

Northeast Algal Society



Salem, MA 2019

58th Annual
Northeast Algal Symposium
Salem State University
April 26th-28th

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The co-conveners would like to acknowledge the generous support of our sponsors for this meeting, the *Biology Department* and the *College of Arts and Sciences* at *Salem State University*, especially Biology Department Chair Ryan Fisher and CAS Dean Gail Gasparich, as well as the *Great Lakes Research Consortium* at *SUNY College of Environmental Science and Forestry*. Special thanks to Dion Durnford, Lindsay Green-Gavrielidis, Stacy Krueger-Hadfield, Amanda Savoie, John Wehr and Brian Wysor for volunteering to serve as judges for the Wilce Graduate Oral Presentation Award, the President’s Undergraduate Oral Presentation and Undergraduate Poster Award, or the Trainor Graduate Poster Award. We appreciate our session moderators: Mary Bisson, Hilary McManus, Gary Saunders and Peter Siver and of course, our intrepid auctioneer, the one and only Craig Schneider. We are grateful to Maureen Horrigan at *Competitive Edge Design* and Lisa Swenson at *Razz-m-Tazz Promotions* for their help designing our meeting logo and NEAS merchandise. Thanks also to our vendor Scott Balogh of *Balogh International Inc.* Finally, we are so grateful to our distinguished guests Kelly Kryc and Jarrett Byrnes for taking time out of their weekends to share their expertise with NEAS.



Welcome to Salem and to the 58th Northeast Algal Symposium!

It is hard to believe since the inception of NEAS in Woods Hole that we have never traveled up the coast to the historic town of Salem, Massachusetts. Residents of Salem will be happy to tell you that Salem was a thriving town when Woods Hole was still a sleepy agricultural village. Founded in 1626 by Roger Conant and a group of immigrants from Cape Ann, the settlement was first named Naumkeag, but the settlers preferred to call it Salem, derived from the Hebrew word for peace. Salem rapidly became a thriving sailing port. The House of the Seven Gables, made famous by American author Nathaniel Hawthorne's novel by the same name, was built in 1668 as a colonial mansion for Captain John Turner. It has been remodeled and expanded over the subsequent 400 years but remains one of the oldest surviving timber framed mansions in the continental United States.



Salem is probably best remembered for the Salem Witch Trials. The 17th Century was a time when people of all educational levels believed you could gain the vast powers of witchcraft by selling your soul to the Devil. Reverend Cotton Mather, a leader in the puritan movement and early medical scientist wrote a book in 1689¹ that described the powers one could gain through such a sale. It was an interesting publication, coming from one of the early advocates of the smallpox vaccine and a proponent of the radical idea that students were better motivated by rewards than by punishment. In 1692, a local physician diagnosed several teenage girls as bewitched, likely based on the descriptions from that book. What followed were charges and countercharges. Slaves were flogged until they confessed to practicing witchcraft and innocent people confessed to flying on broomsticks in an effort to avoid the noose. If you were inhabited by evil spirits and tossed in a well, those spirits would cause you to float, at which time you would be removed from the well and hanged. One man was bound and placed on the ground and heavy rocks placed on his chest— more weight was added until the spirits were forced out of him and he was crushed to death. All told, about 20 people lost their lives during this period, most often women from the fringes of society, or single women who had accumulated wealth or property. This hysteria stopped when the more “respected” members of society began to be charged.

Science has come a long way since these early experiments to determine if you were inhabited by evil spirits. The theme for this year’s symposium is *Translating Science into Action*. We have invited two guest speakers to facilitate that effort: Dr. Kelly Kryc, the Director of Conservation Policy and Leadership at the New England Aquarium and noted environmental policy professional, and Dr. Jarrett Byrnes, a marine ecologist at UMass Boston, who studies the causes and consequences of complexity in nature, including how humans alter the diversity and interconnectedness of life on earth. Our guests will consider the value of citizen science for environmental monitoring work and the influence of science in effecting policy changes. We hope you enjoy the presentations, make time to catch up with your friends, make new friends, and visit the rich historical district of Salem, Massachusetts.

Thea Popolizio and Greg Boyer, NEAS 2019 Co-conveners

¹ *Memorable Providences Relating to Witchcraft and Possession*

Salem State University Map

For your GPS, the address of campus is 352 Lafayette Street, Salem. The entrance to the parking lot is on College Drive. After passing the Sophia Gordon Center (no. 4 on map) and Meier Hall (6) on your right, you will turn right onto College Drive from Lafayette Street. You may park anywhere in the lot on the left. Take the path between the Berry Library (9) and Meier Hall, across the quad (11) to Ellison Campus Center (10). Veteran's Hall is on the second floor.



NEAS EXECUTIVE COMMITTEE & OFFICERS 2018-2019

Office	Officer	Term
President	Louise A. Lewis University of Connecticut louise.lewis@uconn.edu	2018-2020
Treasurer	Lindsay Green-Gavrielidis University of Rhode Island lindsaygreen@uri.edu	2018-2022
Secretary	Thea Popolizio Salem State University tpopolizio@salemstate.edu	2016-2021
Membership Director	Brian Wysor Roger Williams University bwysor@rwu.edu	2015-2020
Nominations Committee	Amy Carlile (Chair) University of New Haven acarlile@newhaven.edu	2017-2019
	Dale Holen (Chair-elect) dah13@psu.edu	2018-2019
Webmaster	Chris Neefus University of New Hampshire Chris.neefus@unh.edu	---
2019 Conveners	Thea Popolizio Salem State University tpopolizio@salemstate.edu	2018-2020
	Greg Boyer SUNY-ESF @ Syracuse glboyer@esf.edu	

2018 Conveners	<p>Amy Carlile University of New Haven acarlile@newhaven.edu</p> <p>Brian Wysor Roger Williams University bwysor@rwu.edu</p>	2017-2019
Members-at-Large	<p>Karolina Fucikova Assumption College Karolina.fucikova@gmail.com</p> <p>Sarah Whorley Daemen College sarahwhorley@gmail.com</p>	<p>2018-2021</p> <p>2016-2019</p>
Development Committee	<p>Greg Boyer SUNY-ESF @ Syracuse gboyer@esf.edu</p>	---
Publications Committee	<p>Elizabeth Lacey Stockton University elizabeth.lacey@stockton.edu</p>	2017-2019
Student Members	<p>Kristen Slodysko SUNY-ESF @ Syracuse knslodys@syr.edu</p> <p>Daniel Wolfe Ohio University dw845316@ohio.edu</p>	<p>2018-2019</p> <p>2018-2019</p>

Nominations for the NEAS Executive Committee 2019

Candidates for Member-at-Large:

Amanda Savoie: “I completed my PhD in the Saunders Lab at the University of New Brunswick in May 2017. My phycological interests lie in the area of red algal systematics, especially the challenging families Delesseriaceae and Rhodomelaceae. I recently began a new position as a Research Scientist at the Canadian Museum of Nature in Ottawa, Ontario, where I am starting a research program focusing on using molecular and morphological techniques to study red algal taxonomy in Canada. I loved attending NEAS meetings as a student, and now I’m looking forward to becoming more involved with the society!”

Craig Schneider earned a B.A. in biology from Gettysburg College and a Ph.D. in botany from Duke University. A faculty member at Trinity College since 1975, he has worked on the marine flora of Bermuda for the past 30 years, at present using molecular-assisted alpha-taxonomy to decipher many new species and genera in the island flora. He is retiring from teaching this year, but will continue his research in retirement. For NEAS, he has co-convened three meetings (1980, 2009, 2017), chaired the Colt Development Committee (1984–1986), was Secretary/Treasurer (1987–1992), President (1996–2000) and a Member-at-Large (2005–2008, 2012–2015).

Sarah Whorley is an Assistant Professor at Daemen College (Go Wildcats!) in Buffalo, NY. She works with freshwater algae as bioindicators of human activities in the landscape. She's already served one term as the NEAS Member-at-Large but would love another chance to do more with the position. As Member-at-Large, Sarah coordinated some of the outreach efforts at the New Hampshire meeting (buttons, letter to the President, banner for group photos). Previously she's served as both a poster and presentation evaluator. In her free time, Sarah is an avid, but slow, runner, and an enthusiastic hiker and camper.

Candidates for VP/President-elect:

Hilary McManus is an Associate Professor of Biological and Environmental Sciences at Le Moyne College in Syracuse, NY. She became a member of the Northeast Algal Society as a graduate student in 2002, and has since supported the society in multiple roles, including nominations committee chair for one year, co-convenor for the 2015 conference, and secretary from 2011-2016. Hilary enjoys the friendly and supportive atmosphere of NEAS, particularly for undergraduate and graduate students.

Deborah Robertson (Warren E. Litsky '45 Endowed Chair and Professor of Biology, Clark University): “I am honored to have been nominated for the position of Vice-President/President-elect of NEAS. I have been a member of NEAS since 1997 and have previously served on the Nominations Committee and as a Member-at-Large. Over the years, I

have enjoyed and benefited from being a member of this vibrant scientific community. As Vice-President/President I look forward to the opportunity to work with both the Executive Committee and the membership to insure the annual meetings are intellectually stimulating and to continue to help scientists communicate the importance of their research to both the public and policymakers. I look forward to exploring ways to support our early career scientists, both students and professionals, and to contribute to the scientific and educational mission of the society.”

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NEAS 2019 Election Ballot

*please vote for one person in each position – thank you!

Member-at-Large:

- Amanda Savoie
- Craig Schneider
- Sarah Whorley

Vice President/President-elect:

- Hilary McManus
- Deborah Robertson

General Program: 58th Northeast Algal Symposium Salem State University

Friday, April 26th

6:00—7:00 Registration
Hawthorne Hotel, 18 Washington Square W

7:00—10:00 PM NEAS Welcome Mixer & Evening Registration
BEERWORKS No. 2 Salem, 278 Derby Street

Saturday, April 27th

7:30—8:00 AM Continental Breakfast, *Veteran's Hall, Ellison Campus Center*

Morning Registration, Auction Drop-off & Preview, Session I and II speakers load presentations, *Veteran's Hall, Ellison Campus Center*

Poster Setup, *Commuter Lounge, Ellison Campus Center*

8:00—8:15 Group Photo

8:15—8:30 Welcome & Opening Remarks

SESSION I STUDENT PRESENTATIONS, Moderator: Hilary McManus

8:30—8:45 *Wilce Award Candidate*
Sarah E. Glass, Louise A. Lewis & Kenneth G. Karol. ORGANELLAR GENOME EVOLUTION IN THE KLEBSORMIDIOPHYCEAE.

8:45— 9:00 *Wilce Award Candidate*
Shaunna Phipps, Charles Goodman, Charles Delwiche & Mary A. Bisson. SALT INDUCED GENE EXPRESSION IN *CHARA LONGIFOLIA* C. B ROB. AND *CHARA AUSTRALIS* R. BR.: IMPLICATIONS FOR SALT TOLERANCE MECHANISMS.

- 9:00—9:15 *Wilce Award Candidate*
Jillian M. Freese & Christopher E. Lane. GENE EXPRESSION DURING THE DEVELOPMENT OF *CHOREOCOLAX POLYSIPHONIAE* INFECTING VERTEBRATA LANOSA.
- 9:15—9:30 *Wilce Award Candidate*
Elizabeth Hunter, Christopher Paight & Christopher E. Lane. CHARACTERIZING THE RELATIONSHIP BETWEEN APICOMPLEXAN *CARDIOSPORIDIUM CIONAE* AND ITS ALPHAPROTEOBACTERIAL ENDOSYMBIONT.
- 9:30—9:45 *Wilce Award Candidate*
Kristina X. Terpis, Matthew W. Brown, J. Craig Bailey & Christopher E. Lane. A PHYLOGENOMIC APPROACH TO INVESTIGATE THE EVOLUTIONARY HISTORY OF PHOTOSYNTHETIC STRAMENOPILES.
- 9:45—10:00 *Wilce Award Candidate*
Erin Borbee, Austin Humphries, Hawis Maddappa & Christopher E. Lane. PATTERNS IN BIOGEOGRAPHY AND BIODIVERSITY OF DINOFLAGELLATES IN INDONESIAN MARINE ECOSYSTEMS.
- 10:00—10:15 *Coffee Break*

SESSION II STUDENT PRESENTATIONS, Moderator: Mary Bisson

- 10:15—10:30 *President's Award Candidate*
Christopher Lee & Dion Durnford. INVESTIGATING HIGH ACETATE AS A REGULATOR OF CONDITIONAL SENESCENCE IN *CHLAMYDOMONAS REINHARDTII*.
- 10:30—10:45 *President's Award Candidate*
Eba K. Mohamed, Marvin W. Fawley, Karen P. Fawley & Hilary A. McManus. A PHYLOGENOMIC RE-EVALUATION OF THE FRESHWATER GREEN ALGA *TETRAËDRON KÜTZING 1845* (SPHAEROPLEALES, CHLOROPHYCEAE).
- 10:45—11:00 *Wilce Award Candidate*
Joshua R. Evans, Susan L. Clayden & Gary W. Saunders. HIDDEN GENETIC DIVERSITY IN THE WIDESPREAD FRESHWATER RED ALGA *AUDOJINELLA HERMANNII* (ACROCHAETIALES, FLORIDEOPHYCEAE).

- 11:00—11:15 *Wilce Award Candidate*
Cody Brooks & Gary Saunders. THE KELP CONVEYOR HYPOTHESIS: LONG-DISTANCE GENE FLOW IN THE NORTHEAST PACIFIC.
- 11:15—11:30 *Wilce Award Candidate*
Brandon S. O'Brien, Christopher D. Neefus & Jennifer A. Dijkstra. GLOBAL DOMINATION: UNDERSTANDING THE SPREAD OF TWO INVASIVE MACROALGAE USING HABITAT SUITABILITY MODELS.
- 11:30—11:45 *Wilce Award Candidate*
Lingjie Zhou & Senjie Lin. ESTIMATING PHYTOPLANKTON CARBON BIOMASS USING DNA.
- 11:45—1:00 PM Lunch, *Veteran's Hall, Ellison Campus Center*
 Session III speakers load presentations
 Executive Committee Meeting, *Presidential Room, Ellison Campus Center*

SESSION III STUDENT PRESENTATIONS, Moderator: Gary Saunders

- 1:00—1:15 *Wilce Award Candidate*
Hannah G. Reich, Irene B. Rodriguez, Todd C. LaJeunesse & Tung-Yuan Ho. IRON AVAILABILITY DICTATES THE RESPONSE OF CORAL SYMBIONTS TO THERMAL STRESS.
- 1:15—1:30 *Wilce Award Candidate*
Kira Turnham & Todd LaJeunesse. SYMBIOTIC DINOFLAGELLATE LINEAGE CAUSES HOST DEATH.
- 1:30—1:45 *Wilce Award Candidate*
Dominique S. Derminio, Kristen N. Slodysko, Zacharias Smith, Bofan Wei, Eric Kilbourn, Anne McElwee & Gregory L. Boyer. BENTHIC PERIPHYTON FROM NEW YORK STATE AS A SOURCE OF MICROCYSTINS, ANATOXINS, AND PARALYTIC SHELLFISH TOXINS.
- 1:45—2:00 **Michael E. Kausch** & John D. Wehr. NUTRIENT STOICHIOMETRY AS A PREDICTOR OF CYANOBACTERIAL BLOOMS AND SPECIES COMPOSITION IN LOWER NEW YORK STATE LAKES.
- 2:00—2:15 *Coffee Break*

2:15—3:15 **KEYNOTE ADDRESS**
Dr. Kelly Kryc, New England Aquarium: THE ROLE OF SCIENCE IN
INFLUENCING DECISION-MAKING IN A POLARIZED DEMOCRACY.

3:15—3:30 *Coffee Break*

SESSION IV POSTER SESSION

3:30—4:30 **Student & Contributed Posters**
Commuter Lounge, Ellison Campus Center

4:30—6:00 **Open Period**
Explore Salem’s downtown and waterfront: stroll Salem Common or the
Essex Street Pedestrian Mall, visit the Salem Witch Trials Memorial,
Pickering Wharf, Salem Witch Museum, House of Seven Gables, &c.

6:00—7:00 **Cocktail Hour – Open Bar**
Hawthorne Hotel

7:00—10:00 **Banquet, Awards, Silent & Live Auction**
Hawthorne Hotel

Sunday, April 28th

8:30—9:15 Continental Breakfast, *Veteran’s Hall, Ellison Campus Center*
Session V speakers load presentations

9:15—9:30 Opening Remarks

9:30—10:30 **KEYNOTE ADDRESS**
Dr. Jarrett Byrnes, University of Massachusetts Boston: CHALLENGES IN
UNDERSTANDING CHANGING KELP FORESTS AT A PLANETARY SCALE

10:30—10:45 NEAS Lab Manual Launch— Elizabeth A. Lacey

10:45—11:00 *Coffee Break*

SESSION V

CONTRIBUTED PRESENTATIONS, Moderator: Peter Siver

- 11:00—11:15 **John D. Wehr**, Nicholas Ballor & Daniel Restifo. UNEXPECTED SALINITY TOLERANCE IN A FRESHWATER BROWN ALGA.
- 11:15—11:30 **Alison I. Feibel**, Bryan L. Morse & Raul A. Ugarte. A HISTORICAL REVIEW OF *ASCOPHYLLUM NODOSUM* HARVESTING IN NORTH AMERICA.
- 11:30—11:45 **Stacy A. Krueger-Hadfield**. MIND THE MATING SYSTEM GAP: THE CONSEQUENCES OF REPRODUCTIVE MODE VARIATION IN HAPLODIPLONTIC MACROALGAE.
- 11:45—12:00 **Daniela Lopes Paim Pinto**, Nicholas Blouin & Christopher E. Lane. REGULATORY MECHANISMS INVOLVING SMALL NON-CODING RNAs IN THE RED ALGAE *GRACILARIOPSIS ANDERSONII*.
- 12:00—12:15 *Coffee Break*
- 12:15—1:00 Closing Remarks, NEAS General Business Meeting & Lunch



BIOGRAPHIES



Dr. Kelly Kryc is an energy and environment policy professional who formerly held positions with the U.S. Senate Committee on Energy and Natural Resources, the U.S. State Department, the White House Office of Science and Technology Policy, and the U.S. Department of the Interior.

Prior to working in the public sector, Kelly spent a decade working for the non-profit sector advancing science priorities in the United States and abroad. Her doctoral and post-doctoral research focused on understanding extreme climate variability in Antarctica during the past 10,000 years. Kelly maintains an appointment as an adjunct faculty member of Georgetown University’s Science in Public Interest Program where she has taught “Science and Society: Global Challenges” and “Shaping National Science Policy.”

Kelly is presently the Director of Conservation Policy and Leadership at the New England Aquarium, focused on transforming science into action that protects the blue planet.

Dr. Jarrett Byrnes is an Assistant Professor of Biology at the University of Massachusetts Boston with expertise in marine ecology, biodiversity and ecosystem function and climate change ecology. His research focuses on the causes and consequences of complexity in nature, with an emphasis on changes in ocean biodiversity in the Anthropocene.



Jarrett was formerly a postdoctoral researcher at the Santa Barbara Coastal Long-Term Ecological Research site where he fell in love, for once and always, with kelp. He then had a dalliance with data synthesis as a postdoc at the National Center for Ecological Analysis and Synthesis where he helped co-found the [#SciFund challenge](#), a nonprofit organization that aims to empower scientists to team up and connect their science to the wider world.

Jarrett’s research team is currently pursuing several different lines of inquiry to look at global effects of climate change on kelp forests and temperate reefs. They have an ongoing working group on data synthesis addressing kelp forests and climate change, and are pursuing citizen science efforts in collaboration with [Zooniverse](#) to look at long-term patterns in giant kelp populations at a global scale. The Byrnes lab has also launched the global [Kelp Ecosystem Ecology Network](#) to run globally coordinated experiments and monitoring of kelp forests.

ORAL PRESENTATION ABSTRACTS (Alphabetical by presenting author)

SATURDAY, APRIL 27th

1. PATTERNS IN BIOGEOGRAPHY AND BIODIVERSITY OF DINOFLAGELLATES IN INDONESIAN MARINE ECOSYSTEMS (*Wilce Award*)

Erin Borbee¹, Austin Humphries², Hawis Madduppa³, and Chris Lane¹. (1) Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, USA, (2) Department of Fisheries, Animal, and Veterinary Sciences, University of Rhode Island, Kingston, RI, 02881, USA; (3) Department of Marine Science and Technology, Faculty of Fisheries and Marine Science, Bogor Agricultural University, Bogor, Jawa Barat 16680, Indonesia.

Indonesia is home to some of the most biodiverse ecosystems in the world, and yet outside of animal systems, few marine biodiversity studies have taken place there. Strict permitting and biodiversity laws have kept recent global surveys, such as the Tara Oceans Project out of Indonesian waters, leaving a significant gap in global ocean data. One group in particular that lacks data is the dinoflagellates. Making up nearly half of sequences in global ocean surveys, the communities in the waters of Indonesia are relatively unknown. Using metabarcoding of the V3 and V9 variable regions of 18S rDNA the dinoflagellate communities in three coastal marine environments spanning across the entire country of Indonesia have been characterized. We measured patterns in both alpha and beta diversity of these communities across the three sampling regions. Beta diversity shows that the three sampling regions have significantly different communities from one another, while Shannon diversity remains statistically the same when compared across all three regions. Future work will be aimed at incorporating water chemistry data to better understand the environmental drivers behind these community shifts. We will also be incorporating fisheries management data from each collection site to evaluate the impact different levels of management have on community composition in these regions.

2. THE KELP CONVEYOR HYPOTHESIS: LONG-DISTANCE GENE FLOW IN THE NORTHEAST PACIFIC (*Wilce Award*)

Cody Brooks & Gary Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton NB E3B 5A3, Canada.

Approximately 10% of Haida Gwaii's seaweed flora is present in California, while being absent from the intermediary Vancouver Island. Given that many of these species are non-buoyant, an explanation for their disjunct distribution presented a conundrum. One possible explanation lies in kelp rafting; large mats of kelp are known to be dislodged from the subtidal annually and subsequently drift on prevailing ocean currents for several weeks before degrading. The kelp conveyor hypothesis posits that these kelp rafts, laden with "hitchhiking" species of algae, drift northward from California on the winter Davidson current to Haida Gwaii resulting in long-distance, unidirectional migration of species. If the kelp conveyor hypothesis has merit, one prediction that should be met is that subtidal species with a continuous distribution along the northeast Pacific should reflect this

pattern at the genetic level owing to gene flow between California and northern BC, whereas intertidal species should not. To test the kelp conveyor hypothesis, specimens of 5 low-intertidal to subtidal and 4 mid- to high-intertidal species were collected and sequenced for the mitochondrial cytochrome *c* oxidase region (COI-5P). Samples were collected from California, Oregon, Vancouver Island and Haida Gwaii and pairwise genetic differentiation was determined for each population pair to assess similarity of adjacent and non-adjacent populations. In support of the kelp conveyor hypothesis, the non-adjacent populations of California and Haida Gwaii tend to be more similar in their subtidal than intertidal species.

3. BENTHIC PERIPHYTON FROM NEW YORK STATE AS A SOURCE OF MICROCYSTINS, ANATOXINS, AND PARALYTIC SHELLFISH TOXINS (*Wilce Award*)

Dominique S. Derminio, Kristen N. Slodysko, Zacharias Smith, Bofan Wei, Eric Kilbourn, Anne McElwee, & Gregory L. Boyer. The State University of New York, College of Environmental Science and Forestry, Syracuse, NY 13210, U.S.A.

Cyanobacterial harmful algal blooms (cHABs) are a common occurrence across New York State, but these samples generally only examine pelagic water. In 2017 and 2018, the New York State Department of Conservation conducted a survey of raw water and benthic rock scrapes from streams across New York State. Within these samples, toxic cyanobacterial species were observed. To identify if the cyanobacterial species present were toxic, these samples were tested using LCMS for microcystins, anatoxins, BMAA, cylindrospermopsin, and paralytic shellfish toxins (PSTs). Also, chlorophyll was measured by bbe Fluoroprobe for raw water and extracted chlorophyll for scrapes. Toxin analysis showed streams had microcystins, anatoxins, and PSTs in both the raw water samples and the benthic scrapes. This shows that there is a potential risk of contact with cHABs that are benthic algae, not only pelagic algae.

4. HIDDEN GENETIC DIVERSITY IN THE WIDESPREAD FRESHWATER RED ALGA *AUDOUINELLA HERMANNII* (ACROCHAETIALES, FLORIDEOPHYCEAE) (*Wilce Award*)

Joshua R. Evans and Gary. W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, Fredericton, New Brunswick, Canada E3B 5A3.

Cases of hidden or cryptic diversity in freshwater red algal lineages have been elucidated with molecular data in recent years and many new taxa have been described to account for this undocumented diversity. The genus *Audouinella* Bory (Audouinellaceae) has undergone numerous taxonomic revisions and currently contains most of the acrochaetoid species that occur in polar, temperate, and tropical streams. However, many of the reported species actually represent genus-level lineages or are misidentified sporophyte stages of batrachospermalean species. The most widespread species in the genus, *Audouinella hermannii* Roth (Duby), is a common component of the freshwater flora in North and South America, Europe, and Australia. In the present study, DNA barcoding with three markers (COI-5P, *rbcL*, and ITS) revealed three or four genetic groups for specimens assigned as *A. hermannii* from near the type locality in Europe, as well as

sites adjacent the western and eastern coasts of North America, and one site in Victoria, Australia. The COI-5P data resolved four genetic groups: *A. hermannii* from Europe (n = 2); *A. sp. 1hermannii* from Atlantic Canada (n = 5); *A. sp. 2 hermannii* from the British Columbia mainland (n = 2) and Oregon (n = 1), and *A. sp. 3hermannii* from Haida Gwaii, an archipelago off the west coast of British Columbia (n = 1). In contrast to COI-5P, the *rbcl* and ITS data resolved three genetic groups, with low sequence divergence observed in the two genetic groups from British Columbia. The *rbcl* data also solidly resolved the single Australian specimen as *A. sp. 1hermannii*. To account for the genetic diversity observed in this species complex, the molecular data will be combined with anatomical observations to propose new species to join “true” *A. hermannii* from Europe.

5. GENE EXPRESSION DURING THE DEVELOPMENT OF *CHOREOCOLAX POLYSIPHONIAE* INFECTING *VERTEBRATA LANOSA* (Wilce Award)

Jillian M. Freese & Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI, USA.

Red algal parasites are a unique type of parasitic organism. Like many other formerly photosynthetic parasites, red algal parasites are physically reduced in size and they have reduced or entirely lost their pigmentation. But unlike others, red algal parasites have extremely close evolutionary relationships to their host, which allows for directly comparing parasites and their hosts to examine the consequences of different lifestyles. *Choreocolax polysiphoniae* was one of the first red algal parasites described, and its ecology and morphology have been well studied. However, the molecular factors involved in the development of *Choreocolax* and its host’s response to infection, remain unknown. Modified single cell transcriptomic methods were used to obtain the transcriptomes of *C. polysiphoniae* and its host, *Vertebrata lanosa* at eight time points of parasite development. Differential gene expression analysis was used to identify up- and down-regulated genes during parasite development and in the host’s response to infection. Within the parasite, there is a dramatic change in the expression profile halfway through its development, likely corresponding to growth (*i.e.* fatty acid biosynthesis and DNA replication). For *Vertebrata*, comparison of infected and uninfected host tissue highlights a number of genes expressed only during infection. The function of these differentially expressed genes and the observed morphology associated with them will be discussed.

6. ORGANELLAR GENOME EVOLUTION IN THE KLEBSORMIDIOPHYCEAE (Wilce Award)

Sarah E. Glass^{1,2}, Louise A. Lewis³, and Kenneth G. Karol¹. (1) Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY 10458, USA; (2) Department of Biology, Lehman College, Bronx, NY 10468, USA; (3) Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06963, USA.

The Klebsormidiophyceae are a class of filamentous green algae with five currently recognized genera: *Entransia*, *Hormidiella*, *Interfilum*, *Klebsormidium*, and *Streptosarcina*, a newly recognized genus isolated from terrestrial habitats in Europe and Central America.

Interfilum has been shown to be phylogenetically imbedded within *Klebsormidium*, and moreover, several *Klebsormidium* species have been resolved as polyphyletic, making this an enigmatic and confusing group. Members of this group have greatly expanded chloroplast genomes due to their large inverted repeat (IR) regions that contain genes usually found in the large and small single copy region. *Entransia* has the largest known IR of any green alga and consequently has one of the largest chloroplast genomes among green algae. The mitochondrial genome of *Entransia* is consistent in size with those of other charophytic green algae, while the mitochondrial genomes of *Klebsormidium* are more dynamic, apparently due to the infiltration of introns and the expansion of intergenic regions. Here we present chloroplast genome sequences from eight additional strains representing *Entransia*, *Interfilum*, and *Klebsormidium*. We found that the chloroplast genomes had consistently expanded inverted repeat regions, and total chloroplast genome length varied in size from about 170 kbp to 206 kbp. We also generated mitochondrial genome data for an additional strain of *Entransia* and an additional strain of *Klebsormidium*. We present a discussion of our data and the patterns and putative processes that underlie organellar genome evolution in this group.

7. CHARACTERIZING THE RELATIONSHIP BETWEEN APICOMPLEXAN *CARDIOSPORIDIUM CIONAE* AND ITS ALPHAPROTEOBACTERIAL ENDOSYMBIONT (*Wilce Award*)

Elizabeth Hunter, Christopher Paight, Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881.

Apicomplexa is a diverse phylum of metazoan-infecting parasites, containing numerous clinically significant genera, including *Plasmodium* (malaria), *Toxoplasma* (toxoplasmosis), and *Cryptosporidium* (cryptosporidiosis). Recently, a single apicomplexan genus, *Nephromyces*, has been described as mutualistic. The sister genus of this mutualist, *Cardiosporidium*, contains a typical parasitic species. These two systems exist in parallel, not only from an evolutionary standpoint, but also from a life history perspective. Species from both genera inhabit closely related host species, and also host their own endosymbiotic bacteria, making them ideal for life strategy comparisons. The term symbiosis encompasses a sliding spectrum of prolonged, intimate associations between species ranging from parasitism to mutualism, and numerous life history traits can tip the scales in either direction. Bacterial endosymbionts are rare in apicomplexans, but genomic data indicates an Alphaproteobacterial symbiont has been retained since *Nephromyces* and *Cardiosporidium* speciated from their last common ancestor. The presence of bacterial endosymbionts in *Nephromyces* may have contributed to the transition from parasitism to mutualism, as well as the low virulence of *Cardiosporidium* species. Characterizing the metabolic capabilities of *Cardiosporidium's* endosymbiotic Alphaproteobacterium is critical to evaluating this hypothesis and understanding apicomplexan interactions with the host tunicate. By sequencing the genome of this bacterial endosymbiont, we provide context to better understand life strategy transitions along the symbiotic spectrum and the role of endosymbiotic bacteria in this process.

8. NUTRIENT STOICHIOMETRY AS A PREDICTOR OF CYANOBACTERIAL BLOOMS AND SPECIES COMPOSITION IN LOWER NEW YORK STATE LAKES

Michael E. Kausch, John D. Wehr. Louis Calder Center – Biological Stations and Department of Biological Sciences, Fordham University, Armonk, NY, USA.

Cyanobacterial blooms have become a widespread water quality issue in recent decades and have resulted in water quality degradation in many lakes in New York State. One of our key goals was to identify ecological factors influencing species composition of blooms of non-diazotrophic cyanobacteria. We collected surface water samples from lakes across southern NY State between June and October in 2018, spanning a wide productivity range (based on chl-*a* concentrations). Samples were analyzed for dissolved nutrients, particulate (phytoplankton) C:N:P ratios, and algal pigments (chl-*a*, phycocyanin). Chl-*a* concentrations varied widely, from 0.4 to 179.2 µg/L, and Secchi depths from 0.15 to 5.7 m, with 20 samples (> 30%) classified as eutrophic or hypereutrophic. Average particulate (phytoplankton) N:P ratios were significantly ($p < 0.05$) below the 16:1 Redfield threshold value in eutrophic and hypereutrophic lakes, suggesting nitrogen supply was a key factor leading to bloom formation in those systems. Dissolved inorganic phosphorus (SRP) concentrations were elevated (> 100 µg/L) in several lakes, particularly in NY City parks. One lake in Central Park, an urban eutrophic/hypereutrophic lake, had high SRP concentrations (67.5-151.4 µg/L) and experienced an intense and extended *Microcystis* bloom from July through October. Another urban eutrophic system, Prospect Park Lake, had elevated SRP concentrations (186.1-474.4 µg/L), although the bloom was composed predominantly of *Planktothrix agardhii*, in combination with diatoms and green algae. Of those lakes whose Secchi depths and chl-*a* concentrations fell within the eutrophic and hypertrophic ranges, 85% of these assemblages were dominated by species of cyanobacteria; notably *Microcystis viridis*, *Dolichospermum crassum*, and *Planktothrix agardhii*. These data suggest that nitrogen supply may have a critical role in bloom formation and that species composition of blooms may be influenced by forms and concentrations of nitrogen.

9. INVESTIGATING HIGH ACETATE AS A REGULATOR OF CONDITIONAL SENESCENCE IN *CHLAMYDOMONAS REINHARDTII* (President's Award)

Christopher Lee & Dion Durnford, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Photoheterotrophic lifestyles allow organisms to harvest light energy through photosynthesis and/or extract energy from organic carbon in the environment such as acetate, glycerol, or sucrose. Heterotrophic metabolism of *Chlamydomonas reinhardtii* is restricted to using acetate, making it an exceptional model organism to study the role of heterotrophic nutrition on conditional senescence. Previous work in this lab has shown that longevity in stationary phase declines with higher acetate conditions, in particular, under limited gas exchange. Using 10 and 30 mM acetate as the low and high condition, we confirmed this relationship and found under my experimental set up, the culture completely collapses within six days. However, this high-acetate-dependent collapse is dependent on the light intensity. Under lower light levels, the cell is protected from

decreases in viability and resembling the low acetate condition. Under higher light levels, senescence is delayed, unexpectedly. This implies that reactive oxygen stress may trigger the rapid senescence, but it is more complicated since at a higher light intensity, there is also some limited protection. This could be due to the induction of ROS detoxification systems in exponential growth that slow down decline in stationary phase. Previous work (Humby et al 2013 J. Phycol. 49, 389–400. <https://doi.org/10.1111/jpy.12049>) showed a decline in starch accumulation in these conditional-senescent conditions and we hypothesized that starch reserve amounts may have a role in determining stationary phase longevity. Using a collection of *Chlamydomonas* starch-deficient and starch over-accumulating mutants, however, we observed the opposite trend then predicted. Cultures with a reduced capacity for starch biosynthesis had increased longevity under high-acetate conditions. These results highlight the complexity of carbon fixation in mixotrophs and display how limiting starch biosynthesis may re-direct carbon resources that allows for enhanced longevity in batch culture.

10. A PHYLOGENOMIC RE-EVALUATION OF THE FRESHWATER GREEN ALGA *TETRAËDRON KÜTZING 1845* (SPHAEROPLEALES, CHLOROPHYCEAE) (President's Award)

Eba K. Mohamed¹, Marvin W. Fawley², Karen P. Fawley², Hilary A. McManus¹. (1) Biology and Environmental Sciences, Le Moyne College, Syracuse, NY, 13214, U.S.A., (2) Science and Mathematics, University of the Ozarks, Clarksville, AR, 72830, U.S.A.

Tetraëdron Kützing 1845 is a genus of green algae currently placed in the class Chlorophyceae, order Sphaeropleales, and family Hydrodictyaceae based on morphology. However, recent molecular studies regarding relationships within the family Hydrodictyaceae have not included representatives of *Tetraëdron*, and other studies of the order Sphaeropleales have suggested placing the genus in the family Neochloridaceae (Sphaeropleales, Chlorophyceae). This study characterizes two plastomes within the genus *Tetraëdron* and uses a phylogenomic approach to determine the correct placement of the genus in relation to the family Hydrodictyaceae. The two assembled plastomes are 131,393 bp and 156,171 bp in size, and each contains two single copy regions and an inverted repeat. The phylogenomic results indicate *Tetraëdron* is not monophyletic and classification revisions are necessary.

11. GLOBAL DOMINATION: UNDERSTANDING THE SPREAD OF TWO INVASIVE MACROALGAE USING HABITAT SUITABILITY MODELS (Wilce Award)

O'Brien, Brandon S.^{*1}; Neefus, Christopher D.¹; Dijkstra, Jennifer A.^{2,3}. (1) Department of Biological Sciences, University of New Hampshire, (2). School of Marine Sciences and Ocean Engineering, University of New Hampshire, (3) Center for Coastal and Ocean Mapping, University of New Hampshire.

Invasive seaweeds are a potent threat to biodiversity in coastal ecosystems worldwide. Only a subset of all introduced seaweeds have made the leap from being locally problematic to global invaders. Here, we explore the use of habitat suitability models for analyzing the regional-scale distribution of invasive macroalgae. In particular, we

attempted to identify locations that may be vulnerable to the introduction of certain highly successful invaders. Models were built for two species: *Undaria pinnatifida* and *Dasysiphonia japonica*. Both species are native to temperate Asia, but have become established in disparate regions of the world. Accuracy of the constructed models was assessed by comparing predicted highly suitable habitat to known occurrence records. They were then used to identify areas that may be vulnerable to introduction by either species in the future: *U. pinnatifida* is already established in a number of areas worldwide, but has yet to reach the Gulf of Maine. *Dasysiphonia japonica* is relatively recent to the Gulf of Maine, and is not as globally widespread, but may have the potential to spread beyond its current extent.

12. SALT INDUCED GENE EXPRESSION IN *CHARA LONGIFOLIA* C. B ROB. AND *CHARA AUSTRALIS* R. BR.: IMPLICATIONS FOR SALT TOLERANCE MECHANISMS (Wilce Award)

Shaunna Phipps¹, Charles Goodman², Charles Delwiche², Mary A Bisson¹, (1) Department of Biological Sciences, University at Buffalo, New York, (2) Department of Biological Sciences, University of Maryland, College Park, Maryland.

Species within the genus *Chara* have different tolerance ranges when exposed to or cultured in varying salinities. We examine salt tolerant *Chara longifolia* and salt sensitive *Chara australis* for mechanisms of salt tolerance and their potential role in adaptation to salt for both species. Since *Chara* is more closely related to embryophytes than to other green algae, we hypothesize that genes similar to those in embryophytes are likely to be the mechanisms behind salt tolerance in *Chara*, especially genes related to Na⁺ export: Na⁺/H⁺ antiport (*NHX/SOS1*) and a H⁺-ATPase (*AHA*). The presence of these candidate genes has been confirmed in *C. longifolia* and *C. australis* using previously established Illumina transcriptomes. Creation of time-course Illumina transcriptomes were made using RNA from multiple time points (0 hr, 6 hr, 12 hr, 24 hr & 48 hr) after a freshwater culture for each species was exposed to salt stress. These transcriptomes reveal differential expression that will enable us to test our hypothesis that Na⁺ export is critical to salt tolerance, as well as identify other genes that may play important roles in adaptation to salt stress. Initial analysis indicated expression of genes involved in photosynthesis and in cell wall maintenance, as well as membrane transport, show different patterns of up- and down-regulation in the two species.

13. IRON AVAILABILITY DICTATES THE RESPONSE OF CORAL SYMBIONTS TO THERMAL STRESS (Wilce Award)

Hannah G. Reich¹, Irene B. Rodriguez², Todd C. LaJeunesse¹, Tung-Yuan Ho². (1) Department of Biology, The Pennsylvania State University, University Park PA 16802, USA, (2) Research Center for Environmental Change, Academia Sinica, Taipei, Taiwan.

Trace metals are critical to the physiology of micro-algae (e.g. phytoplankton). Mutualistic endosymbionts, Symbiodiniaceae, deliver and receive nutrients from their hosts, including reef-building stony corals. Linking the connection between macro (carbon, nitrogen, phosphorus) and micro-nutrient (trace) quotas in relation to energy cycling between host

and symbiont is pertinent to understanding the holobiont's ability to withstand environmental stressors. It is hypothesized that exposure to increased iron availability (and subsequent iron sequestration/retention) may enhance the organism's ability to maintain homeostasis during stress events. To test this hypothesis, cultures of *Breviolum minutum* and *B. psygmophilum*. (formerly *Symbiodinium* clade B) cultures were exposed to a full-factorial set of temperatures and iron concentrations. During exponential growth, cultures were sampled for nutrient content (trace metals and major nutrients), chlorophyll, pigments, and photosynthetic physiology to evaluate *Breviolum spp.* condition. Preliminary results indicate that heat stress halts growth for both species growing under low iron concentrations whereas counterparts at higher iron concentrations are able to persist. Contrastingly, *B. minutum* and *B. psygmophilum* exhibit divergent changes in trace metal stoichiometry in response to changes in temperature. By combining a broad suite of physiological approaches, we have further characterized the Symbiodiniaceae iron requirement by assessing the compounding effects of iron limitation and heat stress on the stability of coral-algal symbioses.

14. A PHYLOGENOMIC APPROACH TO INVESTIGATE THE EVOLUTIONARY HISTORY OF PHOTOSYNTHETIC STRAMENOPILES (*Wilce Award*)

Kristina X Terpis¹, Matthew W. Brown², J. Craig Bailey³, Christopher E Lane¹. (1) University of Rhode Island, Kingston, RI, 02881, U.S.A., (2) Mississippi State University, Mississippi State, MS, 39762, U.S.A., (3) University of North Carolina-Wilmington, Center for Marine Science, Wilmington, NC, 28409, U.S.A.

Stramenopiles are a major eukaryotic clade, branching with Rhizaria and Alveolata to form the supergroup SAR. Members of this diverse clade of protists are found in marine, freshwater, and terrestrial habitats and contain large numbers of both photosynthetic and non-photosynthetic species. There are currently at least 15 described classes of photosynthetic stramenopiles. Whereas much is known about diatoms, due to their contribution to global biogeochemical cycles, and how large kelps create entire ecosystems, little is known about many of these organisms. The expansion of transcriptomic datasets has enabled the inclusion of a greater number of lineages, some of which have been ambiguously assigned in single gene phylogenies. In an effort to establish a robust phylogeny for photosynthetic stramenopiles (Ochrophyta), novel transcriptomes were constructed to investigate evolutionary relationships within this diverse group. Here we cultured 23 photosynthetic stramenopiles from 8 different classes (Chrysophyceae, Chrysochromophyceae, Dictyochophyceae, Eustigmatophyceae, Phaeothamniophyceae, Pinguicophyceae, Raphidiodiphyceae, and Xanthophyceae) concentrating on undescribed species and those of uncertain taxonomic affinity. Transcriptomes were sequenced for each culture and these data were combined with existing data for phylogenomic analysis. Our phylogeny robustly places taxa among the ochrophytes, which were previously considered *insertae sedis*. Novel resolved relationships among the Ochrophyta will be discussed.

15. SYMBIOTIC DINOFLAGELLATE LINEAGE CAUSES HOST DEATH (*Wilce Award*)

Kira Turnham, Todd LaJeunesse. Biology, Penn State University, State College, PA 16802, U.S.A.

The family Symbiodinaceae is best known for species forming symbioses with various invertebrates including reef-building corals. However, when presented to host species, Symbiodinaceae members elicit contrasting responses including mutualism and mortality. Our attempts to experimentally induce stable symbioses of four *Fugacium* cultured isolates resulted in death of the model organism, the mangrove jellyfish *Cassiopea xamachana*. We sought to determine if *Fugacium* constitutively release putative harmful substances without presence of a host and if physical contact between and/or ingestion of *Fugacium* was needed to cause host response. Identifying the mechanism by which *Fugacium* species induce mortality will have implications for further analysis of putative toxicity within the family Symbiodinaceae. This group thus represents a model system to study dinoflagellate ecology and evolution as well as mutualism dynamics.

16. ESTIMATING PHYTOPLANKTON CARBON BIOMASS USING DNA (*Wilce Award*)

Lingjie Zhou & Senjie Lin. Marine Science Department, University of Connecticut, Groton, CT 06340, U.S.A.

Phytoplankton are one of the most important and fundamental groups of organisms in the ocean. In most phytoplankton studies, species composition and their contribution to the phytoplankton community are essential; however, it is technically challenging to assess an individual species biomass in a phytoplankton assemblage. With the development of molecular techniques, DNA analysis has the potential to work as a proxy for estimating species composition and species-specific biomass simultaneously. This requires an established correlation between biomass and DNA content at the species level with a correlation of a measurable DNA index, such as 18S rDNA. To address this shortcoming, species representing major phyla of micro algae are being studied. The results from 12 species that have been examined so far showed an apparent log-log linear correlation for carbon and DNA content as well with DNA and 18S rDNA and with Carbon and 18S rDNA. Furthermore, this 18S rDNA-to-carbon approach enables high-throughput sequencing (HTS) work for natural plankton assemblages. DNA extracted can be used for rDNA HTS (metabarcoding) and its total quantity in a sample can be used to calculate community total Carbon biomass in the environment. The resulting rDNA sequences provide taxon resolution, whereas taxon-specific rDNA sequence read numbers out of the total sequencing reads can be used to estimate taxon-specific carbon contribution (%) in the community. If validated, an accurate and efficient determination of phytoplankton species composition and species-specific biomass will become feasible.

ORAL PRESENTATION ABSTRACTS (Alphabetical by presenting author)
SUNDAY, APRIL 28th

17. A HISTORICAL REVIEW OF *ASCOPHYLLUM NODOSUM* HARVESTING IN NORTH AMERICA

Alison I Feibel, Bryan L Morse & Raul A Ugarte. Acadian Seaplants Ltd. 30 Brown Ave. Dartmouth, Nova Scotia, Canada, B3B 1X8.

Commercial harvesting of *Ascophyllum nodosum* (Rockweed) has taken place in the Northwest Atlantic for 60 years. Over this time the geographical spread of harvesting and the overall biomass landed have increased significantly. *A. nodosum* harvesting began in Nova Scotia, Canada, in 1959, and now takes place across the provinces of Nova Scotia and New Brunswick and the state of Maine. The method of harvesting has also changed over time. Initially, mechanical harvesters were responsible for the majority of the harvest, however over the past 40 years the primary method of harvest has been manual, utilizing hand held cutter rakes from small boats. This project aims to correlate the historical changes that have occurred in the *A. nodosum* harvest over the past 60 years with the harvestable biomass of *A. nodosum* available over that time. Published literature provided historical biomass estimates before and during early harvesting years, which was then compared to recent biomass data collected by Acadian Seaplants Ltd in the same locations.

18. MIND THE MATING SYSTEM GAP: THE CONSEQUENCES OF REPRODUCTIVE MODE VARIATION IN HAPLODIPLONTIC MACROALGAE

Stacy A. Krueger-Hadfield, Department of Biology, University of Alabama at Birmingham, Campbell Hall 464, Birmingham, AL 35294.

While the balance between reproductive modes and breeding systems are well characterized in animals and seed plants, understanding the evolutionary consequences of this variation in haplodiplontic macroalgae is more challenging. The mechanisms by which these evolutionary processes operate differ subtly, but fundamentally, because in haplodiplontic life cycles, fertilization and meiosis are spatiotemporally separated by a prolonged haploid stage. As a consequence, haplodiplontic macroalgae face unique eco-evolutionary constraints as each ploidy stage is linked to the other, whereby impacts on one ploidy may cascade through the entire life cycle. First, there are two possible ways for selfing to occur, depending on whether or not a species has separate sexes. Separate sexes are often used as a proxy for an outcrossed mating system in haplodiplontic species, but selfing can occur in which cross-fertilization occurs between full-sib males and females that share the same diploid parent. Second, asexuality will result in the dominance of one ploidy stage, and loss of the other due to the spatiotemporal separation of meiosis and fertilization. Third, the haploid stage is a critical window in which selection can act, as no deleterious mutation can be masked, but the impacts of inbreeding depression are less well known. Fourth, the maintenance of haplodiplontic life cycles is hypothesized to be

driven by ecological niche differentiation, but empirical tests of this are rare. Red macroalgae are excellent models with which to test eco-evolutionary hypotheses addressing the maintenance of sex, but there are critical gaps in our ability to use these algae as models because data are lacking or taxonomically restricted. I will discuss recent work on several marine and freshwater red algae in which we can readily address mating system and life cycle evolution.

19. REGULATORY MECHANISMS INVOLVING SMALL NON-CODING RNAS IN THE RED ALGAE *GRACILARIOPSIS ANDERSONII*

Daniela Lopes Paim Pinto¹, Nicholas Blouin², Christopher E. Lane¹. (1) Department of Biological Sciences, University of Rhode Island, Kingston RI, 02881, U.S.A, (2) INBRE Bioinformatics Core, University of Wyoming, Laramie, WY 82071, U.S.A.

Genetic and epigenetic gene regulations are crucial in understanding many aspects of organismal development and responses to biotic and abiotic factors. Small non-coding RNAs (sRNA) play a role in controlling multiple epigenetic phenomena. They have entered into the gene regulation scenario as ubiquitous and adjustable repressors of gene expression across a broad group of eukaryotic species. However, very few studies have been conducted in algal systems to identify their presence and potential function. Although endogenous sRNAs and specific proteins involved in sRNA biogenesis have been reported for few species of green, brown and red algae, the gene regulatory mechanisms involving non-coding RNAs in algae remain mostly uncharacterized. By employing next-generation sequencing and bioinformatics tools, we attempted to describe the landscape of small RNA in *Gracilariopsis andersonii*. The sequencing of a small RNA library constructed from *G. andersonii* tissues produced ~ 55 million reads which were used as input to a pipeline designed for identification of sRNAs based on the characteristics of known land plants sRNAs. The resulting sRNA candidates identified were partitioned into different classes of small non-coding RNA and their potential targets predicted *in silico*. This study will provide essential insights to comprehensively understand the regulatory processes mediated by sRNAs in red algae. It will also be instrumental in setting the stage for a wide range of studies related to algae biology, and the role of epigenetics throughout under-studied eukaryotes.

20. UNEXPECTED SALINITY TOLERANCE IN A FRESHWATER BROWN ALGA

John D Wehr, Nicholas Ballor, & Daniel Restifo. Louis Calder Center – Biological Station, Fordham University, Armonk, NY 10504, USA.

The freshwater brown alga *Pleurocladia lacustris* A. Braun was originally described by Alexandro Braun in 1855 from Tegeler See, a freshwater, inland lake in Berlin, Germany. Most populations subsequently discovered were from calcareous freshwater streams and lakes in Sweden, Latvia, Denmark, U.K., Austria, and the USA. A smaller number of brackish populations have been reported, mainly from coastal Sweden, northern Canada, and Greenland. The physiological adaptations and potential evolutionary variation in this species has not yet been examined. We isolated and cultured populations of *Pleurocladia*

from three freshwater, low-conductivity streams (0.3-0.7 mS / cm; 0.1-0.3 PSU), situated at markedly different distances from marine water: 100 m above the high tide, 600 km upstream, and more than 2000 km upstream from the ocean. All were maintained and grew well in MiEB12 freshwater medium. Replicated growth experiments were conducted in enriched seawater medium with salinities of 0.1, 1, 5, 10, and 25 PSU and measured growth based on dry mass and Chl-a concentrations. Filaments grew successfully when transferred directly from freshwater to experimental media, without intermediate adaptation steps. We predicted that each strain would grow best in freshwater conditions, but differ in their tolerance to seawater as a function of their original proximity to the ocean. Surprisingly, all three strains tolerated the full range of salinity, with specific growth rates ranging from 0.6 – 0.9 d⁻¹ and maximum yields at 10 PSU (6 to 7-fold increase in DM and Chl-a). This pattern differs strongly from prior experiments with a freshwater strain of *Ectocarpus* (both members of Ectocarpaceae). The wide salinity tolerance in freshwater strains of *Pleurocladia* suggests that this species may have migrated into and out of marine habitats several times in its evolutionary history. Future experiments are aimed to examine possible biochemical mechanisms permitting this highly plastic physiology.

POSTER ABSTRACTS (Alphabetical by presenting author)

1. ISOLATION AND CHARACTERIZATION OF MUTANTS DEFECTIVE IN CILIA REGENERATION IN *CHLAMYDOMONAS REINHARTII* (President's Award)

Ellen Acheampong & Jason Brown, Department of Biology, Salem State University, Salem, MA.

Cilia and flagella are identical brush-like organelles found on the surfaces of eukaryotic cells and are involved in motility, sensing, and signaling. Defects in cilia assembly or function lead to PKD, congenital heart disease, Bardet Biedl syndrome, and other ciliopathies. In *Chlamydomonas reinhardtii*, one of the most well-studied flagella model organisms, regeneration of flagella to normal length and functions occurs within 90 minutes of acid-shock deflagellation where hundreds of genes are induced. Less is known about how the cells regulate expression of these genes: How do the cells detect the presence or absence of cilia and signal the nucleus? How are the genes encoding cilia proteins coordinated with each other? Previous experiments found that cells that failed to upregulate a reporter of flagella gene expression also had a delay in flagella regeneration.

The goals of this experiment were to generate *C. reinhardtii* mutants defective in cilia regeneration, to identify the mutated genes in these strains, and to identify transcription factors and signaling components needed for flagella assembly. 3000 hygromycin-resistant colonies were generated by the insertion of *aph7* DNA fragment. 42 of the 3000 colonies exhibited defective flagella structure, defective motility, or delayed flagella regeneration; 14 of these 42 mutants had delay in regenerating their flagella. To identify the mutated genes, genomic DNA for a subset of mutant strains was extracted, and PCR reactions were set up using the Restriction Enzyme Site Directed Amplification polymerase chain reaction (RESDA PCR) protocol with primers specific for the *aph7* insert combined with four different degenerate primers. DNA fragments from successful PCR reactions were purified and sequenced. Mutated genes were identified and characterized to identify the proteins encoded by these genes. Flagella regeneration and reporter gene assays were conducted to further characterize the phenotypes of two of the mutants originally identified as having a delay.

2. THE EFFECTS OF ALGAECIDES AND HERBICIDES ON A *MICROCYSTIS* WINTER BLOOM IN LAKE OKEECHOBEE, FLORIDA (USA) (Trainor Award)

Max Barbosa¹, D.E. Berthold¹, F.W. Lefler¹, C.M. Baird², H.D. Laughinghouse IV¹.

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Microcystis-dominated cyanobacterial harmful algal blooms (cyanoHABs) are a reoccurring problem within the Lake Okeechobee Waterway resulting in widespread economic and health impacts. As public awareness on the risks of blooms increases, there is an urgent need for studies on both short-term and long-term management of cyanoHABs. In order

to provide science-based best management practices or eradication/treatment options, we tested various concentrations and combinations of algaecides and herbicides. Bloom waters were collected from Lake Okeechobee in November/2018 and were dominated by *Microcystis wesenbergii*, with some *M. aeruginosa* and *Dolichospermum circinale* colonies present. The bloom material was exposed to fifteen different algaecides, herbicides, or combinations, using four different concentrations. Cell abundance and morphology, chlorophyll a/b, phycocyanin and microscopic analyses were undertaken at the time of collection and 24 and 72 hours post-treatment. Microcystin concentrations were measured from the crude bloom, but were determined too low to undertake microcystin degradation analyses. Overall, the effectiveness of the chemicals varied. The most efficacious at treating this bloom included sodium carbonate peroxyhydrate, copper sulfate pentahydrate, copper ethanolamine complex, and combinations of diquat dibromide with endothall, copper gluconate/citrate, and/or copper ethanolamine. Other promising treatment methods included combinations of flumioxazin with copper gluconate/citrate and endothall with liquid H₂O₂. Some chemicals, including liquid H₂O₂ and endothall alone, were unable to deplete cyanobacterial abundance and therefore considered an ineffective treatment option for the treatment of *M. wesenbergii*-dominated blooms. Future work aims at treating toxic blooms and monitoring cell abundance together with toxin production and release for effective treatments *in situ*.

3. A NOVEL, EFFICIENT METHOD TO MAP AND QUANTIFY A SLOW-GROWING FRESHWATER ALGA (*HERIBAUDIELLA FLUVIATILIS* (ARESCH.) SVED) (*Trainor Award*)

G. C. Barker & J. D. Wehr. Louis Calder Center – Biological Station, Fordham University, Armonk, NY 10504, USA.

River ecology studies commonly utilize outdated and inadequate methods. Non-random sampling, using visual estimates as a reliable form of measuring data, and poor spatial resolution are all standard. Yet the technological capacity to overcome all of these challenges not only exists, but is readily available. This project aims to establish randomized, spatially explicit, observation-based field methods for the study of crustose river algae.

Methods were developed to investigate microhabitat preferences of *Heribaudiella fluviatilis* (Aresch.) Sved in Macedonia State Park, CT. *H. fluviatilis* is regarded as the most common species among the relatively rare group of freshwater brown algae. It is likely but unconfirmed that this species is more strongly impacted by abiotic factors than by grazing and has remarkably slow growth, at a rate of up to a few millimeters per year. Evaluating these and other ecological questions requires randomized data at a spatial scale relevant to their small thallus size. To achieve this, a photographic, image-analysis method was developed to quantify fine-scale abundance and growth patterns.

For each sampling day, random points were generated along a detailed map of a 40-m reach. A quadrat was centered on each of these points and surveyed for *H. fluviatilis*, which was photographed when present. Photographs were processed using photoQuad freeware, providing a high degree of accuracy and objectivity in estimating percent and absolute cover. From this, we will build a thorough map of *H. fluviatilis* within the reach

and overlay it with canopy cover data to determine whether canopy cover or proximity to other colonies influences *H. fluviatilis* location. These methods are readily adaptable and easy to implement for any sessile species at a range of spatial scales, making randomized, quantitative, spatially-explicit methods more accessible.

4. EFFECT OF LIGHT ON CADMIUM ACCUMULATION IN *CHARA LONGIFOLIA* C.B ROB. AND *CHARA AUSTRALIS* R. BR. (President's Award)

Amber Bartlett¹, Megan Montroy¹, Austin Nottingham^{1,2}, and Mary A Bisson¹. (1) Department of Biological Sciences, University at Buffalo, New York; (2) Graduate Program in Evolution, Ecology, & Behavior, University at Buffalo, New York.

Cadmium (Cd) is a heavy metal, adversely affecting nearly all organisms. Remediation is recommended when Cd exceeds 1 ppm in soil or sediments. Phytoremediation uses plants to remove pollutants and restore desired ecosystem functions. We investigated the effect of light intensity on Cd uptake in two Charophyte species (*Chara australis* and *Chara longifolia*) to assess light's effect on efficacy of phytoremediation. *C. australis* is salt sensitive and samples were grown in freshwater. *C. longifolia* samples are salt tolerant and were grown in fresh and saltwater. Plants were exposed to different light intensities (14 moles m⁻²s⁻¹ and 57 moles m⁻²s⁻¹) and 0 ppm Cd (control) or 50 ppm Cd (experimental). Digestion was performed using HNO₃ and H₂O₂ to prepare samples for inductively coupled plasma mass spectrometry (ICP-MS). Results in 50 ppm Cd show *C. australis* in freshwater with intense light exposure (n=7) accumulates an average of 700 ppm (SD= ±478), whereas *C. australis* exposed to low intensity light (n=9) has an average accumulation of 497 ppm (SD= ±358). *C. longifolia* in freshwater with intense light exposure (n=7) accumulated an average of 545 ppm (SD= ±201), and those exposed to lower light intensity (n=9) accumulated an average of 892 ppm (SD= ±339). *C. longifolia* in saltwater exposed to intense light (n=9) accumulated 599 ppm (SD= ±256) and in low intensity light exposure, (n=9) *C. longifolia* accumulated an average of 1005 ppm (SD= 645). Differences in Cd accumulation with respect to light intensity were not significant (p<0.05). Cd accumulation between the control and experimental samples were significant (p<0.05). In plants exposed to elevated Cd, plant concentration exceeded 100 ppm, indicating that *C. longifolia* and *C. australis* have potential as effective phytoremediation candidates.

5. THE RELATIVE ABUNDANCE OF *SACCHARINA NIGRIPES* IN THE BAY OF FUNDY OVER TIME (President's Award)

Marie Dankworth and Gary W. Saunders. Centre For Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

Since the early 1980's, the sea surface temperature (SST) in the Bay of Fundy has risen on average 1°C per decade, particularly during spring and autumn. It is likely that cold water adapted kelps will no longer survive if SST in the Bay of Fundy continues to rise. For the seaweed species *Saccharina nigripes* it was hypothesized that an initial decline recorded in 2012 in the Bay of Fundy correlated to a winter of unusually warm SST. During the

investigated period between 2010 and 2012, the relative abundance of *S. nigripes* dramatically declined and did not fully recover to 2010 values by the end of the study in 2014. We have completed a local ecological survey of *S. nigripes*, *Laminaria digitata* and *Saccharina latissima* to provide new insights on biogeography and survivorship of kelp species in a warming Bay of Fundy. Recent data from 2018 revealed a rebound of *S. nigripes* at Lepreau (Bay of Fundy), which is again the dominant contributor in the intertidal kelp community. An inverse correlation of the relative abundance of *S. nigripes* and *L. digitata* was observed. *S. nigripes* was highly abundant (70–80%) in 2010–2011 and again in 2018 compared to *L. digitata*, which had a low abundance (20%) in 2010 and 2018. The low relative abundance of *S. nigripes* in 2012 resulted in enhanced relative abundance of *L. digitata* (64%). Winter SST in the Bay of Fundy is a major factor that varied and was approximately 4°C warmer in 2012–2013 (8°C) compared with 2010 (2–5°C), 2011 (3–5°C) and 2018 (3–5°C). Thus our preliminary data continue to support the hypothesis that unusually high SST contributed to the relative decline in *S. nigripes* in 2012.

6. A MORPHOLOGICAL INVESTIGATION OF FOUR MESOPHOTIC ADDITIONS OF RHODOPHYTA TO THE FLORA OF BERMUDA

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Four species are added to the mesophotic zone benthic marine algal flora of the Bermuda Islands: *Contarinia* sp. 1Bda, *Gloiocladia pelicana*, *Halarachnion louisianense* and *Halopeltis* cf. *willisii*. The deepwater collections were made by technical divers and submersibles. The four species were compared morphologically and anatomically with protologue descriptions and we present our results here. Molecular *rbcL* sequence data was compared with molecular records from North Carolina and the Gulf of Mexico in BOLD and GenBank to determine relatedness. *Halopeltis willisii* was presently known only in North Carolina and others are known from the sister warm temperate zone of the Gulf of Mexico. *Contarinia* sp. 1Bda has previously unrecorded morphological differences from *C. magdae* and *C. peyssonneliiformis*, the two species presently known in the Western Atlantic Ocean.

7. COMPARISON OF GROWTH RATE AND LIPID CONTENT IN DESERT AND POLAR ALGAE

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Thanks to their ability to produce lipids and carbohydrates, microscopic algae are a potential source of renewable fuels. Determining what conditions are most favorable to the growth and lipid production of specific algal strains can aid in the search for an alternative to fossil fuels. Desert and polar strains of *Bracteacoccus bullatus* were grown on different media and tracked for their growth rates over a month. In another

experiment, the same strains were frozen for two hours, grown for several weeks, and subsequently harvested. The cellular lipids were chemically extracted and analyzed using GC/MS. The results suggested that the polar strains grew best in nutrient-enriched media while the desert strains grew best in the nutrient-poor media. In response to freezing, total lipid content increased in the desert strains and decreased in the polar strains. This suggests major physiological differences between the desert and polar strains of the same species.

8. ASSESSING CHANGES IN COASTAL ECOSYSTEM ENGINEERS AND ASSOCIATED COMMUNITIES IN NARRAGANSETT BAY

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Habitat-forming seaweeds, such as rockweeds and kelps, are ecosystem engineers that form dynamic habitats in cool-water regions and support complex food webs. Rockweeds, such as *Fucus* spp. and *Ascophyllum nodosum*, are dominant, temperate seaweeds in the intertidal and shallow subtidal of rocky shorelines, while kelps form complex habitats in the subtidal. Changes in the distribution or abundance of habitat-forming seaweeds can have dramatic consequences for the associated food webs and ecosystem health. Recent anecdotal reports suggest that habitat-forming seaweeds have decreased in Narragansett Bay. Accordingly, we hypothesize that the abundance and species composition of coastal ecosystem engineers (e.g. rockweed and kelp), and their associated communities in Rhode Island (RI), have shifted over time. Our research project is assessing the current health of economically and ecologically important habitats in Narragansett Bay. Our objectives are fourfold: (1) survey fish, invertebrate, and seaweed communities by combining traditional methods (e.g. random quadrat sampling) with a novel video transect method at sites dominated by rockweed or kelp; (2) quantify habitat quality through assessments of fish abundance, growth, and foraging ecology; (3) determine changes in habitat-forming seaweeds and associated faunal communities by comparing new data with historical records; and (4) examine the abiotic drivers of ecosystem change using existing Narragansett Bay data. During the fall of 2018, we conducted 10 surveys combining quadrat sampling and video in 6 rockweed and 4 kelp habitats using a novel, cost effective video transect device; an additional 12 rockweed and 12 kelp habitats will be surveyed during the summer of 2019. Here, we will report the results of the surveys conducted in fall of 2018 and analyze how these habitats have changed over the past 30+ years.

9. UNDERSTANDING SPECIES DIVERSITY AND DISTRIBUTION OF *CYLINDROCYSTIS* SPECIES (ZYGNETOPHYCEAE)

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Cylindrocystis species may be found in almost any habitat, anywhere in the world except permanently frozen polar areas. Some species, such as *Cylindrocystis brebissonii*, appear to be nearly cosmopolitan while others are so localized as to be considered endemic. In the course of a phylogenetic study of the genus *Cylindrocystis* we encountered two species which appeared to be new to science. In order to better understand the taxonomy and distribution of *Cylindrocystis* species, we undertook a global and comprehensive review of the known species. Several discoveries and observations will be discussed. Amended taxonomic concepts of the most widely reported species *Cylindrocystis brebissonii* and *C. crassa* indicates that each broadly-defined species includes at least one other species. This taxonomic assessment affects our understanding of the distribution of these reportedly cosmopolitan species.

10. THE DISTRIBUTION OF *PRORODON VIRIDIS* (CILIOPHORA, PROSTOMATIDA), A CILIATE WITH ENDOSYMBIOTIC *CHLORELLA* (TREBOUXIOPHYCEAE, CHLORELLALES), AT THE OXIC/ANOXIC INTERFACE IN A FRESHWATER LAKE.

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Measuring the vertical distribution of the mixotrophic ciliate *Prorodon viridis* Ehrenberg-Kahl in 2018 revealed a narrow but distinct seasonal band located at the oxic / anoxic interface in Lake Lacawac, a mesotrophic lake in Northeast, Pennsylvania. *Prorodon viridis*, which harbors green algae endosymbionts, establishes a peak in concentration at 9 m depth from June - September, a depth with mid-day nominal light illumination and dissolved oxygen. The ciliate band appears to dissociate at night. Cells of *Prorodon viridis*, with a mean size of 60 x 70 µm, contained on average 111 algae cells, which ranged in size from 3 – 7 µm in diameter. Numerous larger algal cells appeared to be in the process of cell division. DNA extraction of uncultured algae cells was performed on isolated ciliate cells, and the *rbcL* gene was PCR amplified and sequenced. The symbiont is in the genus *Chlorella* Beijerinck but is distinct from *C. vulgaris*, and *C. variabilis*, symbionts of the common ciliate *Paramecium*. Data from the ITS2 gene of the green symbiont are needed to verify its taxonomic placement. Likewise, an understanding of the metabolic interaction of these two partners, along with possible other (bacterial) endosymbionts is needed.

11. SEQUENCING OF THE FRAGMENTED CHLOROPLAST AND MITOCHONDRIAL GENOMES OF *PITHOPHORA* SP. (HORSEHAIR ALGAE)

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Pithophora is a filamentous green alga within the order Cladophorales that can be found growing on the bottom or on the surface of ponds or other slow-moving water sources that are rich in nitrogen and phosphorus in very dense mats. *Pithophora* mats are a nuisance occurring as a result of eutrophication and are difficult to prevent and control. Genera within the order Cladophorales appear to have unusual chloroplast genomic conformations where the genes do not connect to make a single circular chromosome. Instead they occur on linear fragmented pieces of DNA, usually without another gene. These fragments can fold into secondary structures, but it is unknown if they associate into a single chromosome or remain as linear fragments throughout the life of the algal cell. In this study, an isolate of *Pithophora* was collected in central Georgia and cultured to be used to further explore the sequence, conformation, and, eventually, the expression of chloroplast genomes from this order. Total DNA was isolated and deep sequenced using Illumina's MiSeq technology.

Using sequences from other Cladophorales genera as templates for assembly, twelve complete coding regions have been assembled from the chloroplast (*atpA*, *atpB*, *atpH*, *petA*, *petB*, *psaA*, *psaB*, *psbB*, *psbC*, *psbD*, *psbN*, and *rbcL*) and one from the mitochondria (*coxI*). So far, all the assemblies have followed the pattern seen in other genera from Cladophorales, i.e. the genes occur on non-overlapping fragments and a single full-length coding region occurs on each fragment. Also of interest are the presence of non-canonical codons. Phylogenetic analysis of the sequences demonstrate that the coding regions are consistent with the genus *Pithophora*, but the species cannot be confirmed.

12. A MOLECULAR-ASSISTED ALPHA TAXONOMIC (MAAT) STUDY OF SOME WESTERN ATLANTIC SOLIERIACEAE (GIGARTINALES) (*President's Award*)

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This project involves the description of three novel species of red algae within the family Solieriaceae, one in the recently described genus *Eucheumatopsis* and two in *Meristotheca*. Using the chloroplast *rbcL* gene as a marker, as well as morphological characteristics, *Eucheumatopsis sanibelensis* sp. nov. from the Gulf of Mexico coast of Florida is distinguished from *E. isiformis* with a type locality in the eastern Caribbean Sea. Further, using the same genetic marker and its morphological characteristics, a red algal species previously identified as *Meristotheca gelidium* in Bermuda is shown to be the new species *M. odontoloma*. A second Bermuda species of *Meristotheca* collected in the mesophotic zone from 60 m is shown by using MAAT to be *M. muriamans* sp. nov. An early collection of *M. muriamans* in Bermuda from 1953 was misidentified as *Agardhiella ramosissima*.

13. CHLOROPLAST AND MITOCHONDRIAL GENOMES OF A *PEDIASTRUM DUPLEX* ISOLATE FROM CENTRAL GEORGIA

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Pediastrum is a freshwater colonial green alga in the family Hydrodictyaceae. A *Pediastrum* sp. was isolated from a freshwater system in Milledgeville, Georgia and cultured. The purpose of this project was to sequence chloroplast and mitochondrial genomes of this isolate to 1 – phylogenetically identify the isolate to the lowest possible taxonomic level, 2 – provide new sequences to improve resolution within the Hydrodictyaceae family, and 3 – potentially provide genomic sequences to explore gene expression in this genus. Total DNA was deep sequenced using Illumina MiSeq technology and the chloroplast and mitochondrial genomes assembled with de novo assembly strategies using Geneious software. The chloroplast genome was circular, 199,241 base pairs in size, and contains 107 protein coding genes, 26 tRNA's, and 3 rRNA's. The coding region sequences were nearly identical to an archived *P. duplex* isolated from Eastern Europe in the 1960s (UTEX LB1364) so the new isolate was given the working name of *P. duplex* - Milledgeville. The LB1364 strain's plastome has not been fully sequenced but fragments have been archived in GenBank, despite the high sequence similarity between LB1364 and *P. duplex*-Milledgeville, their gene orders differ. The gene order of *P. duplex*-Milledgeville does match other archived *P. duplex* chloroplast genomes except for an inverted region in *P. duplex*-Milledgeville. The mitochondrial genome was a total of 40,756 base pairs containing 43 protein coding genes, 24 tRNAs, and 3 rRNA's. The mitochondrial gene sequences match coding regions from the UTEX LB1364 strain with 100% similarity. Two other *P. duplex* chondriomes are in GenBank and comparison of them to *P. duplex*-Milledgeville shows that intra-specific rearrangements of the mitochondrial genome may be common. These sequences provide chloroplast and mitochondrial genomes from a wild *P. duplex* isolate and provide more evidence that organelle genome rearrangements occur within this species.

14. DIVERSITY OF TERRESTRIAL GREEN ALGAE FROM CHILE AND PANAMA, WITH A FOCUS ON *DIPLOSPHAERA* (TREBOUXIOPHYCEAE, CHLOROPHYTA) (*President's Award*)

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Terrestrial green algae participate in biofilms and serve as potential partners for lichen symbiosis. As part of a larger biodiversity survey in Chile and Panama, we collected algae from lichens and substrates, including bark. We report results on the diversity of sampled terrestrial green algae as assessed by DNA barcode analysis using data from the plastid-encoded gene *rbcl*. First, we examined the diversity of green algae on substrates from Chile and Panama. These were distributed into several trebouxiophyte genera.

Diplosphaera was the most frequently sampled genus in our study and these samples were distributed into several well-supported clades. DNA barcode gap analysis supports many distinct species of *Diplosphaera* beyond the four already known. Some clades (species) contained algae from broad geographic locations and diverse habitats, pointing

to ecological flexibility. Some clades are correlated with high or low elevation, suggesting ecological specialization. Next, we obtained green algal sequence data associated with two species of the lichen fungus *Pseudocyphellaria*. The algal sequences from these lichens are members of *Diplosphaera* and are closely related. Both samples originated from low elevation sites in Chile. *Diplosphaera*, a common genus of terrestrial unicellular green algae that lives on bark and other substrates, has not yet been reported as being associated with *Pseudocyphellaria*. Using published data, we also analyzed sequences of *Diplosphaera* associated with other lichenized fungi and show that they do not form a monophyletic group, indicating that different species of *Diplosphaera* can participate in symbiotic associations.

15. AULACOSEIRA GIRAFFENSIS SP. NOV., A NEW DIATOM SPECIES FORMING MASSIVE POPULATIONS IN AN EOCENE LAKE (*President's Award*)

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Diatoms began to inhabit freshwater by at least the Late Cretaceous, becoming well established by the early to middle Eocene. *Aulacoseira*, an important diatom in numerous ponds, lakes and rivers today, was one of the earliest known genera to colonize freshwater ecosystems. Members of this genus with characteristics familiar to those found on modern species became increasingly more abundant by the Eocene, and continued to thrive throughout the Miocene to the present. We describe a new species of *Aulacoseira* from an early to middle Eocene site near the Arctic Circle in northern Canada. The new species, *Aulacoseira giraffensis*, has valves with a length:width ratio close to 1, a hyaline valve face, straight mantle striae, a shallow ringleist, branched linking spines, concave-convex complementarity on adjacent valve faces, and rimoportulae with simple papillae-like structure. The suite of characters, especially the highly branched spines, concave-convex valves and simple rimoportulae, is unique for this species. Large numbers of *A. giraffensis* specimens were found over a ten meter section of the core, representing thousands of years. These high concentrations are indicative of abundant, bloom-like, growth. Findings confirm that the morphological body plan for the genus was well established by the Eocene. Although findings indicate evolutionary stasis in morphological structure for *A. giraffensis* over a time scale of thousands of years, oscillations in valve morphometrics could potentially be used to trace changes in the environment of this ancient Arctic waterbody, especially periods of high growth alternating with periods of reduced growth.

16. VARIATION IN VEGETATIVE DESICCATION TOLERANCE BEHAVIOR OF INDEPENDENTLY-EVOLVED DESERT SPECIES OF *TETRADESMUS* (*Trainor Award*)

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Vegetative desiccation tolerance (VDT) — the ability of vegetative cells to recover from extreme loss of protoplasmic water — is a rare but phylogenetically widespread phenomenon. Some VDT species can survive rapid and long-lasting desiccation and recover their physiological activity once water becomes available. Unlike embryophytes, green algae show multiple origins of terrestriality, with algae of desert soil crusts being perhaps the most dramatic example. In Chlorophyta desert species are embedded in aquatic taxa, such as a common freshwater genus *Tetradismus* (Sphaeropleales, Chlorophyceae). More importantly, desiccation tolerance in different desert *Tetradismus* species has evolved independently from aquatic ancestors, and we expect them to show variation in VDT traits.

We demonstrated dramatic differences in response to desiccation of aquatic and desert *Tetradismus* using PSII chlorophyll fluorescence as a proxy for the physiological state of cells. When hydrated the effective quantum yield of photosynthesis was similar for all strains. Likewise, desiccation resulted in a complete loss of effective quantum yield. Upon rehydration a clear and significant distinction between aquatic and desert species was apparent: only desert species recovered their photosynthetic activity, the aquatic species remained inactive even after 15 h. The behavior upon rehydration varied among species depending on intensity of desiccation. Rapid desiccation reaching low relative humidity (RH) values (RH ~5% reached in 23 h) appears to cause the most damage. Upon rehydration desert species initially had photosynthetic activity but lost it later. Less severe modes of desiccation (RH ~65% reached in 8 h and RH~85% reached in 12 h) resulted in differences among the independently-evolved desert species.

This complex of closely related species of *Tetradismus* from different habitats is an ideal system for future investigations of the underlying mechanisms and evolution of desiccation tolerance in chlorophycean algae.

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