corresponds to four distinct species: *G. cervicornis*; a resurrected *G. ferox*; a new species, *Gracilaria baiana* sp. nov., and *G. domingensis sensu stricto*, which includes the later heterotypic synonym, *G. yoneshigueana*. Our study demonstrates the value of multipronged approaches, including DNA barcoding approaches, to decipher cryptic species of red algae.

P12. THE CHLOROPLAST GENOME OF A MICROSCOPIC MARINE GREEN ALGA FROM ANTARCTICA

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An unknown microscopic epiphytic marine green alga was collected in Antarctica growing heavily on the surface of a green seaweed, *Lambia antarctica*. Both, host and epiphyte, were sequenced via Illumina HiSeq. Two large plastid contigs were obtained, one corresponding to *Lambia* and the other one to a taxon related to *Entocladia*, the epiphytic chlorophyte. The epiphyte's plastid genome was assembled, edited, and annotated using the A5 pipeline and Geneious. The plastid genome is circular and 134,250 base pairs long. A total of 100 genes (71 protein-coding genes, 26 tRNAs, and 3 rRNAs) were identified, and 7 introns were present in five genes: psbB(1), petB(2), petD(1), atpB(2), psbD (1). This plastid genome revealed a highly

rearranged architecture when compared with other taxonomically related plastomes. A phylogenetic analysis of this microscopic epiphyte also revealed its position in the Ulvophyceae and sister to GenBank entry EF595342.1 (*Ulva* sp.). The taxonomic identity of this epiphyte may represent an unknown lineage found in the underexplored Antarctic region.

P13. MORPHOLOGICAL AND MOLECULAR ASSESSMENT OF SEaweEDS IN THE UNDERSTUDIED COAST OF ALABAMA

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The benthic marine algae from the Gulf of Mexico have been of great interest to several phycologists since 1802 for their ecological and economic importance in addition to their beauty. Biodiversity assessments from the Gulf of Mexico have identified 673 species of seaweeds. Despite previous works performed in the area, seaweeds of Alabama have largely been overlooked due to the belief that Alabama's short coastline would prove to be unproductive of marine algae (Taylor 1954). The last checklist that included marine benthic algae from Alabama in 1901 focused mostly on vascular land plants (Mohr 1901). Therefore, a modern biodiversity assessment of these algae from coastal Alabama is long overdue. Here, we investigate the Alabamian seaweed diversity (i.e. red, green, and brown algae) with a morphological and molecular approach. Thus far, since 2003 our studies has revealed up to 26 red, 14 green (eight *Ulva* species), and four brown seaweeds, which includes several new records and putative new species. This study is providing baseline information on the biodiversity, distribution, and seasonality of the marine algae of coastal Alabama, and will be useful to help discover and monitor for future introductions.

P14. METACOMMUNITY STRUCTURE AND COMMUNITY-ENVIRONMENT RELATIONSHIPS IN THE DELAWARE RIVER WATERSHED: IMPLICATIONS FOR BIOASSESSMENT USING DIATOMS

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The Delaware River Watershed Initiative (DRWI) is a long-term, collaborative water quality monitoring effort aimed at eight sub-watershed clusters in the Delaware River basin. The DRWI collects fish, macroinvertebrates and diatoms and associated environmental factors at streams targeted for restoration or habitat protection as well as baseline conditions at "integrative" control sites. We analyzed Elements of Metacommunity Structure (EMS; coherence, turnover, and boundary clumping) from diatom samples collected by the DRWI from 2013-2015. We determined environmental gradients most strongly related to EMS along primary and secondary axes of a detrended correspondence analysis (DCA) using CCA. Diatom communities were organized in a Clementsian structure along the primary axis, indicating distinct community types correlated with pH and conductivity gradients across the watershed. Along the secondary axis, sites were organized in nested subsets along a gradient of habitat quality. Notably, it appears that the observed Clementsian structure may be an artifact of uneven sampling distribution along pH

and conductivity gradients, despite no significant outliers. One of the major goals of the DRWI, like many other watershed bioassessment programs, is to use bioindicators to monitor changes in water quality by quantifying species' response to environment. An artificial Clementsian structure has important implications for describing species' environmental optima. EMS are important factors to consider in experimental design, sampling effort, and developing water quality metrics.

P15. DECLINES IN PHYTOPLANKTON ABUNDANCE IN THE SOUTH OF THE WESTERN ANTARCTIC PENINSULA (WAP) - A RESPONSE TO CLIMATE CHANGE?

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Since 1997, scientists at the British Antarctic Survey have been collecting data on parameters of physical oceanography, extent of sea ice cover, and phytoplankton abundance. Two decades of data suffice in providing an evaluation of seasonal patterns and long-term change, and comparisons with higher latitudes of the WAP. These data have been collected weekly from Ryder Bay on Adelaide Island. Physical measurements are taken with a CTD (Conductivity, Temperature, Depth Recorder). Seawater samples are collected from 15m depth and analyzed for size fractionated chlorophyll content. The results indicate that historically, seasonal phytoplankton blooms occur in the summer. Diatoms and chains of smaller cells (>20 µm) form those blooms. In recent years, less winter sea ice has accumulated. Additionally, stronger winds have been mixing surface waters. Phytoplankton blooms have decreased in size. Similar changes have been observed further north on the WAP. This pattern, in turn, impacts the marine ecosystem as phytoplankton compose the base of the coastal food web. A decline in krill abundance has been correlated to the decrease in phytoplankton which reduces food resources for local populations of Adelie penguins. It is likely that these dramatic changes are linked to anthropogenic climate change and will progress southwards to Ryder Bay.

P16. STRESS, HYPOXIA, AND HERBICIDAL TENDENCIES: MICROALGAE IN THE UNDERGRADUATE BIOCHEMISTRY LABORATORY

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A series of three biochemistry laboratory experiments is described which is an accompaniment to a metabolism-focused second term lecture course in biochemistry. The exercises each use selected species of microalgae to investigate (i) redox dynamics under salt stress, (ii) herbicide-induced metabolite depletion, and (iii) hypoxic metabolism. In the first experiment, salt-tolerant and freshwater microalgae are exposed to salt stress, and its impact on antioxidant status in the algae is evaluated using a luminescence assay. The second experiment examines the sensitivity of four classes of microalgae to an ALS-inhibitor type herbicide in terms of growth inhibition and depletion of branched chain amino acids. The third experiment demonstrates the effect of hypoxia on ATP and protein synthesis in diatoms. The students initiated and maintained algal cultures throughout the experiments, and their work in pairs enhanced their interest and encouraged peer learning. The experiments are discussed in the order performed, however any order of the exercises should be similarly engaging, economical, and convenient. Students are

exposed to the fascinations of microalgae while developing aseptic technique and exploring the principles of cell culture and spectrophotometry. Biochemistry lecture topics that are made more interesting and accessible include enzyme inhibition, metabolic intervention, low-oxygen metabolism, amino acid biosynthesis, redox dynamics, and cellular stress responses.

P17. NEW RECORD OF *GEITLERIA* IN NORTH AMERICA FROM THE GREAT SMOKY MOUNTAINS

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Morphological characterization of cyanobacteria has been utilized since their discovery in the microscope to understand the diversity and evolutionary relationships among and within them. With the advent of molecular techniques to analyze the 16S rRNA and associated 16S-23S ITS region, researchers have begun to test the taxonomic hypotheses made in the past, and revision and new discoveries have resulted over the last decade. However, many of the “old” described genera that were described using only morphologically techniques are relatively poorly understood in the study of cyanobacteria evolution. *Geitleria* was once a genus thought to only be found creeping along limestone substrates in caves of Spain but have now been reported in other locations such as *Geitleria floridiana* that was found on a limestone cave fissure in Marianna, Fl. Now another physical reporting is from a limestone substrate from the Great Smoky Mountain National Park. This adds interesting ecological details to a once ecologically narrow genus. However, it has yet to be cultured like many other ecologically peculiar cyanobacteria. Difficulties collecting DNA evidence and culturing have been linked to the habitat in which it is found and the deposition of calcium carbonate onto the filaments. From photograph images it appears to have a heterocyte. The future aim is to recollect the sample and to obtain molecular evidence and access the evolutionary relatedness as well as the condition of molecular markers of heterocyte formation. In doing this it will add much needed confirmation or clarification among the Symphonemataceae and the Hapalosiphonaceae.

P18. UNDERSTANDING THE DEEP PHYLOGENETIC RELATIONSHIPS OF THE THIN FILAMENTOUS SYNECHOCOCCALES (CYANOBACTERIA)

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Over the past decade considerable work has been conducted on the thin (<3.5 µm wide) simple filamentous cyanobacteria known as the Pseudanabaenales. In the most recent higher level classification scheme, these taxa were all placed in the Synechococcales in four families: Romeriaceae, Leptolyngbyaceae, Heteroleibleiniaceae, and Pseudanabaenaceae. Our recent analysis of over 300 OTUs in this group reveals that this new system is incorrect. Bayesian analysis revealed the existence of seven family-level clades, with generic representation different from the above. The major clades include the Leptolyngbyaceae (with *Leptolyngbya*, *Plectolyngbya*, *Tapinothrix*, *Phormidesmis*, *Planktolyngbya*, *Alkalinema*, *Romeria*, and several undescribed genera), "Neosynechococcaceae" (with *Stenomitos*, *Neosynechococcus*,

Pantanalinema, *Scytolyngbya*, and several undescribed genera), "Arthronemataceae" (with *Arthronema* and two undescribed genera), "Oculatellaceae" (with *Oculatella* and several undescribed genera), "Nodosilineaceae" (with *Nodosilinea*, *Jaaginema*, *Halomicronema*, *Prochlorothrix*, *Cyanobium*, and several undescribed genera), "Trichocoleaceae" (with *Trichocoleus* and one undescribed genus), and Pseudanabaenaceae (*Pseudanabaena*, *Limnothrix*). The new proposed family-level taxa are defined phylogenetically, and none can be distinguished morphologically.

P19. DESCRIPTION OF A NOVEL, CRYPTIC EPIPHYTIC CYANOBACTERIUM ISOLATED FROM A FRESHWATER LAKE IN NORTHEAST FLORIDA

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Cyanobacteria, also known as blue-green algae, are a group of photosynthetic organisms ubiquitous to both aquatic and terrestrial habitats. While genetically diverse, many cyanobacteria are indistinguishable by morphology alone due to phenotypic plasticity and dearth of characters. In order to assess phylogenetic placement of cryptic species, a polyphasic or total evidence approach is commonly used combining ecology, morphology, and molecular data (e.g., 16S rDNA gene data). An epiphytic, cyanobacterial sample was obtained from *Nuphar advena* leaves in Northeast Florida, a subtropical habitat. The cultured organism appeared as thin, unbranching filaments with no specialized cells, resembling *Leptolyngbya*. 16S rDNA gene and Internal Transcribed Spacer (ITS) data returned $\leq 93\%$ sequence similarity via BLAST search. Maximum Parsimony and Likelihood analyses did not place the strain in any supported clade. The ITS region was unique compared to the closest relatives. Based on ecology, 16S, and ITS data, we propose the erection of a new genus *Glomerolinea* (Latin for beaded thread) to describe this monospecific group.

P20. WHICH NAME SHOULD BE APPLIED *SONDEROPELTA* OR *SONDEROPHYCUS*?

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In the past decade there has been some confusion over the application of the name *Sonderophycus*. *Sonderophycus* originally was placed as incertae sedis within the red algae. Today, individuals who apply the name *Sonderophycus* recognize that it belongs to the red algal crustose order Peyssonneliales. Recently, there has been revisionary research conducted in the Peyssonneliales that has led to apparent problems with the use of the name *Sonderophycus* by some Phycologists. A systematic study conducted in the early 1980s resolved the nomenclatural issues with *Sonderophycus* in which the name was to be no longer applied; however, it appears that some are no longer following this treatment of *Sonderophycus*. In this study herein, we clarify why the name *Sonderopelta* should be used over that of *Sonderophycus*.

P21. MITOCHONDRIAL AND CHLOROPLAST GENOMES OF THE FRESHWATER RED ALGA *PARALEMANEA GRANDIS* (BATRACHOSPERMALES, RHODOPHYTA)

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Paralemanea grandis was collected from a turbulent flow region of the Cahaba River in Birmingham, AL USA. The sample was found growing from rock substrata adjacent to a USGS monitoring site (02423496). Mitochondrial and chloroplast DNA genome sequences were assembled and annotated from Illumina HiSeq pair-end reads. The mitochondrial genome was circular in construction and was 28,954 base pairs in length. There were 23 protein-coding genes, 17 tRNA genes, and 2 rRNA genes annotated to the mitochondrial genome. The *cox1* gene, which is commonly used as a “barcoding” marker for red algal species delimitation, contained a 2,257 base pair intron that might be problematic for PCR based Sanger sequencing methods. The chloroplast genome features the presence of two inverted repeat regions that include copies of the rRNA genes and makes the assembly problematic. The plastome is at least 179,531 base pairs in length with a minimum of 160 protein coding genes and at least 25 tRNA genes. A 2,022 base pair intron was found in the *chlB* gene. We are currently performing analyses to sequence through a short single copy (ssc) region of the plastome found in between the inverted repeat regions. Although *P. grandis* is a freshwater red alga, the mitochondrial and chloroplast genomes have a similar gene content to marine Rhodophyta.

P22. DEVELOPMENT OF A DIATOM-BASED, COST-EFFECTIVE BIOMONITORING TOOL FOR THE SAUDI ARABIAN RED SEA COASTLINE

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Diatoms are diverse group of single-celled algae with siliceous cell walls that are resistant to dissolution. Different species of diatoms are adapted to different environmental conditions. These properties make them useful indicators of environmental conditions, such as the Saudi Arabian Red Sea coastline, which has habitats that span a range of impacts. Diatoms can be used there to monitor nearshore environments and provide early warning of possible harmful or undesired water quality affects, or as monitoring tools that can be used to help provide objective goals for any efforts that might be implemented to mitigate water quality issues in a cost-effective fashion. Obstacles to utilizing diatoms in this way are: 1) the diatoms, particularly the benthic diatoms of the Red Sea are not well known taxonomically, 2) there is little information on the distribution of Red Sea diatoms in relationship to environmental parameters, and 3) identifying diatoms can be a time-consuming effort requiring highly specialized training. We hope to overcome these obstacles with an international collaboration to build a database of benthic marine diatoms and their habitats, in one of the first studies of marine benthic diatom tolerance and distribution in relationship to coastal pollution in a tropical region. This poster reports on our progress so far in collecting and cataloging hundreds of benthic diatoms, including dozens of undescribed taxa, from the reefs and harbors of the Red Sea.

P23. AEROTOPE PRODUCTION IN THE BENTHIC GENUS *NOSTOC*: MOLECULAR CONFIRMATION THAT *N. KIHLMANII* BELONGS TO *NOSTOC SENSU STRICTO*

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Historically, the ability to produce aerotopes (clusters of gas vesicles) was commonly considered to be a trait variably expressed within genera. *Anabaena*, *Coelosphaerium*, *Oscillatoria*, *Lyngbya*, *Nostoc*, and *Nodularia* all had aerotope-producing and aerotope-lacking species. With the advent of molecular sequencing it was discovered that in most instances, taxa occurring in aerotope-producing genera were unrelated to species in that genus incapable of aerotope production. This led to the separation of species into new genera, such as *Dolichospermum*, *Woronichinia*, *Planktothrix*, and *Limnoraphis*, and even to the splitting of the Aphanizomenonaceae out of the Nostocaceae. We were able to collect *Nostoc kihlmanii*, an aerotope-producing member of what is commonly held to be a terrestrial genus with the near universal lack of aerotope production from a wetland habitat in western Pennsylvania in the spring of 2014 and 2015. We directly sequenced the 16S rRNA gene, and phylogenetic analysis demonstrated that the species was certainly within *Nostoc sensu stricto*. We had expected different results. Now it can be stated that two genera in the Nostocaceae possess both species with and without the ability to produce aerotopes: *Nostoc* and *Nodularia*.

P24. ASSESSING THE APPLICATION OF INTERNAL TRANSCRIBED SPACER (ITS) REGION SECONDARY STRUCTURES TO CYANOBACTERIAL SYSTEMATICS THROUGH ORGANISM WIDE COMPARISONS

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Molecular phylogenetic studies have revolutionized cyanobacterial taxonomy. Classical morphology based systematics are not consistent with phylogenetic data, and do not accurately predict evolutionary relationships. Additionally, cryptic diversity and phenotypic plasticity make assessing cyanobacterial morphology particularly difficult. Cyanobacterial taxonomy is currently transitioning from morphological to molecular based taxonomic systems. Thus molecular tools have become increasingly important as taxa are defined and redefined during this period of flux. Conformations of the highly conserved Internal Transcribed Spacer (ITS) regions, located between the 16S and 23S rDNA genes, have proved phylogenetically informative in previous systematics research. Comparisons of the secondary structures of ITS regions for closely related taxa have become the standard when defining new taxa, especially when few morphological differences are observed but significant ecological differences exist. This study aims to compare ITS secondary structures from all orders of cyanobacteria. Secondary structure motifs will be compared between and among genera and species to evaluate to what degree they are consistent with molecular phylogenetic relationships. In addition to elucidating the viability of this molecular tool for large scale systematic application, this research will create the largest data set of folded ITS secondary structures against which future taxonomic comparisons can be made.

P25. GENOME-WIDE COMPARISON OF *PICOCHLORUM* (CHLOROPHYTA, TREBOUXIPHYTE) SPECIES

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Members of the *Picochlorum* genus are considered candidates for biofuel, nutraceutical, and wastewater applications due to their robustness, high biomass productivity, protein and lipid content. Physiological, photosynthetic, and genomic differences were compared for two closely related and highly salt tolerant species, *Picochlorum SENEW3* and *Picochlorum oklahomensis*. Although closely related, these species show large differences in genome size and gene family expansion in *P. oklahomensis*. The genomes were compared for evidence of positive selection on genes and we find that some of the fastest evolving genes and included genes involved in response to heat and high light, glutamate synthesis, starch production, and helicase activity, highlighting key functions that may be involved in adaptation to each respective habitat. Photosynthetic efficiency is similar between the two species and photosystem related proteins show evidence of extreme negative selection or selection for protein conservation. Several instances of horizontal gene transfer are also shared between the two species. An additional two *Picochlorum* species will be included in further comparison analyses.

P26. TESTING HYPOTHESES OF EUNOTIOPHYCIDAE EVOLUTION: HAVE WE REALLY DISCOVERED ANYTHING OVER THE LAST CENTURY, AND WHY DO WE BELIEVE THAT *PERONIA* IS ANCESTRAL?

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The Eunotioid group is considered to be the first raphe-bearing lineage in diatoms. Despite this, few investigations have undertaken detailed consideration of the raphe's evolutionary development either among Eunotioid species or within a broader systematic system of pennate and raphid diatoms. Contributing to the difficulty in clarifying and understanding is that multiple questions are being simultaneously asked. These simultaneous queries are not 100% compatible. Here, we look at evolutionary arguments relating to the evolution of the raphe and evaluate them in a hypothesis testing fashion, thus clarifying multiple questions concerning raphe evolution. We then select the single evolutionary question that can be corroborated or refuted with existing understanding of the morphological diversity of diatoms. Specifically, is *Peronia* a likely candidate to be the first raphe-bearing diatom? Using known morphological diversity analyzed via cladistic analysis, multiple hypotheses concerning the phylogenetic position of *Peronia* are tested. In all cases the idea of *Peronia* being a basal Eunotioid or raphid lineage is rejected. This conclusion has been further corroborated by recent molecular investigations. This study then demonstrates the need to test historically accepted evolutionary statements that have not been tested with modern methodologies.

P27. A NEW MOLECULAR CLOCK ESTIMATE FOR DIATOMS

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Speculation on the temporal appearance and diversification of diatoms is varied. This work has largely focused on identifying an origin time for diatoms. Estimates based upon fossil speculation range from the late Precambrian or early Paleozoic to Triassic. Molecular clock estimates range from the late Paleozoic to Middle Triassic. Little effort, comparatively, has been focused on identify the timing and divergence of evolutionary subgroups within diatoms. This work has been largely focused on freshwater Thalassiosiroid taxa utilizing both fossil and molecular datasets. Estimates for the origin of these taxa range from the Eocene to late Miocene. An abundant literature base exists with ample “well-dated” species specific observations as a result of IODP/ODP/DSDP efforts. Additionally, phylogenetic hypotheses based upon molecular data for diatoms are beginning to coalesce (sort of). We present a densely calibrated diatom molecular clock estimate. This estimate was created using the BEAST software package and utilized stratigraphic data gleaned from IODP/ODP/DSDP literature and a 250+ taxon, 3 gene phylogenetic hypothesis based upon genbank submissions. Results support a Triassic/Jurassic diatom origin and reveal multiple, concurrent diversification events within major diatom subgroups. The estimate also corroborates specific fossil and molecular estimates of subgroups and supports diversification events driven by major geological and ecological transitions. Finally, areas in need of greater taxon sampling are identified for the focus of future investigation.

P28. AN OVERVIEW OF THE TRIBAL CLASSIFICATION OF THE FAMILY RHODOMELACEAE (RHODOPHYTA)

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The family Rhodomelaceae is the largest within the Rhodophyta with 145 genera and over 1,000 species. In the past, 17 tribes have been proposed but currently only 12 are recognized for the Family. Despite its taxonomic and systematic significance, relationships between the genera in Rhodomelaceae have been rarely investigated and its tribal classification remains elusive. Most of the tribes constitute hypothesized monophyletic groups that need to be tested. In an ongoing study, 270 sequences have been produced with different markers (*rbcL*, *psbA* and LSU) including taxa representing most of the accepted tribal groupings. In the phylogenies recovered, although mostly unresolved, it was clear that the Family is partially represented by strongly supported monophyletic groups, including the Bostrychieae, Amansieae, Laurencieae, Chondrieae, Rhodomeleae, and Polyzonieae. However, the Polysiphonieae and Pterosiphonieae appear to be polyphyletic. Polysiphonieae Clade I includes a small group of taxa that clusters within the Pterosiphonieae. Polysiphonieae Clade II comprises taxa from the *Polysiphonia sensu lato* group while *Polysiphonia sensu stricto* (Clade III) was recovered as sister of Clades I and II. An independent monophyletic group formed by species of *Digenea*, *Bryothamnion* and *Alsidium* was also recovered and this comprises Polysiphonieae Clade IV. Morphological characters delimiting these new groups are being investigated and they are given informal names.

P29. THE DIVERSITY OF HOUSE GUTTER EUKARYOTIC MICROORGANISMS

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Assessing the microbial diversity of various habitats is leading to the discovery of new lineages, particularly within the bacteria. Recent studies have turned their focus to the microorganisms found in houses, sampling interior surfaces and comparing the microbial diversity throughout the home. This study assesses the eukaryotic diversity of house gutter communities as part of an undergraduate botany class project at Le Moyne College. Samples were obtained from five separate house gutters around Raleigh, North Carolina, USA. Initial observations were made concerning general appearance of the samples, then algal growth medium was added to subsamples that were then placed in a lighted environment to encourage growth of the photosynthetic eukaryotes. After several weeks, samples were imaged using light microscopy and DNA was extracted and sent to the University of North Carolina Microbiome Core Facility for targeted high-throughput sequencing of the V9 hyper-variable region of the 18S rRNA gene. The resulting sequence data were analyzed to determine the eukaryotic diversity, with a focus on the photosynthetic lineages.

P30. THE PLASTID GENOME OF *BALBIANIA INVESTIENS* A FRESHWATER RED ALGAL EPIPHYTE (BALBIANIALES, NEMALIOPHYCIDAE)

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The red algal subclass Nemaliophycidae is comprised of ten orders most of which are marine. However, there are three strictly freshwater orders, Balbianiales, Batrachospermales and Thoreaales. The Batrachospermales and Thoreaales have been well studied, but much less is known about the Balbianiales, which is taxon-poor with only two genera and three species. The phylogenetic relationships among the orders of the Nemaliophycidae are unresolved using multigene analyses prompting the need for phylogenomic data. Currently, there is no genomic data for the Balbianiales to be included in such analyses. Here, we present the plastid genome of *Balbiana investiens*, an epiphyte on *Batrachospermum spp.* in European streams. This alga is available in a few public culture collections and these cultures were utilized for this study. Prior to next-gen sequencing, the identity of the culture was confirmed by PCR amplification and sequencing of the *rbcL* marker. Total genomic DNA was sequenced using the Illumina MiSeq system. The *De Novo* plastid genome assembly (>160 Kbp) for *B. investiens* was shown to be similar to other plastid genomes for taxa in the Florideophyceae. As well, it is comparable in terms of the number of tRNA's and protein-coding genes including the presence of the *ycf* gene

family. Knowledge of the *Balbiania investiens* plastid genome will greatly enhance future studies of phylogenetic relationships among freshwater and marine Rhodophyta.

P31. BREVETOXIN PERSISTENCE IN MACROALGAE AFTER A *KARENIA BREVIS* BLOOM EVENT IN SOUTH TEXAS

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Red tide blooms composed of *Karenia brevis* have become bi-annual events along the South Texas coast. Last year's bloom persisted in local bay systems from September 15 – November 23, 2015. The bloom caused mass fish kills coupled with marine and terrestrial animal mortalities. This study examined the accumulation of brevetoxin in *Sargassum spp.* collected from Padre Island National Seashore during a *Karenia brevis* bloom. *Sargassum* was cultured with *Karenia brevis* and time course sampling was performed over a 3-day period. The brevetoxin concentration was determined using ELISA. Concentrations of brevetoxin increased from 24 – 51 ng/g wet wt. *Sargassum* over the 3-day period. Pelagic *Sargassum* can transfer brevetoxins into regions not experiencing red tides and cause impacts on the organisms that utilize this resource.

P32. RENDERING MICROALGAE IN VIRTUAL ENVIRONMENTS

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Light and electron microscope observation of microbes, including most algae, present a two-dimensional rendering of three-dimension organisms. Even when observers mentally or digitally reconstruct the three-dimensional morphology, much is lost in the mental of physical presentation of this aggregate data. Emerging technology allows observers to view true three-dimensional renderings in virtual reality. This experience allows the observer to acquire a more accurate and satisfying estimate of microbial morphology. To generate this three-dimensional rendering, multiple microscopy techniques must be used to create the virtual specimen. In this presentation, multiple three-dimensional renderings are presented in a virtual reality landscape for select diatom species. The images include atomic force and confocal microscope image mergers constructed by an interdisciplinary team of artists, biologists, and digital engineers. The products represent one of the most detailed and accurate single representations of microbes to date. Import to this technique is that while constructing the three-dimensional renderings requires significant infrastructure, disseminating and viewing the specimens does not. Low cost visualization can be performed with consumer mobile devices and extreme low cost virtual reality headsets, making the opportunity to experience these images available to most.

P33. MIDDLE SCHOOL PROJECT LEADS TO THE DISCOVERY OF A NEW ALGAL SPECIES

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We initiated a project with an 8th grade science class at Monticello Middle School to demonstrate the isolation and characterization of new stains and taxa of algae. The main goal of the project was to isolate new strains of algae from the class Eustigmatophyceae. These algae are of interest because they produce high levels of polyunsaturated fatty acids and hydrocarbons. The project was initiated in March 2015 with a class presentation that described algae and how they are characterized. We presented the project to the class as a chance for the students to isolate and characterize a new algal species. Initially, the students observed two water samples from roadside ditches that contained mats of *Zygnema*, a green alga unrelated to the Eustigmatophyceae. We showed the students how to prepare cultures of *Zygnema*, with the possibility that one or more Eustigmatophyceae would grow up with the *Zygnema*. All the students received 50-ml collection tubes with instructions to collect their own algal samples to culture. One of our initial *Zygnema* cultures contained a Eustigmatophyceae alga and we showed the students how to isolate the alga of interest. The eustigmatophyte strain grew well and we were able to characterize the strain by light microscopy and DNA sequence analysis. The new strain from a ditch on the University of Arkansas at Monticello campus proved to be a new species of the proposed family, Neomonodaceae. We were able to complete the characterization by the end of the Spring 2015 school term.

P34. THE BCCM/ULC COLLECTION FOR THE *EX-SITU* CONSERVATION AND THE EXPLORATION OF POLAR CYANOBACTERIAL DIVERSITY

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The BCCM/ULC public collection, funded by the Belgian Science Policy Office since 2011, aims at gathering a representative portion of the polar cyanobacterial diversity with different ecological origins (limnetic microbial mats, soil crusts, cryoconites, endoliths, etc.). It is publicly available for researchers that want to study the taxonomy, evolution, adaptations to harsh environmental conditions, and genomic make-up of cyanobacteria. The collection presently includes 226 cyanobacterial strains, with more than half being of polar origin (catalogue: <http://bccm.belspo.be/catalogues/ulc-catalogue-search>). The morphological identification shows that the strains belong to the orders Synechococcales, Oscillatoriales, Pleurocapsales, Chroococciopsidales and Nostocales. The large diversity is also supported by phylogenetic analyses based on 16S rRNA sequences. This broad distribution makes the BCCM/ULC

collection particularly interesting for phylogenomic studies. In addition, cyanobacteria produce a range of secondary metabolites (e.g. alkaloides, cyclic and linear peptides, polyketides) with different bioactive potential. Bioassays have shown antifungal activities of the cell extracts of strains *Plectolyngbya hodgsonii* ULC009 and *Phormidium priestleyi* ULC026. Due to the geographic isolation and the strong environmental stressors of the habitat, the exploration of these metabolites in Antarctic cyanobacterial strains seems promising for biotechnology or biomedical applications.

P35. FLOCKING BEHAVIOR OF *VOLVOX BARBERI* AND OPTIMAL SPHERE PACKINGS
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Volvox barberi forms spherical colonies consisting of 10000-50000 cells. Somatic cells form the exterior matrix of the colonies and beat flagella to propel them in a rolling motion. Here, I demonstrate that *V. barberi* colonies can show flocking behavior. An application of the Clark-Evans index to *V. barberi* colonies swimming in culture wells shows that their spatial distribution is typically aggregated (average p-value $\ll 0.005$), while other motile algae including *Volvox carteri* are randomly organized. Time lapse photography revealed the dynamics of flocking as follows: small groups (1-4 colonies) gathered initially, and over several minutes attracted other groups to form single flocks of more than 100 colonies. These flocks grew and shrank dynamically but often persisted over many tens of minutes or even hours. *V. barberi* colonies in typical flocks had a wide distribution of radii, and formed striking triangular lattices with polygonal defects. Comparison of these lattices with dense packings of polydisperse spheres, suggests that *V. barberi* flocks can achieve optimal random packing. I propose that *Volvox barberi* use water currents created through flagellar beating to pull each other together.

P36. ZINC PROTECTS AGAINST CADMIUM TOXICITY IN THE MACROALGA *CHARA*: ROLE FOR REACTIVE OXYGEN SPECIES?

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The macroalga *Chara australis* R Br takes up cadmium from the water column or the sediment. Zn protects against Cd toxicity, increasing the survival rates to Cd stress by 8 to 42%. Zn does not prevent Cd uptake. We explored the possibility that the effects of Zn are due to protection against damage from reactive oxygen species (ROS) via a glutathione-mediated pathway. During 24 h of Cd stress with and without Zn, we followed ROS species using the fluorescent probe DCHF and measuring the reduced (GSH) and oxidized (GSSG) forms of glutathione using liquid chromatography/triple quadrupole mass spectroscopy. We were unable to show an increase in ROS species in the shortest time measured (30 min), at which time ROS had decreased to 25% of

control. There was no significant difference with Zn, and no significant change over 24 h. At 2 h, decreases in GSH (6%) and GSSG (18%) occurred, but there was no significant difference with the addition of Zn. By 24 h, Cd-treated plants showed a significant increase over the earlier levels (GSH to 32 times the controls, and GSSG to 164% of controls). Zn treatment significantly increased the concentration of both, but the increase in GSSG was proportionately greater, so that the ratio of GSH:GSSG, which was 328 in the controls, was 4630 in the Cd-treated plants and 2180 in the plants treated with both cadmium and zinc. These data are not consistent with Zn protection against oxidative stress.

P37. GENOME-WIDE COMPARISON OF *PICOCHLORUM* (CHLOROPHYTA, TREBOUXIPHYTE) SPECIES

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Members of the *Picochlorum* genus are considered candidates for biofuel, nutraceutical, and wastewater applications due to their robustness, high biomass productivity, protein and lipid content. Physiological, photosynthetic, and genomic differences were compared for two closely related and highly salt tolerant species, *Picochlorum SENEW3* and *Picochlorum oklahomensis*. Although closely related, these species show large differences in genome size and gene family expansion in *P. oklahomensis*. The genomes were compared for evidence of positive selection on genes and we find that some of the fastest evolving genes and included genes involved in response to heat and high light, glutamate synthesis, starch production, and helicase activity, highlighting key functions that may be involved in adaptation to each respective habitat. Photosynthetic efficiency is similar between the two species and photosystem related proteins show evidence of extreme negative selection or selection for protein conservation. Several instances of horizontal gene transfer are also shared between the two species. An additional two *Picochlorum* species will be included in further comparison analyses.

P38. PHOTOSYNTHESIS INHIBITION EFFECT OF NAPHTHOQUINONE DERIVATIVES ON *MICROCYSTIS AERUGINOSA* AND *DOLICHOSPERMUM SMITHII*

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We developed harmful cyanobacteria specific algicide naphthoquinone (NQ) derivatives. However, mechanism on selective algicidal effect of NQ derivatives to cyanobacteria have not been understand. We investigated algicidal mechanisms of NQ derivative in photosynthesis system. We evaluated the difference of algicidal activity of NQ derivative under presence or absence of light on *Microcystis aeruginosa* and *Dolichospermum smithii*. Interestingly, two species were almost eliminated (more than 99 %) under light condition, whereas the algicidal activity was significantly low as 36.7 % and 10.3 % under dark condition at 7th day after

inoculation, respectively. To investigate the effects of photosynthesis system after inoculation of NQ derivative, we measured oxygen evolution rate and chlorophyll fluorescence from PhotosystemII (PSII). The oxygen evolution rate was rapidly reduced after inoculation of NQ derivative. The chlorophyll fluorescence showed similar patterns in the NQ inoculated and non-inoculated groups. In addition, we analyzed chlorophyll fluorescence patterns after inoculation of 3-(3,4-dichlorophenyl)-1,1- dimethylurea (DCMU), which is known to block the Q site in PSII. As a result, the chlorophyll fluorescence pattern of DCMU showed significantly different pattern with NQ derivative. These results indicated that NQ derivative enabled to mitigate target cyanobacteria by affecting photosynthesis system, except the Q site in PS II. We will be investigating algalicidal mechanisms of NQ derivatives in photosystemII and reactive oxygen species (ROS) evolution.

P39. PHYLOGENY AND TAXONOMIC REVISION OF *SPYRIDIA HYPNOIDES* (SPYRIDIAEAE, CERAMIALES, RHODOPHYTA) WITH UNCINATE SPINES

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Nineteen samples belonging to species of *Spyridia* Harvey with characteristic uncinata spines were investigated for comparative chloroplast-encoded *rbcL* and nuclear LSU rDNA sequence analysis and for their vegetative morphology. Three species are currently well known to possess uncinata spines: *Spyridia hypnoides* (Bory de Saint-Vincent) Papenfuss, *S. cupressina* Kützing, and *S. horridula* F. Schmitz ex J. Agardh. Our molecular analyses and morphological studies indicate that there are two distinct entities with two different distribution ranges going under the name *S. hypnoides*. Our material from India is recognized as *Spyridia hypnoides*, whereas our collection of “*S. hypnoides*” from the Red Sea, Israel, is actually *Spyridia aculeata* (C. Agardh ex Decaisne) Kützing, a species which was previously considered a synonym of *S. hypnoides*. *Spyridia aculeata* may be widely distributed in the Mediterranean Sea, the western Atlantic Ocean, the Caribbean Sea, the Gulf of Mexico and the Red Sea.

P40. SILICATE UTILIZATION OVER 14L:10D DAY:NIGHT CYCLE CONFIRMS NIGHT METABOLISM IN LAKE MICHIGAN DIATOM ENRICHMENTS USING NITRATE OR AMMONIUM AS A NITROGEN SOURCE

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As diatoms only take up silica when they replicate, measuring the amounts of dissolved and particulate silicate were an important aspect of this study. Silica was used as a proxy of the diatom reproduction. Depending on growth conditions, some algal species divide throughout the day and night; this suggests that protein synthesis can be an important component of algal night metabolism and hence nitrogen utilization. The goal of this experiment was to measure the amount of night protein synthesis occurring in a culture of diatoms from Lake Michigan. Diatoms were enriched with light for energy and excess nutrients—including phosphate, silicate, nitrate and limited ammonium for some—along with use of physical separation methods. Growing conditions were prepared in a way which anticipated the diatoms would synchronize to

a 14:10 day:night cycle and store energy, during their day phase, to use for night protein synthesis and replication. Their growth was monitored by taking samples before and after the transitions of light to dark along with midday and midnight samples. Assays of dissolved and particulate silicate were used to measure utilization, which confirmed their nighttime growth. As hypothesized, the diatoms had significant growth during their night phase. There were decreases in the nighttime dissolved silicate and increases in the nighttime particulate silicate. When available, the diatoms preferred to use ammonium instead of nitrate. Cell division during the night phase indicated sufficient daytime energy storage to fuel night protein synthesis and cell replication.

P41. IN CHARACEAE: "EVERYTHING IS EVERYWHERE, BUT THE ENVIRONMENT SELECTS"

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The Characeae, commonly called stoneworts or muskgrasses, are a group of freshwater green algae. Species in this family are integral parts of aquatic ecosystems. Previous studies have shown that the Northeast U.S.A. has a particularly rich Characeae flora. Over 25 species from four genera have been reported from New York and New England. The pattern of richness in Northeast lakes was complex: with equal sampling effort some lakes were found to have only a single species while at others up to seven species were found. Furthermore, certain species were found to cluster in geographic regions of New York and New England, while others were widespread. These differing distribution patterns have been hypothesized to be biological (e.g., waterfowl dispersal) or chemical (e.g., pH or conductivity). In 2014 and 2015 we surveyed 740 water bodies across New York and New England, collecting all species of Characeae encountered and water chemistry data for each site. This dataset allows investigation of species richness using multivariate analyses and species distribution models. Species with uneven distributions (e.g., western New York and northern Maine) such as *Chara contraria* were very well supported by the species distribution models (AUC 0.98), while more evenly distributed species such as *Nitella flexilis* were poorly supported (AUC 0.67). Taken together, the twelve species analyzed for this study suggest that water chemistry constrains species in different ways, with generalist and specialist species identified.

P42. SOIL CYANOBACTERIA FROM KOLA PENINSULA, RUSSIA

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Kola Peninsula is located in the north-western part of Russia in the tundra and northern taiga zones, at high latitudes. In that region with the harsh climate, acidic soils and high levels of anthropogenic transformations obtained cyanobacterial species richness is low, containing 33

morphospecies. Representatives of Synechococcales, Chroococcales and Oscillatoriales were most abundant by the number of species. *Nostoc*, *Leptolyngbya* and *Aphanocapsa* were found to be the most commonly seen genera in the all soils samples. Further, using 16s rRNA gene sequencing, we confirmed that *Nostoc* and *Microcoleus* certainly belongs to the respective lineages. Also, we have found, supposedly, new species of the recently described genus *Stenomitos*, based on polyphasic approach. Analysis of the 16S-23S ITS region will be performed in the near future for more distinct demarcation of current species of *Nostoc*, *Microcoleus* and *Stenomitos*.

P43. STRAIN AND LIPID VARIETY OF THE DIATOM *PHAEODACTYLUM TRICORNUTUM*

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Phaeodactylum tricornutum is a great model organism for bio-fuel production and genomic sequencing. This diatom has very diverse potential as is it can be found in saltwater, freshwater, and soil environments with growth morphology differences. Additionally, *P. tricornutum* creates various internal cellular lipid concentrations naturally and relative abundance can vary depending on both environmental conditions and genetically unique strain expression. Lipids analyzed in this paper use Gas Chromatography or High Performance Liquid Chromatography/Mass Spectrometer techniques. The two lipids of interest are diesel length hydrocarbon and betaine lipid production. The hydrocarbon chain lengths studied in this experiment vary between ten to twenty-two carbons long. For both types of lipids analyzed in this experiment, strain variety and growth temperature were used as variables and relative abundance of each are analyzed using liquid organic solvent extractions lipid chromatograms produce from a GC/MS or HP-LC/MS. This type of research offers insight for the alternative fuel industry of diatoms and the wide variety of growth outcomes that need to be understood and harnessed.

P44. A NEW SPECIES OF *STANIERIA* (CYANOBACTERIA) ISOLATED FROM A SMALL POOL ON MEXICAN RIVIERA

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A sample from a small pool in the Mexican Riviera region (the eastern coastline of the Yucatan Peninsula) was collected in January 2015. Enrichment cultures from this sample were made, and a small coccoid cyanobacterium was isolated into unialgal culture from the enrichment cultures. This isolate is purplish in color, and produces numerous small endospores each division cycle called baeocytes. Morphologically it belongs to the genus *Stanieria*, which currently has four species, mostly isolated from marine environments. Our taxon is most similar to the type species, *S. cyanosphaera*, but differs in its reddish color and larger baeocytes. In a phylogenetic analysis based on the 16S rRNA gene, it is distant from the type species and paraphyletic to the *Stanieria* clade. From the information presently on hand, we conclude it is certainly a new species, but it could represent a new genus sister to *Stanieria*.

P45. NEW INSIGHTS IN THE SYSTEMATICS OF *POLYSIPHONIA SENSU LATO* (RHODOMELACEAE, RHODOPHYTA): RESURRECTION OF THE GENUS *POLYOSTEA* FROM THE NORTHERN PACIFIC

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Twelve genera were listed in synonymys with *Polysiphonia* in a recent review of red algal genera. One of them, the genus *Polyostea* is resurrected here for taxa that are characterized by branches of spiral origin but with bilateral phyllotaxy of laterals, 6-13 pericentral cells, ecorticate throughout, lacking trichoblasts, unicellular rhizoids cut off from pericentral cells, four-celled carpogonial branches, and tetrasporangia arranged in straight series. The genus *Polyostea* contains three taxa, namely, *Polyostea bipinnata*, *P. gracilis* comb. nov., and *P. hamata* comb. nov. from the north Pacific. *rbcL* and concatenated *rbcL* and *cox1* phylogenies strongly support the resurrection of *Polyostea* as a valid and separate genus in *Polysiphonia sensu lato* and not in *Pterosiphonia*, where these three species have been placed previously. Thus, *Polysiphonia sensu lato* is currently composed of multipericentral group, *Neosiphonia*, *Polyostea*, and *Polysiphonia sensu stricto*.

P46. *WILSONOSIPHONIA* GEN. NOV. (RHODOMELACEAE, RHODOPHYTA) BASED ON A MOLECULAR PHYLOGENY WITH A REVIEW OF KEY MORPHOLOGICAL CHARACTERS IN *POLYSIPHONIA SENSU LATO*

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We assessed specimens previously identified as *Polysiphonia howei* from Belize, Brazil, Florida, and India and established the genus *Wilsonosiphonia* based on the new combination, *Wilsonosiphonia howei*. The *rbcL* and *cox1* phylogenies support the status of *Wilsonosiphonia* as a new genus that is sister to the genus *Herposiphonia*. The diagnostic features for *Wilsonosiphonia* are: 1) the location of rhizoids at the distal end of pericentral cells and 2) the taproot shaped multicellular ends of rhizoids. *Wilsonosiphonia* includes *W. howei* comb. nov., *W. fujiae* sp. nov., and *W. indica* sp. nov. These three species resemble each other in external morphology but *W. fujiae* is distinguished by having two tetrasporangia per segment rather than one, *W. indica* by having abundant and persistent trichoblasts, and *W. howei* by having few and deciduous trichoblasts.

P47. TAXONOMIC REVISION OF TWO PHYMATOLITHON SPECIES: *P. LAEVIGATUM* AND *P. PURPUREUM* BASED ON SEQUENCING TYPE MATERIALS AND MORPHOLOGICAL OBSERVATION

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Phymatolithon laevigatum was originally described as *Lithothamnion laevigatum* by Foslie on collections of Kuckuck from Helgoland in Germany. Subsequently, he reduced *L. laevigatum* to the rank of forma and treated as *P. polymorphum* f. *laevigatum*, and then he reelevated to species rank as *P. laevigatum*. The undated material designated as lectotype by Adey & Lebednik was presented in TRH herbarium in Norway. Many other materials from the same shipment were presented in elsewhere. In PC, Thuret-Bornet herbarium, Woelkerling selected a material as paratype which was consisted of a single fertile piece accompanied by a label in Foslie's script with the basionym. We collected samples of *P. laevigatum* from Canada, England, and France. Of them, sample from Canada is corresponded with lectotype of *P. laevigatum*, whereas samples from England and France with paratype of *P. laevigatum* based on molecular data of psbA and COI-5P gene. However, there are 2.6% gene sequence divergence between samples of lectotype and paratype of *P. laevigatum*. In our phylogenetic analysis, paratype of *P. laevigatum* is recognized as lectotype of *P. polymorphum* f. *papillata*. In this study, we propose elevating this *P. polymorphum* f. *papillata* to the rank of a species based on its molecular and morphological data. *Phymatolithon papillatum* sp. nov. is characterized by the growth pattern and the shape and size of basal and epithallial cells.

P48. THE CONSPECIFICITY OF *PTEROSIPHONIA DENDROIDEA* AND *P. TANAKAE* (RHODOMELACEAE, RHODOPHYTA) INFERRED FROM MORPHOLOGICAL AND MOLECULAR ANALYSES

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Recent phylogenetic studies in the genus *Pterosiphonia* have suggested that *P. dendroidea* and *P. tanakae* are conspecific and show its wide geographic distribution in the Pacific. *Pterosiphonia dendroidea* was originally described as *Polysiphonia dendroidea* from Peru and transferred to *Pterosiphonia*. *Pterosiphonia dendroidea* was characterized by diagnostic features as its light cortication, presence of trichoblasts, 8-12 pericentral cells, branches with the production of three to five-order laterals, and congenital fusion of 2-3 segments. *Pterosiphonia tanakae* shares such as features. Our phylogenetic analysis using rbcL sequences reveals low gene sequence divergence (0.6-0.7%) between samples of *P. dendroidea* and *P. tanakae* and suggesting that these two species are conspecific. We propose that *P. tanakae* is a later synonym of *P. dendroidea*, and our study indicates the wide occurrence of *P. dendroidea* in the northern and southern Pacific Ocean.

P49. PRODUCTION OF *KAPPAPHYCUS ALVAREZII* (DOTY) DOTY CLONES BY MICROPROPAGATION

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Tissue culture technique has proven to be a reliable method to mass produce certain crops. This method was also tested in macroalgae to produce clones for seaweed farming. Callus production and shoot regeneration from protoplast has established protocols for some seaweed species and *Kappaphycus alvarezii*. Cells and larger tissues whether in solid or suspension media were used to propagate clones were tested for suitability for farming and successful. However, the length of culture in-vitro limits the production process making the growing of *Kappaphycus* in vitro an expensive technique to produce clones. In this study, *Kappahycus alvarezii* (KA) was grown in-vitro to obtain a more efficient protocol for the production of clones. Small sections of *Kappahycus* were grown in suspension for one month under the same light and salinities. Media, source of explants, length of explants, and stocking density were determined to obtain higher growth rate and survival rate. Growth rate of KA is significantly higher in media with Grund medium + organic nitrogen than Grund medium only and *Ascophyllum nodosum* media. Shoots develop in explants from tips is significantly faster than sections from older branches. Growth rates of explants approximately 3 and 5 mm are significantly higher than 10 mm sections. Growth rate of KA grown at 10, 15, 20, 25 individuals per 200 mL of media are not significantly different. The appearance of shoot primordia as early as 7 days was observed in the media with higher nitrogen concentration. This protocol could be adapted to reduce the time of culture in-vitro and make propagules for farming affordable to the stakeholders.

P50. A SURVEY OF BENTHIC CYANOBACTERIA IN THE MIDDLE BASIN OF THE ST. JOHNS RIVER

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The St. Johns River is an integral part of an ecosystem in Florida that stretches all the way from Indian River County to Duval County. It is one of the lowest flowing rivers in Florida, leaving it extremely susceptible to nutrient pollution due to its inability to quickly flush out any extraneous input. Nitrate nitrogen is a great source of pollution in the springs of the St. Johns River as a result of urban development and agricultural use of fertilizer. The excess nitrates stimulate the growth of filamentous algae, and can be related to harmful algal blooms in the springs as well. Benthic cyanobacteria, including the genera *Dolichospermum*, *Leptolyngbya*, and *Oscillatoria*, are well adapted to effectively cycle nutrients like nitrates regardless of their abundance. In this survey, benthic samples were collected from multiple sites in areas of the middle basin of the St. Johns River, with additional focus being placed on Silver Springs. Examination of the morphology and 16S rDNA genes of isolates from this area revealed dominance by the common, widely distributed genus *Leptolyngbya*. We explore the relationship between nutrient levels and cyanobacterial diversity from these habitats.

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