60th Annual
Northeast Algal Symposium

Burlington, Vermont
April 8 - 10, 2022

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Special thanks to our judges for the Wilce Graduate Oral Presentation Award (Anne Lizarralde, Ira Levine, Dale Holen, Mary Bisson), the President's Undergraduate Oral Presentation and Undergraduate Poster Award (Diba Khan-Bureau, John Wehr, Lesleigh Kraft), and the Trainor Graduate Poster Award (Jeff Johansen, Amanda Savoie, Trevor Bringloe, Ron Hoham). Many thanks to all who have volunteered to judge award presentations - we had a very strong showing and did not need everyone who signed up, but thank you all! We appreciate our session moderators: Greg Boyer, Hilary McManus, Louise Lewis, Susan Brawley, Sarah Caltabiano, and Chelsea Villanueva, and of course, our intrepid auctioneer, the one and only Craig Schneider. We are grateful to Vermont's own Nick Bezio for designing our meeting logo and NEAS merchandise, and Domenic D'Amore (Daemen University) for designing our anniversary logo.

Finally, we are so grateful to our distinguished guests Greg Boyer and Mindy Morales for sharing their insights and expertise with NEAS.

Meeting Code of Conduct

NEAS is committed to creating a safe and welcoming environment for all attendees. To do so, all attendees are expected to abide by the following Code of Conduct:

- All attendees will treat each other with respect.
- Considerate, respectful and collaborative communication is expected.
- Personal attacks directed toward individuals, or disruptions of the virtual portions of the meeting (e.g., “zoom-bombing”), will not be tolerated.
  - Examples of unacceptable behavior include, but are not limited to, written and verbal comments related to physical appearance, body size, race, religion, national origin, gender, gender identity and expression, sexual orientation, as is use of nudity and/or sexual images in presentations or chats.
- Downloading and capturing information presented is strictly prohibited without the written permission of the authors. This applies to oral and poster presentations.

Individuals engaging in behaviors that violate this code of conduct will be removed from the meeting by the moderator/host.

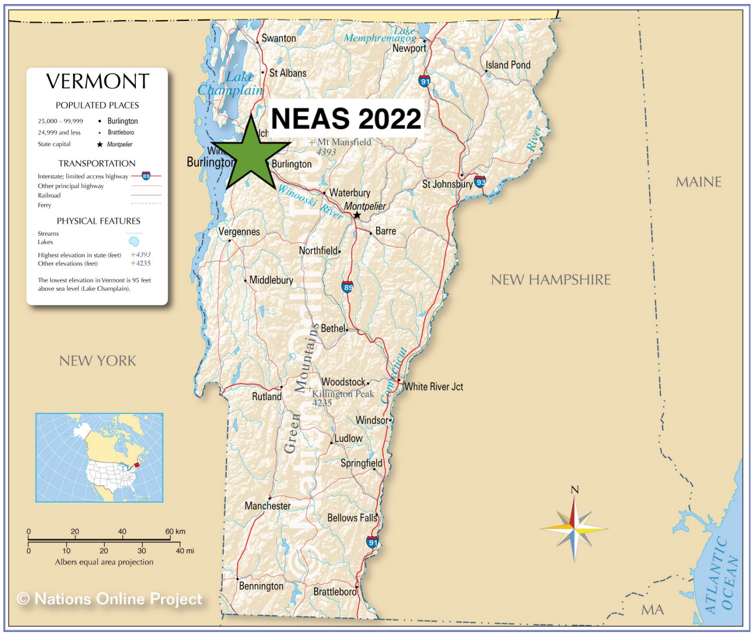
Did you know? It’s NEAS’ 60th anniversary.
Some might call it a diamond anniversary. We call it a DIATOM anniversary!

PS: You can get various conference-themed merchandise in our online store:
https://www.redbubble.com/shop/ap/50324084

Welcome Message

Welcome to the ***60th*** Northeast Algal Symposium! Our 60th NEAS is being held in Burlington, VT, on the land of the Abenaki People of the Dawn, and on the very shore of Lake Champlain. According to the wonderful History of the Northeast Algal Society, NEAS has never been held in the state of Vermont. After 60 years, we thought it was time to change that.

Vermont seems a particularly suitable place for a freshwater-themed meeting. Much of Vermont’s border with New Hampshire is defined by the Connecticut River, the longest stream in New England. The border with New York runs through another major water body - Lake Champlain, which despite its smaller size is sometimes called the Sixth Great Lake. The lake is part of UNESCO’s Champlain-Adirondack Biosphere Network and provides drinking water and diverse ecosystem services to the population of Vermont and New York. It also (allegedly) harbors a monster called Champ!



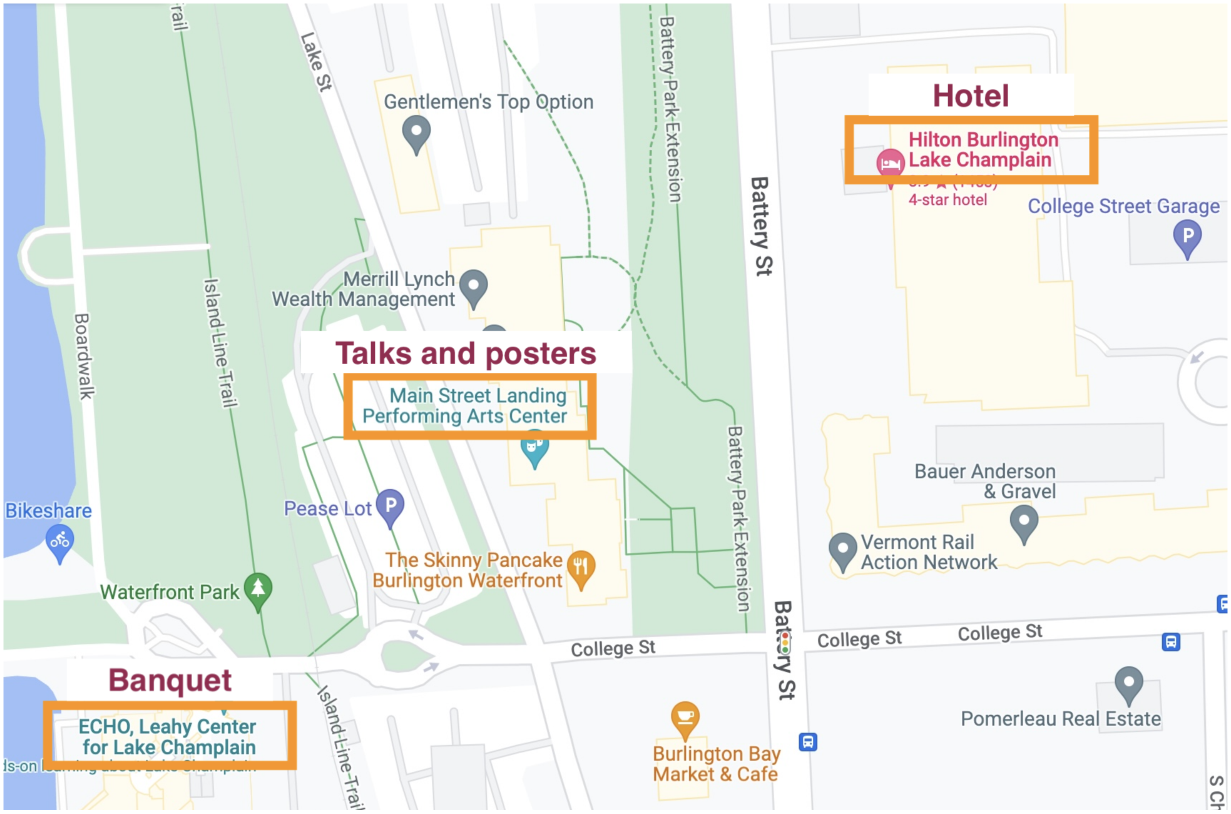
Map by Nations Online Project.

Today, Lake Champlain is the subject of cutting-edge scientific research, much of it centered at the University of Vermont. The Rubenstein Ecosystem Science Laboratory is a major research hub for Lake Champlain studies, and houses among others a phycologically named research vessel, the Melosira! One of our keynote speakers, Dr. Ana (Mindy) Morales-Williams is affiliated with the Rubenstein Lab, and in her presentation will tell us about her research on lake ecosystems. Our other keynote speaker, Dr. Greg Boyer, will provide insights into lake ecology by focusing on harmful algal blooms, especially toxic cyanobacterial blooms. We hope you will enjoy this impressive line-up of lake experts, in addition to many other fantastic presentations on our roster - it should be an exciting meeting!

Sarah Whorley and Karolina Fučíková, NEAS ~~2020~~ 2022 Co-conveners

Map & Directions to Meeting

Most of our meeting will take place at Main Street Landing: 60 Lake St, Burlington, VT 05401, which is a short walking distance from the hotel. The Hilton Burlington Lake Champlain hotel is located at 60 Battery St. Our Saturday evening banquet will be at the ECHO Museum (Leahy Center for Lake Champlain), 1 College St.



Parking in Burlington is limited and a little pricey - but the city is very pedestrian friendly and has a public transit system (https://ridegmt.com/). We recommend parking at the hotel (for a daily fee) and walking between venues. We have planned all venues to be close together and within easy walking distance.

Virtual Directions

Zoom link for talks (Saturday and Sunday, 8am-noon, with breaks):
https://assumption.zoom.us/j/91534682741?pwd=UUUyWllIRjhvZGpydUs1WFBUYWpKZz09
Password: NEAS2022

DIFFERENT Zoom link for virtual poster session (Saturday 2pm):
https://assumption.zoom.us/j/95371645437?pwd=eHRqVnIrNUpZTDV2dC9mWFVwQTZqdz09
Password: NEAS2022

Website to preview all poster presentations ahead of the live virtual session:
https://sites.google.com/daemen.edu/neas2022posterpresentations/home

General Program

Friday, April 8th

Time	Event	Location
4:00pm - 7:00pm:	Registration	Main Street: Lake Lobby
	Auction Donation	Main Street: Lake Lobby
	Poster Hang Up	Main Street: Classroom
6:00pm - 9:00pm:	Welcome Mixer	Main Street Lake Lobby
	Small plate appetizers and a cash bar will be available	

Saturday, April 9th

Time	Event	Location
7:00am - 8:15am:	Breakfast	Main Street: Lake Lobby
	Continental breakfast and coffee will be available	
	Registration	Main Street: Lake Lobby
	Auction Donation	Main Street: Lake Lobby
	Presentation Upload	Main Street: Lake Lobby
	Poster Hang Up	Main Street: Classroom
8:15am - 8:30am:	Welcoming Remarks	Main Street: Filmhouse
8:30am - 9:00am:	NEAS Memorials	Main Street: Filmhouse
9:00am - 9:45am:	Oral Session 1	Main Street: Filmhouse
9:45am - 10:15am:	Break	
10:15am - 11:15am:	Oral Session 2	Main Street: Filmhouse
11:15am - 11:30am:	Coffee Break	Main Street: Lake Lobby
11:30am - 12:15pm:	Oral Session 3	Main Street: Filmhouse
12:15pm - 1:45pm:	Lunch, EC meeting	Main Street: Lake Lobby
	A buffet of sandwiches and salads from Panera will be available	
2:00pm - 3:00pm:	Virtual Posters	Zoom Breakout Rooms
3:00pm - 3:30pm:	Break	
3:30pm - 5:00pm:	In-Person Posters	Main Street: Classroom
5:00pm - 6:30pm:	Break	Burlington's many attractions.
6:30pm - ???	Gather for Banquet	Leahy ECHO Museum
	A buffet meal will begin being served at 7:00pm. There will be a cash bar available	
	Auction	Leahy ECHO Museum

Sunday, April 10th

Time	Event	Location
7:00am - 8:00am:	Breakfast	Main Street: Lake Lobby
	Continental breakfast and coffee will be available	
8:00am - 9:00am:	Keynote Speakers	Main Street: Filmhouse
9:00am - 9:15am:	Break	
9:15am - 10:15am:	Oral Session 4	Main Street: Filmhouse
10:15am - 10:30am:	Coffee Break	Main Street: Lake Lobby
10:30am - 11:30am:	Oral Session 5	Main Street: Filmhouse
11:30am - 1:00pm:	Lunch, Business Meeting	Main Street: Lake Lobby, Filmhouse
	Boxed sandwiches from Panera will be available	

~Depart~
We will see you next year!

2021-2022 Executive Committee

President: Hilary McManus

Treasurer: Lindsay A. Green-Gavrielidis

Secretary: Thea Popolizio

Membership: Brian Wysor

Nominations: Dale Holen

Members at Large: Karolina Fučíková, Sarah Whorley

Development: Amanda Savoie, Greg Boyer, Craig Schneider, John Wehr

Publications: *vacant*

Website: Chris Neefus

Graduate Member: Rachel Cray

2021 Convenors: Louise Lewis, Peter Siver

2022 Convenors: Sarah Whorley, Karolina Fučíková

2023 Convenors: Dale Holen, Louise Lewis, Anne Lizarralde, Peter Siver

In Memoriam

Edwin A. Boger (1923–2019)

For those of you who knew and remember Ed Boger, you can probably picture him at the Development Committee Table during our annual meetings. He was most happy to sell NEAS t-shirts and mugs, but most of all to chat with all the attendees – to tell a joke, to catch up with old friends, to meet new grad and undergrad students, and to hear what was going on in their phycological and personal lives. A veteran of WWII, Ed received his B.A. from Valparaiso University, M.S. from the University of Connecticut with F.R. Trainor, Ph.D. from Clark University under H.W. Johansen, and was a member of the biology faculty at Worcester State University from 1968–2000. Soon after the "Ideas Committee" of NEAS was established in 1984, Ed was appointed to it by then President R.T. Wilce, and he continued to serve on it for nearly three decades as it morphed into the Development Committee (1985) and then the Le Baron Colt Jr. Development Committee (2007). His steadfast service raising funds for students on this committee earned him the inaugural Frank Shipley Collins Award of NEAS in 1996. As dedicated servants to students, Ed and his wife Margaret endowed a student scholarship at Worcester State awarded annually to an outstanding junior majoring in Biology who shows great potential for graduate studies and career success.

C.W. Schneider & P.A. Siver

Robert Thayer Wilce (1926–2022)

Who is Professor Robert T. Wilce? If you'd attended NEAS meetings several years prior to his passing at 97 this past February 26th, while Bob was still a regular participant, you would know who he was, and had he asked you a probing question on your presentation you most certainly would remember him.

Bob was a major driving force of NEAS for over 50 years from its early evolution from a Manhattan group of plant physiologists, biochemists and algal scientists who utilized mostly unicellular algae (*Euglena* and *Chlamydomonas*) in their research. Professor Frank R. Trainor of University of Connecticut and Bob of University of Massachusetts, Amherst attended one of the Manhattan groups informal meetings and soon thereafter Dr. Trainor invited that group and all New England phycologists to the Connecticut campus at Storrs for a spring 1969 meeting, referred to by Trainor as the Algal Discussion Group, hosted by himself and Joanna Page.

On extending out from the Metropolitan area the new group focus shifted from physiology and biochemistry to broader ecological, developmental, cytological taxonomic and other studies of micro and macro algae. In the fall of that year Bob Wilce, with me, his graduate student, hosted the second of these broad based meetings of phycologists drawing 135–140 participants from New England and the northeast beyond and called it the Northeast Algal Symposium (The History of the Northeast Algal

Society, W. Johansen and P. Bradley, NEAS contr. #4). These two 1969 meetings set the tone and format for future and even current meetings with additions and minor changes along the way. From Trainor and Page's "Algal Discussion Group" to Wilce and Sears' Northeast Algal Symposium, the group soon took on today's name, the Northeast Algal Society or NEAS. Always congenial and supportive of students, members and attendees have benefitted from this collegial, professional and welcoming group.

During his long involvement with NEAS, Bob was always offering new ideas for the organization, focusing on: student support and involvement; as President; Honorary Chair; Host or Cohost for three NEAS meetings; recipient of the Frank Shipley Collins Award; as judge for student participant's presentations (the Wilce Award, the namesake for two student awards complementing the Frank R. Trainor Award); and generally providing unbridled energy and enthusiasm throughout.

Bob stands among few if any phycologists in still working on a manuscript (this one on *Rhodymenia delicatula* Dangeard), with ideas for others still gestating at 97 years of age at the time of his passing. All through his academic life and well into retirement, Bob was passionate about phycology and NEAS in particular.

Bob received many awards during his professional life, among them a Guggenheim Fellowship, a Fulbright-Hayes Research Abroad Fellowship, but perhaps the one he cherished most was an Honorary Doctor of Science from the University of Copenhagen and presented by The Dane's Queen Margrethe in 1998 for his sustained interest and research on the marine algae of Greenland and adjacent Arctic waters.

Always curious and strong in work ethic, Bob faced age and its health issues by hardening his determination to work as best he could, right to the end. After spending the morning likely thinking of his nearly finished *Rhodymenia* manuscript while waiting patiently for lunch, he passed quietly among loved ones, Donna Parker, his daughter-in-law and caregiver in particular and his nurse Maria by his side. He talked daily with his attentive son Alex Wilce, Professor of Mathematics, Susquehanna University.

His curiosity nourished his pursuits and a broad spectrum of phycological interests including but not limited to the intricacies of red algal sexual reproduction, early study of red and brown algal crusts, sublittoral algal ecology, biogeography, practical aspects of fouling of beaches by *Pylaiella*, discovery and publication of undescribed algal species, nuclear plant monitoring of algal populations in heated effluents and annual review of reports, graduate student involvement, challenging current paradigms of molecular based algal taxonomy and his lifetime study of Arctic seaweeds. Colleagues often invited him to speak to their classes not only for the content of his presentations but to introduce their students to a professor who was not just enthusiastic, but even passionate about his work with the algae and the world around him. Perhaps some of you have been encouraged by Bob's infectious enthusiasm when doubts clouded your progress or have benefitted from his probing questions.

Bob's interests were broad and well informed. He loved reading history, biographies, ancient sea and land battles, just about anything in science and world events. He became an avid fly fisherman, tying his own fishing flies, some of which have been auctioned here at NEAS.

Bob did not begin his life with academic aspirations. Rather in the time of war, he signed up with the paratroopers in 1942 and was eventually sent to the European theater where he was later wounded and sent home to recover. As a wounded WWII veteran and after some years in recovery he eventually enrolled at the University of Scranton under the GI Bill and graduated with a BS in Zoology in 1950. This cast a new path leading to a MS in Botany at the University of Vermont. With several botanical options open to him, from Vermont Bob decided University of Michigan the best support and provided the most interesting options. He took his Ph.D. with Wm. Randolph Taylor there in 1957. Taylor wanted him to work on tropical marine algae, but Bob wanted none of that. Rather, he set his course to the north, eventually to Arctic waters. He set out in small boats for an adventurous and challenging series of collections of littoral and sublittoral algae for taxonomic, floristic and ecological study from the Labrador Peninsula and northwest Newfoundland. These studies became the subject of his Ph.D. thesis published in the Bulletin of the National Museum of Canada in 1959, the same year he began teaching at the University of Massachusetts in Amherst.

Prior to Bob's cold-water studies, much of the work on Arctic and subarctic seaweeds had been done by Europeans. The Danish phycologist Kolderup Rosenvinge was early but Bob's ties with European phycologists began with a University of Michigan post-doctoral and a Lincoln Ellsworth Fellowship grant to study with Mat's Waern of Uppsala, Sweden and Tyge Christensen of Denmark, two strong influences and mentors to Bob. He spoke and often referred to the influence and work of these two European mentors and other European phycologists who had worked in northern and Arctic waters. The name of the r*ed crust Waernia mirabilis* Wilce, Maggs and Sears honored Mats Waern.

While showing Mats Waern a red alga he'd collected from Woods Hole, Mats asked him, "Is this our *Rhodymenia delicatula*?" referring to a similar alga in European waters. That question set the stage for Bob's last manuscript on this small red alga collected from about 8 m off the Woods Hole Fisheries Jetty. Intrigued by the apparent disjunct distribution of *R. delicatula* led Bob into possible hypotheses accounting for its and other disjunct distributions. While he all but completed his manuscript on the reproductive and vegetative biology and ecology of this little red, he hoped someone would see it to publication if he didn't finish it himself. His work on its disjunct distribution was stuck at the level of speculation. Were he to have a second life he still would never run out of interesting questions about the algae. Even at 78 years old, 13 years after his retirement in 1990, Bob Wilce was awarded a NSF grant for a 4th Arctic expedition to Canada's Baffin Island to study a foliar brown alga which he considered a combination of two genera, *Platysiphon* and *Arcticophycus glacialis* gen et comb nov. which he assigned to a new brown algal order the Stschapoviales, Phaeophyceae.

But let me summarize how I and many others likely remember Professor Robert T. Wilce. Above all, curious and enthusiastic, having a strong work ethic, passionate about working with the algae, encouraging and inspirational to students, and always ready to challenge the current paradigm such as molecular phylogenetics. With his international reputation and broad correspondence, Bob was a driving force during the origins and growth of NEAS. He was a great conversationalist always probing and attentive while engaging with students, colleagues and friends. Bob was also a great fly fisherman and human being, and a good friend to many.

Jim Sears, Professor Emeritus, Biology, UMass Dartmouth
Graduate student, colleague and close personal friend of Bob Wilce

Candidates for NEAS Executive Committee

We have the following nominations and will hold a virtual election during the meeting. The ballot will be available from 8am Saturday until 10am Sunday.
https://pennstate.qualtrics.com/jfe/form/SV_etjUmJyU4VAEuzj

You can read more about each position in the NEAS Officers Manual.
https://northeastalgae.org/organization_docs/NEASofficersmanual.Feb2011.pdf

Secretary:

A) Sarah Princiotta

Member at Large:

A) Ken Karol
B) Anne Lizarralde
C) Jessie Muhlin

Nominations Committee Chair:

A) Chris Lane

Candidate Biographies

Sarah Princiotta (she/her/hers) is an aquatic microbial ecologist and phycologist. She uses a combination of field sampling, laboratory work in culture, and mesocosm approaches to better understand how trophic relationships between members of freshwater microbial communities contribute to the structure of those communities over time, and how these patterns may change against the backdrop of anthropogenic changes in global climate and land use. One of the major themes of her research is mixotrophic protists that combine photosynthesis and ingestion of particulate prey. Dr. Princiotta is currently an Assistant Professor of Biology at Penn State Schuylkill, where she conducts research with and teaches with undergraduate students. Her research program involves a field campaign of 15 lakes across NE Pennsylvania in a partnership with a regional lake monitoring program hosted by Lacawac Sanctuary. She is also an active member of the science committee that guides PLEON, the Pocono Lake Ecological Observatory Network. Prior to joining Penn State, Dr. Princiotta was a postdoctoral research associate at Hancock Biological Station (Murray, KY; 2017-2019) and served as the Director of Research and Education at Lacawac Sanctuary Biological Field Station (Lake Ariel, PA; 2016-2017). Her doctoral and undergraduate degrees are earned from Temple University (Philadelphia, PA) under the guidance of Robert Sanders.

Ken Karol, My primary research interest focuses on utilizing several molecular and morphological approaches toward understanding the evolution of green algae in a broad sense, and, more restrictively, the biology, evolution, systematics, and classification of the Characeae.I am also part of a NSF funded Tree of Life project, The Green Algae Tree of Life (GrAToL). This project involves the collaboration of five institutions to understand the evolutionary relationships of all of the major groups of green algae, a diverse group of more than 14,000 photosynthetic species worldwide.

Anne-Marie (Lott) Lizarralde, Senior Research Scholar, Botany Department, Connecticut College. Anne started working in the lab of Peter Siver the summer after she graduated from Connecticut College as an Environmental Studies major (1991) and then also received her Master's degree in Botany (1997). She has been working as a laboratory manager and her research focuses on the modern scaled chrysophytes along the Eastern coastline of the United States and Canada, as well as more recent work on fossil specimens from an Eocene lake from the Canadian Arctic. Anne has co-authored numerous papers on scaled chrysophyte floras, has served as co-editor for the Proceedings Volume for the 2008 International Chrysophyte Symposium, supervised the summer research programs, and is responsible for continuing research on Dr. Siver's NSF grants.

Jessie Muhlin is a Professor of Marine Biology at Maine Maritime Academy where she teaches in and is Chair of the Corning School of Ocean Studies. Her research interests focus on the reproductive ecology, population genetics, and food web ecology of fucoid seaweeds in the northwestern Atlantic. Jessie is involved in art-science collaborations using marine algae as inspiration. She has a deep commitment to public outreach and routinely participates in outreach programs with the National Park Service, Schoodic Institute, and Maine Sea Grant, among others. You can often find her feeding her students an assortment of edible sea vegetables and encouraging everyone to understand and appreciate the algae.

Chris Lane, My lab focuses on the evolution of algae from a molecular, ecological and phylogenetic context, and in particular the mechanisms and consequences of genome reduction and gene transfer. Algae are fascinating subjects because they have adapted to exploit a variety of niches and habitats (marine, freshwater, snow, hot springs and almost anywhere moisture persists) and employ an array of life-history strategies (e.g., free-living, symbiotic and parasitic). Of interest to us are the algae that have taken on a parasitic lifestyle, and specifically, how this strategy affects the organism over evolutionary time.

Presentation Schedule

Saturday, April 9th

7:00 am - 8:15 am

Main St. Lake Lobby: Breakfast, Registration, Auction Donations, Presentation Upload
Main St. Classroom: Poster Hang-up.
Main St. Lake Lobby: Exhibitors.

8:15 am - 8:30 am

Main St. Filmhouse: Welcoming Remarks
Join on zoom:
https://assumption.zoom.us/j/91534682741?pwd=UUUyWllIRjhvZGpydUs1WFBUYWpKZz09
Password: NEAS2022

8:30 am - 9:00 am

Main St. Filmhouse: NEAS Memorials
We remember Dr. Edwin Boger and Dr. Robert Wilce, long-time and dedicated NEAS members who recently passed away. Contributions by various NEAS members.
Join on zoom:
https://assumption.zoom.us/j/91534682741?pwd=UUUyWllIRjhvZGpydUs1WFBUYWpKZz09
Password: NEAS2022

9:00 am - 9:45 am

Main St. Filmhouse: Oral Session 1, Wilce Award
Moderator: Susan Brawley
Join on zoom:
https://assumption.zoom.us/j/91534682741?pwd=UUUyWllIRjhvZGpydUs1WFBUYWpKZz09
Password: NEAS2022

9:00-9:15. Brandon O'Brien: Biogeography and invasion potential of five invasive seaweeds under projected ocean warming.
9:15-9:30. Josephine Crichton: An environmental DNA metabarcoding approach to study red algal biodiversity.
9:30-9:45. Stephen Gottschalk: Landscape genetics and inferred gene flow of aquatic green algae (*Chara* subsection *Willdenowia*) in eastern North America.

9:45 am - 10:15 am: Break

10:15 am - 11:15 am

Main St. Filmhouse: Oral Session 2, Wilce Award
Moderator: Greg Boyer
Join on zoom:
https://assumption.zoom.us/j/91534682741?pwd=UUUyWllIRjhvZGpydUs1WFBUYWpKZz09
Password: NEAS2022

10:15-10:30. Michael Kausch (last year's Graduate Research Award recipient): Growth of the bloom-forming cyanobacterium *Limnoraphis birgei* under near-zero nitrogen conditions.
10:30-10:45 Natalie Flores: Toxic cyanobacterial blooms in a eutrophic lake: evaluating the detection of microcystins in select fish species.

10:45-11:00. Mildred Akagha: *Albertania* and *Egbenema gen. nov*. from Nigeria: expanding biodiversity in the Oculatellaceae (Cyanobacteria).
11:00-11:15. Brian Jusko: *Atlanticothrix*: Novel strains of the *Nostoc*-like genus from San Nicholas Island and Ethiopia.

11:15 am - 11:30 am
Main St. Lake Lobby: Coffee Break

11:30 am - 12:15 pm
Main St. Filmhouse: Oral Session 3, Wilce and President's Award
Moderator: Louise Lewis
Join on zoom:
https://assumption.zoom.us/j/91534682741?pwd=UUUyWllIRjhvZGpydUs1WFBUYWpKZz09
Password: NEAS2022

11:30-11:45. Sarah Caltabiano: Characterization of nitrate reductase in *Microcystis aeruginosa* PCC7806 wild type and non-toxic mutant strain. (Wilce)
11:45-12:00. Chelsea Villanueva: What a difference a tRNA makes: defining when and how much tRNA insertions, in otherwise orthologous operons, skew the phylogenetic potential of the 16S-23S ITS. (Wilce)
12:00-12:15. Emanuel Eagle: Developing a database for estimating the impact of climate on freshwater algae in the northeastern United States. (President's)

12:15 pm - 1:45 pm
Main St. Lake Lobby: Lunch - *A buffet of sandwiches and salads from Panera.*
Main St. Board Room: Executive Committee meeting.

2:00 pm - 3:00 pm
Virtual Poster Session (access from anywhere on your computer or phone). Posters 1-4, Trainor and President's Award. Preview for posters 5-22 are also available on the website; we **encourage all poster presenters to attend the virtual session**.
https://sites.google.com/daemen.edu/neas2022posterpresentations/home
Join on Zoom (different link than talks):
https://assumption.zoom.us/j/95371645437?pwd=eHRqVnIrNUpZTDV2dC9mWFVwQTZqdz09
Password: NEAS2022

3:00 pm - 3:30 pm
Break - gather back at Main St. Landing.

3:30 pm - 5:00 pm
Main St. Classroom: In-Person Poster Session. Posters 5-22. Trainor and President's Award.

5:00 pm - 6:30 pm
Break: Catch up with your colleagues, network, explore Burlington, or take a nap!
Vote online in the Executive Committee elections:
https://pennstate.qualtrics.com/jfe/form/SV_etjUmJyU4VAEuzj

6:30 pm - ???

Leahy ECHO Museum: Banquet (buffet meal served at 7:00 pm), Auction.

Sunday, April 10th

7:00 am - 8:00 am

Main St. Lake Lobby: Breakfast, Registration, Auction Donations, Presentation Upload
Main St. Classroom: Poster Clean-up

8:00 am - 9:00 am

Main St. Filmhouse: Keynote Talks.
Join on zoom:
https://assumption.zoom.us/j/91534682741?pwd=UUUyWllIRjhvZGpydUs1WFBUYWpKZz09
Password: NEAS2022

8:00-8:30. Ana (Mindy) Morales-Williams: Understanding phytoplankton response to disturbance across space and time.
8:30-9:00. Gregory Boyer: Evolution of our understanding of harmful algal blooms and their monitoring.

9:00 am - 9:15 am: Break

9:15 am - 10:15 am

Main St. Filmhouse: Oral Session 4, Contributed Talks.
Moderator: Chelsea Villanueva
Join on zoom:
https://assumption.zoom.us/j/91534682741?pwd=UUUyWllIRjhvZGpydUs1WFBUYWpKZz09
Password: NEAS2022

9:15-9:30. Ron Hoham: Snow and glacial algae with emphasis on climate change and global warming and snow algae in Vermont.
9:30-9:45. Daniel Remias: Differences and commonalities in community composition of Arctic and Central European glacial ice and snow algae.
9:45-10:00. Lenka Procházková: *Chloromonas* sp. “Milena-type” (Chlorophyta) causing unusual mountain bright red snow in association with broadleaf shrubs.
10:00-10:15. Jeff Johansen: *Mojavia aguilerae* and *Mojavia dolomitestris* - two new species of *Mojavia* (Nostocaceae, Cyanobacteria)

10:15 am - 10:30 am

Main St. Lake Lobby: Coffee Break

10:30 am - 11:30 am

Main St. Filmhouse: Oral Session 5, Contributed Talks.
Moderator: Hilary McManus

Join on zoom:
https://assumption.zoom.us/j/91534682741?pwd=UUUyWllIRjhvZGpydUs1WFBUYWpKZz09
Password: NEAS2022

10:30-10:45. Mary Bisson: The Evolution of an unusual Na-ATPase important for salt tolerance in *Chara*: the possible role of whole genomic duplication.
10:45-11:00. Trevor Bringloe: Ushering in an era of high-resolution genetics in phycology: introducing an accessible workflow leveraging whole genome sequencing for biodiversity detection and phylogenetic analyses.
11:00-11:15. Ira Levine: Algae Foundation's AlgaePrize, education and workforce development.
11:15-11:30. John Wehr: Changes in the epiphytic algal assemblages following major changes in the macrophyte flora in the Colorado River.

11:30 am - 1:00 pm
Main St. Filmhouse: Closing remarks and General Business Meeting.

12:00 pm - 1:00 pm
Main St. Lake Lobby: Lunch - *A buffet of sandwiches and salads from Panera.*

~Depart~

Keynote Speakers' Biographies

The theme for this year's symposium is "***Keeping It Fresh: Water Quality in Northeastern Lakes and Reservoirs***". We have invited two speakers to facilitate that effort.

Dr. Greg Boyer

First, our own Dr. Greg Boyer of SUNY College of Environmental Science & Forestry who is a world-renowned expert on cyanobacterial blooms. Lake Champlain is not immune from these blooms and the topic has received much public attention in recent years. Dr. Boyer has been with SUNY ESF for over 30 years and director of the Great Lakes Research Consortium since 2007. He is a biochemist by training with broad interests in the chemistry and ecology of biologically-active natural products produced by plants, algae and bacteria. This includes algal toxins as well as small peptides called siderophores important in metal homeostasis.

EVOLUTION OF OUR UNDERSTANDING OF HARMFUL ALGAL BLOOMS AND THEIR MONITORING. <u>Gregory L Boyer</u>, SUNY-College of Environmental Science and Forestry, Syracuse NY, USA 13210.

Harmful algal blooms dominated by cyanobacteria (cHABs) are increasing in occurrence and severity in many North American inland waters. In the mid-1900's, our understanding of the field was that toxins were produced by three taxa ('Annie, Fannie and Mike' – *Anabaena* (*Dolichospermum*), *Aphanizomenon*, *Microcystis*) and focused on three toxins (saxitoxin, microcystin-LR and anatoxin-a). Over the last few decades, our knowledge of toxin (bio)chemistry has expanded; we now recognize more than 300 different toxins in five or six chemical classes, with multiple different cyanobacterial genera capable of their biosynthesis. CHABs were primarily reported from smaller water bodies and associated with animal fatalities, but are now observed across multiple systems - the Great Lakes, riverine and benthic environments and the freshwater – saltwater interface. They can have ecosystem-wide impacts and affect far more than just animals. Management actions initially focused on protecting from exposure via drinking water must evolve to protect from exposure through multiple avenues including drinking water, aerosolization and recreational contact. Drawing from the New York State experience, this talk will trace both the evolution in our understanding of cHABs, and the current gaps and limitations in that understanding for both immediate control and management. The benefits and limitation of the democratization of cHAB monitoring, e.g., moving away from Federal, State, and Provincial-based monitoring programs to increased community-based monitoring will be discussed.

Dr. Mindy Morales

Additionally, we are inviting Dr. Mindy Morales, Assistant Professor in the Rubenstein School of Environment and Natural Resources at the University of Vermont. Dr. Morales is a limnologist specializing in phytoplankton community ecology and carbon biogeochemistry. Her research focuses on the role of anthropogenic disturbance and climate change in algal community assembly, linking fine scale physiological and ecological mechanisms with ecosystem and landscape scale processes. Dr. Morales is a founding member of the Phycological Research Consortium which meets annually at Iowa Lakeside Laboratory, and a steering committee member of the Global Lake Ecological Observatory Network (GLEON).

UNDERSTANDING PHYTOPLANKTON RESPONSE TO DISTURBANCE ACROSS SPACE AND TIME. **Ana M. Morales-Williams[1].** [1]Rubenstein School of Environment and Natural Resources, University of Vermont, Burlington, VT, 05405, U.S.A.

Aquatic ecosystems are experiencing multiple interacting climate change pressures, representing a shifting baseline of environmental conditions. Lakes respond quickly to regional and global change relative to terrestrial systems, and because of this are considered sentinels of environmental disturbance. Within lakes, benthic algae and phytoplankton communities are equivalent sentinels, responding to disturbance and shaping biogeochemical cycles through fluctuation in their biomass, primary productivity, and functional traits. Although phytoplankton and benthic microalgae generally have doubling times of hours to days, traits such as dormancy and alternative metabolic strategies allow persistence of populations across annual to multi-decadal timescales. Spatially, extreme storm events and hydrologic fluctuation may be experienced differently by primary producers in the nearshore benthic zone compared to lake phytoplankton, thus understanding the heterogeneity of phytoplankton response to disturbance across spatial and temporal scales is critical to predicting lake ecosystem function. My research seeks to understand community assembly and ecosystem function in a non-equilibrium disturbance framework, integrating paleolimnological and modern data to predict feedbacks and threshold shifts in response to environmental stressors. In Vermont, most oligotrophic lakes have doubled in phosphorus concentrations over the past 40 years, but the phytoplankton response to these trends is variable, and in many lakes, largely unknown due to incomplete or nonexistent biological monitoring data. Our group is characterizing biotic indicators of environmental change utilizing landscape-scale paleolimnological records from 103 lakes across the state. Preliminary results suggest that while lakes are chemically recovering from stressors such as acidification and land-use alteration, phytoplankton communities have not consistently returned to pre-disturbance taxonomic composition, but are functionally similar. Ongoing work will identify algal functional traits that are resilient to disturbance across space and time. This information will allow us to understand and predict feedbacks between phytoplankton phenology and lake ecosystem function in response to a rapidly changing climate.

Oral Abstracts (Saturday)

Oral Session I - Wilce Award

9:00. BIOGEOGRAPHY AND INVASION POTENTIAL OF FIVE INVASIVE SEAWEEDS UNDER PROJECTED OCEAN WARMING.

Brandon O'Brien[1], Chris Neefus[1], Jenn Dijkstra[2]. 1. University of New Hampshire, Department of Biological Sciences. Durham, NH 03824. USA. 2. University of New Hampshire, Center for Coastal and Ocean Mapping. Durham, NH 03824. USA.

Introduced seaweeds can have severe negative impacts on their introduced ecosystems, often through the alteration of physical habitat space. One question surrounding every invasive species is whether or not it has reached its geographic limit, or if it will continue to spread. In this study we investigate the invasion potential of five widely introduced seaweeds: *Caulerpa taxifolia*, *Codium fragile* subsp. *fragile*, *Dasysiphonia japonica*, *Sargassum muticum*, and *Undaria pinnatifida*. Species distribution models were used to predict the potential geographic distribution of each species under present-day and future climate warming scenarios. The most important driving environmental variables for each species were also investigated. Under current conditions, minimum sea surface temperature had the highest percent contribution in the models of all species. Under current conditions, all five species were found to have significant potential to invade new territory. Under future conditions, evidence of potential range contraction and poleward expansion were apparent in several species. The projected models showed *C. taxifolia* to have the greatest loss in potential highly suitable habitat, and *U. pinnatifida* to have the greatest gain. These results show that there will be species-specific responses to ocean warming, making it difficult to make broad statements about future threats by invasive species.

9:15. AN ENVIRONMENTAL DNA METABARCODING APPROACH TO STUDY RED ALGAL BIODIVERSITY.

Josephine Crichton and Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Biodiversity monitoring is an important tool in ecosystem conservation, as it provides a baseline of species composition and evidence of successful management practices. These data can inform policymakers to ensure ecologically and economically valuable marine ecosystems are being sufficiently monitored and protected. As red algae become more popular in large-scale industry, the threat of biodiversity loss grows due to overexploitation, habitat loss and invasive harvesting practices. Thus, finding non-invasive, comprehensive, and accessible methods to monitor species of interest is a large part of the biodiversity and conservation challenge. Monitoring is typically conducted using molecular-assisted-alpha-taxonomic (MAAT) surveys, which require extensive taxonomic expertise, long field hours, SCUBA equipment and personnel, and invasive sampling techniques. This project uses environmental DNA (eDNA) metabarcoding to simultaneously identify multiple red algal species from a single rock scrape sample. This type of sampling is less invasive than traditional sampling, and offers reduced reliance on taxonomic expertise, tide times and weather. The floristic lists generated using both MAAT surveys and the eDNA surveys will be compared to determine if eDNA offers improved detection of red algal species and if there are species routinely being left out of current surveys due to insufficient sampling. Improved

accessibility makes these data easier and faster to generate and staying on top of the proliferation of invasive species, ecosystem collapse, and the health of valuable species and ecosystems becomes less laborious and expensive.

9:30. **LANDSCAPE GENETICS AND INFERRED GENE FLOW OF AQUATIC GREEN ALGAE (CHARA SUBSECTION WILLDENOWIA) IN EASTERN NORTH AMERICA.**

Stephen D. Gottschalk[1, 2], John D. Wehr[2], and Kenneth G. Karol[1]. 1 The Lewis B. and Dorothy Cullman Program for Molecular Systematics, New York Botanical Garden, Bronx, NY, U.S.A.; 2 Louis Calder Center—Biological Field Station and Department of Biological Sciences, Fordham University, Armonk, NY, U.S.A.

The movement of aquatic macrophytes between waterbodies is a major component of aquatic ecosystem health, and a necessary step for genetic exchange between populations. *Chara* – a group of macrophytic green algae – comprise an important part of native freshwater flora worldwide. Broad species concepts and assumed widespread water-fowl dispersal have resulted in members of this genus being considered ubiquitous and cosmopolitan. However, recent genetic information and taxonomic revisions have indicated that some species may be more limited in their ranges, and possibly rarer than previously described. Rather than being panmictic, bird-dispersed organisms, could some of these algae have local or regional genetic structure? What factors allow them to be genetically connected or genetically isolated across their ranges? In this study, isolation by distance, isolation by landscape resistance, and isolation by habitat suitability (based on water chemistry) are examined as possible mechanisms influencing genetic structure as measured by GBS generated SNP data. In our present study, we examined members of *Chara* subsection *Willdenowia* to serve as a study group to examine the conditions that are likely to play a role in gene flow between waterbodies in the eastern United States of America.

Oral Session II - Wilce Award

10:15. **GROWTH OF THE BLOOM-FORMING CYANOBACTERIUM *LIMNORAPHIS BIRGEI* UNDER NEAR-ZERO NITROGEN CONDITIONS.**

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

Harmful algal blooms (HABs) are a global water quality issue with detrimental impacts on ecosystems and economies. *Limnoraphis birgei* is an understudied, bloom-forming species of cyanobacteria (Order Oscillatoriales) for which blooms have been documented in many US states. We isolated unialgal cultures of *L. birgei* from the plankton in North Lake, Westchester County, New York, which has been impacted by annual blooms of this species. We conducted laboratory experiments to test the influence of different forms and concentrations of nitrogen on growth rate and nutrient uptake. Experiments were run with replicated 125-mL Erlenmeyer flasks inoculated with nutrient-depleted *L. birgei* filaments in 50 mL modified BG-11 medium amended with either nitrate (NO_3^-) or ammonium (NH_4^+) as the sole N source at concentrations of 0 mM, 0.1 mM, or 1 mM nitrogen. Filaments were randomly harvested for measurements of dry mass (mg) and dissolved nutrients. In the 0 mM N treatments, dry mass increased 3.5 to 9-fold, highlighting the ability of *L. birgei* to sustain growth in the absence of dissolved nitrogen. In all experiments, phosphorus uptake continued independent of N treatment, and was significantly correlated with growth rate, suggesting that growth of *L. birgei* and nitrogen availability are uncoupled. Phosphate was depleted by 87% in the 0 mM NO_3^- treatment, compared to 96% in 0.1 mM and 99% in 1 mM treatments. In the 0.1 mM and 1 mM NO_3^-experiments, dry mass increased 15-fold and 19-fold, respectively; the same concentrations of added NH_4^+ resulted in an increase in dry mass of 3.5-fold and 6-fold, respectively. Our results indicate that *L. birgei* is able to sustain growth in nitrogen-depleted conditions and suggest that this species can proliferate in lakes characterized by low dissolved nitrogen availability.

10:30. **TOXIC CYANOBACTERIAL BLOOMS IN A EUTROPHIC LAKE: EVALUATING THE DETECTION OF MICROCYSTINS IN SELECT FISH SPECIES.**

Natalie Flores[1], Todd Miller[2] & Jason Stockwell[1], [1]The University of Vermont, Burlington, VT, [2]The University of Wisconsin-Milwaukee, Milwaukee, WI.

Cyanobacteria blooms are a persistent issue in freshwater habitats globally, and are projected to continue, if not worsen, with climate change and eutrophication. Cyanobacteria can produce bioactive molecules, some of which can be toxic to eukaryotic organisms. However, the long-term effects of exposure to cyanobacteria toxins (cyanotoxins) range from tumor promotion to unknown effects. One of the primary concerns of cyanotoxins in aquatic ecosystems is their potential presence in fish and subsequent consumption by humans. Relatively limited information is known about how cyanotoxins transfer through wild fish, if certain species are more likely to transfer toxins, and whether detectable patterns exist that would help limit human exposure. We hypothesized that cyanotoxin (microcystin) concentrations in water are positively correlated to concentrations in fish. We conducted a field study to measure concentrations of cyanotoxins in water and two species of fish (yellow perch, *Perca flavescens*, and golden shiners, *Notemigonus crysoleucas*) from a shallow eutrophic lake in Vermont during the summer-fall seasons (2016-2017). Water samples throughout the period contained numerous cyanobacterial secondary metabolites, including microcystins, anabaenopeptins, and cyanopeptolins. We concurrently detected a subset of some of these metabolites in the brain, liver, and muscle tissues of the fish, however we will focus on microcystin for this presentation. Our preliminary results suggest that fish in water bodies with cyanobacteria that are actively producing toxins may contain cyanotoxins and highlight the need to better understand the movement of cyanotoxins through the food web.

10:45. ***ALBERTANIA* AND *EGBENEMA GEN. NOV.* FROM NIGERIA: EXPANDING BIODIVERSITY IN THE OCULATELLACEAE (CYANOBACTERIA).**

Mildred U. Akagha[1], Nicole Pietrasiak[2], Alžběta Vondrášková[3], Sandra C. Lamb[4], Jeffrey R. Johansen[1,3]. [1]Department of Biology, John Carroll University, University Heights, OH 44118, U.S.A.; [2]Environmental Soil Microbiology, Plant & Environmental Sciences Department, New Mexico State University, Las Cruces, NM 88003, U.S.A.; [3]Department of Botany, Faculty of Science, University of South Bohemia, České Budějovice, 37005 Czechia; [4]Department of Marine Sciences, University of Lagos, Akoka, Nigeria.

A total of eight soil/subaerial samples were collected in Lagos State, Nigeria, and used to isolate cyanobacterial cultures which were characterized microscopically, sequenced, and phylogenetically analyzed. Within the resulting set of cultures, a number of Synechococcales were observed, particularly belonging to the family Oculatellaceae. *Egbenema gen. nov.* and two new species of the recently described genus *Albertania* were found. Both genera belong to a supported clade within the Oculatellaceae that includes *Trichotorquatus* and *Komarkovaea.* The two new species of *Albertania, A. egbensis sp. nov*. and *A. lattericola sp. nov*., were from the same sample, but phylogenetically were separate based on 16S rRNA gene phylogenies, percent identity below the 98.7% threshold, and ITS percent dissimilarity >7.0%. *Egbenema aeruginosa gen et sp. nov.* was phylogenetically separated from *Trichotorquatus* and *Albertania* but was in a clade with other strains belonging to *Egbenema*. Two of these *Egbenema* strains were also named in order to provide a more complete taxonomy of the genus, *Egbenema epilithica sp. nov.* from Puerto Rico and *Egbenema gypsiphila sp. nov.* from biological soil crusts in New Mexico. Our results support the hypothesis that further species discoveries of tropical cyanobacteria will likely be made as West African aquatic and subaerial habitats are sampled and studied using modern methods.

11:00. ***ATLANTICOTHRIX*: NOVEL STRAINS OF THE *NOSTOC*-LIKE GENUS FROM SAN NICHOLAS ISLAND AND ETHIOPIA.**

Brian Jusko & Jeffrey Johansen. Department of Biology, John Carroll University, University Heights, OH, 44118, USA

The cyanobacteria as a whole are in the process of undergoing considerable taxonomic revision due to the adoption of a polyphasic approach to classification and a trove of new species identifications. One group in particular with significant unresolved polyphyly are the nostocaleans. Genus *Nostoc* and other *Nostoc*-like genera play important roles, including nitrogen and carbon fixation, in biological soil crusts and other terrestrial biomes. Although their ecological importance is documented, there are taxonomic issues including polyphyly as a result of the incomplete knowledge surrounding their diversity. The *Nostoc*-like *Atlanticothix* was recognized as a novel genus in 2021 from a set of strains isolated from Brazilian forests based on a body of evidence separating them from previously recognized species. Although little is known to this point about the global distribution of this genus, two new strains have been isolated from geographically distant regions relative to the original sampling site: one from the soil crusts of San Nicholas Island, California, and one from a religious monument in Ethiopia. Based on morphological and genetic evidence, it appears that the new strains are indeed members of *Atlanticothrix.* The vast distance and environmental diversity among the three locations provides an important look into not only the distribution of *Atlanticothrix,* but also a clearer idea of the diversity of species within the genus and of the nostocaleans as a whole. This finding should serve to reduce the unresolved polyphyly and increase understanding of global nostocalean diversity.

Oral Session III - Wilce and President's Award

11:30. **CHARACTERIZATION OF NITRATE REDUCTASE IN *MICROCYSTIS AERUGINOSA* PCC7806 WILD TYPE AND NON-TOXIC MUTANT STRAIN.**

Sarah K. Caltabiano[1] & Gregory L. Boyer[1]. 1: Department of Chemistry, State University of New York, College of Environmental Science and Forestry, Syracuse, New York

Nitrogen is an essential element for the growth of cyanobacteria. Runoff of nitrate fertilizers into freshwater systems can contribute to the proliferation of cHABS and their toxicity. Characterizing the enzyme activity of nitrate reductase (NR) in *Microcystis aeruginosa* is an important step to understanding the bloom dynamics of this organism when nitrate is present.

Nitrate reductase isolated from the toxin-producing wild type (WT) strain *Microcystis aeruginosa* PCC7806 and in its non-toxic *-mcyB* mutant was characterized for suitable electron donors, pH optimum, and substrate affinity. Suitable electron donors for both strains included ferredoxin reduced by ferredoxin-NADP+ reductase and methyl viologen. No NR activity was detected using NADH, NADPH, $FADH_2$ or ferredoxin reduced by sodium dithionite. Using methyl viologen as the electron donor. The WT NR activity showed Michaelis Menten kinetics with a Km(nitrate) of 3.4-7.40 mM.. The pH optimum was 8.5 for ferredoxin reduced by ferredoxin-NADP+ reductase, and 10.5 for methyl viologen. These results indicate *M. aeruginosa* WT NR activity is typical of a bacterial NR and very different from purified NR obtained from *Arabidopsis thaliana* and *Aspergillus nidulans*. Differences NR activity between WT and its *–mcyB* mutant under laboratory conditions will be presented.

11:45. **WHAT A DIFFERENCE A TRNA MAKES: DEFINING WHEN AND HOW MUCH TRNA INSERTIONS, IN OTHERWISE ORTHOLOGOUS OPERONS, SKEW THE PHYLOGENETIC POTENTIAL OF THE 16S-23S ITS.**

Chelsea D Villanueva[1], Markéta Krautová[2] and Jeffrey R. Johansen[3]. [1] Department of Biological, Geological, & Ecological Sciences, Cleveland State University, Cleveland, OH, 44115 U.S.A.; [2]Department of Biology and Ecology, University of Hradec Králové, Hradec Králové, Czech Republic; [3]Department of Biology, John Carroll University, University Heights, OH, 44118 U.S.A.

The polyphasic approach, in cyanobacterial taxonomy, has employed characterization of the potentially regulatory 16S-23S Internal Transcribed Spacer region secondary structures and percent dissimilarity calculations, to distinguish separate species. Conventionally, the presence of $tRNA^{Ile}$ and $tRNA^{Ala}$ genes within some ITS operons, and their absence in others, was a likely marker of paralogous operon copies. However, an analysis of clonal sequence data from 32 *Brasilonema* strains (Scytonemataceae, Nostocales), showed that within the genus, 3 distinctly orthologous operons [A, B, &C] were distributed among taxa, and each was present in a $tRNA^+$ [A, B, C] and $tRNA^-$ [A_o, B_o, C_o] form. We found that while helices, often used in classical ITS secondary structure comparisons, displayed species specific phylogenetic signals, spacer regions between conserved domains displayed strong signals relating them to either the [A,B,C] or the [A_o,B_o,C_o] operons. This data suggests the possibility that tRNA insertions may be due to ancient and variable movement of transposable elements within the genome. Inclusion of the potentially transitory domain in p-distance calculations increased the percent dissimilarity of orthologous operons from the same species, by an average of 3.16%. The presence/absence of tRNA genes within ITS sequences should not be considered as routinely demonstrating orthology. Further, the methods of ITS analyses should be refined to reflect the complex evolutionary histories of orthologous operons, especially if the presence of a transitory domain is validated.

12:00. **DEVELOPING A DATABASE FOR ESTIMATING THE IMPACT OF CLIMATE ON FRESHWATER ALGAE IN THE NORTHEASTERN UNITED STATES.**

Emanuel Eagle & Peter A. Siver. Department of Botany, Connecticut College, New London, CT, 06320, U.S.A.

The development of long term databases consisting of chemical, physical and algal records for freshwater lakes and ponds has been a focus of work in our laboratory for decades. Data has been assembled using direct measurements, historical studies, and incorporating information from paleolimnological investigations. In addition to expanding the databases, we have used the data to trace changes in algal diversity over time, shifts in trophic and acidic conditions, and long-term impacts of wind speed on thermocline development and subsequent growth of cyanobacteria. Reports on the impacts of warmer climates on all types of aquatic and terrestrial organisms appear almost daily in the media. In addition, we have witnessed governmental agencies and private lake associations advocate that climate warming is to cause for problems associated with specific lakes, including eutrophication, HABs and fish kills. However, the source of the climate data in the majority of these reports is either not given, or is not necessarily reflective of the climate for the specific geographic area in question. Given the potential impacts of increasing temperatures on algal populations and subsequent lake conditions, we wanted to expand our long term database to include air temperature records for specific lake regions. To date we have added air temperature data for 12 locations, each spanning 70 years. The data were derived from continuous records taken at established weather stations, mostly situated at airports, and are highly correlated with NOAA data. At almost all of the sites, and for all months investigated, there were no significant trends (increasing or decreasing) in air temperature, and none of the shifts in algal populations could be linked to warming air temperatures. Variability in air temperature relative to season, proximity to the ocean and latitude will also be discussed.

Oral Abstracts (Sunday)

Oral Session IV

9:15. SNOW AND GLACIAL ALGAE WITH EMPHASIS ON CLIMATE CHANGE AND GLOBAL WARMING AND SNOW ALGAE IN VERMONT.

Ron Hoham[1] & Daniel Remias[2]. [1]Department of Biology, Colgate University, Hamilton, NY 13346, U.S.A.; [2]School of Engineering, University of Applied Sciences Upper Austria, Wels 4600, Austria.

Snow and/or glacial algae are found on all continents and are mostly green algae belonging to the Chlorophyta (Chlamydomonadales) and Streptophyta (Zygnematales), but also include chrysophytes, cryptomonads, cyanobacteria, dinoflagellates, euglenoids, and xanthophytes. Drones and satellite imagery has increased our understanding of their distribution and abundance. Algae color snow and glaciers green, red, pink, golden-brown, orange, or purple-grey and microbial communities include in addition to algae, other eukaryotes, bacteria, archaea, and viruses. Chlamydomonad algae have invaded the snow habitat at least twice in their evolutionary history. Secondary metabolites in green algae (astaxanthin and purpurogallin) protect chloroplasts and nuclei from damaging PAR and UV, and IBPs and PUFAs reduce cell damage in subfreezing temperatures. Snow and glacial algae reduce albedo (sun reflectivity), increase the melt of snowpacks and glaciers, and record air temperatures and levels of CO^2 are contributing to their increased growth. Snow and glacial algae reduce albedo more than impurities (cryoconite) and increase melting of glaciers by as much as 26%. In six mountains ranges in the northern hemisphere, the number of snow days have decreased in the past 21 years by as much as 31 days. Glaciers that have existed on Mt. Kilimanjaro, Africa, for over 11,000 years, may be gone by the year 2050. There is the need for more collections of these microbes before some habitats disappear. Snow algae occur in several sites in the Green Mountains of Vermont, which we plan to visit after this meeting.

9:30. **DIFFERENCES AND COMMONALITIES IN COMMUNITY COMPOSITION OF ARCTIC AND CENTRAL EUROPEAN GLACIAL ICE AND SNOW ALGAE.**

Daniel Remias[1], Lenka Procházková[2], Linda Nedbalová[2], Liane G. Benning[3] & Stefanie Lutz[4].
1:School of Engineering, University of Applied Sciences Upper Austria, 4600 Wels, Austria; [2]Charles University, Faculty of Science, Department of Ecology, Viničná 7, 12844 Prague, Czech Republic; [3]GFZ German Research Center for Geosciences, Telegrafenberg, 14473 Potsdam, Germany; [4]Agroscope, Competence Division Method Development and Analytics, Müller-Thurgau-Strasse 29, 8820 Wädenswil, Switzerland.

Melting snowfields and glacial surfaces are known for blooms of photoautotrophic microbes, causing striking discolorations during summer in polar and mountainous regions. The aim of this study was to recognize the dominating taxa by molecular means using high-throughput sequencing, and to compare biogeographically selected sites of the European Alps with Subarctic and High Arctic ones. The amplicon metagenomes of field communities were acquired using both 18S and ITS2 rDNA markers. Earlier biodiversity studies of cryoflora at species level were hampered due to dominance of closely related green algal taxa in snow and ice habitats. Because of the limited resolution of partial 18S rDNA Illumina sequences, the hypervariable ITS2 region was used for discriminations between the genotypes. The results showed that red snow was caused by the cosmopolitan *Sanguina nivaloides* (Chlamydomonadales, Chlorophyta) and two yet undescribed *Sanguina* species in northern regions and Central Europe. Arctic orange snow was dominated by *S. aurantia*, which was not found in the Alps. On glaciers, at least three *Ancylonema* species (Zygnematales, Streptophyta) dominated, and they showed biogeographical patterns in their individual distributions. Golden-brown blooms consisted exclusively of *Hydrurus* sp. (Hydrurales, Stramenophiles) and were a phenomenon of Arctic slush habitats; similar flagellates were found in the Alps only at low amounts. From these chrysophytes, only 18S but not ITS2 sequences were amplified, showcasing how delicate the selection of eukaryotic "universal" molecular primers can be. In general, the geographic distribution of distinct species was probably influenced by individual abiotic conditions of their habitats.

9:45. ***CHLOROMONAS* SP. "MILENA-TYPE" (CHLOROPHYTA) CAUSING UNUSUAL MOUNTAIN BRIGHT RED SNOW IN ASSOCIATION WITH BROADLEAF SHRUBS.**

Lenka Procházková[1], Daniel Remias[2], Linda Nedbalová[1] & Milena Kociánová[3]. [1]Charles University, Faculty of Science, Department of Ecology, Viničná 7, CZ-12844 Praha, Czech Republic, [2]University of Applied Sciences Upper Austria, Campus Wels, Stelzhamerstr. 23, A-4600 Wels, Austria, [3]Krkonoše National Park Administration, Dobrovského 3, CZ-543 01 Vrchlabí, Czech Republic

Melting mountain snowfields harbor complex microbial communities. Amongst phototrophic psychrophiles, "watermelon snow" and its flagship species *Sanguina nivaloides* are most common. Evidently, further chlamydomonadacean taxa cause similar phenomena once robust cyst stage reach the snow surface. While *Sanguina nivaloides* is restricted to open, high alpine sites, here an undescribed alga thriving at lower altitudes in semi-exposed snow packs is presented. The blooms were observed in early summer showed site-fidelity from year to year. Aim of the work was a preliminary taxonomic and cellular characterization. The alga was found as virtually monospecific communities, causing small but intense bright red spots in the Krkonoše Mts., Jeseníky Mts. (Czech Republic) and High Tauern (Austria). Phylogenetic analysis using 18S rDNA revealed that the cells represent an independent *Chloromonas* lineage, in distinct sister relationship to *Chloromonas hoshawii* UTEX SNO66. Applying Illumina MiSeq with paired 300 bp reads, an ITS2 rDNA metagenomic analysis of the red snow samples confirmed that more than 80% of algal reads accounted to this species. Culturing efforts have been unsuccessful so far. TEM observation revealed oval to spherical cells with a robust multi-layered cell wall, sometimes the outermost was detached. The alga exhibits different cellular strategies compared to "conventional" snow dwelling algae from other *Chloromonas* clades, a more pronounced astaxanthin-accumulation in relationship to chlorophylls, and a putative dependence on a specific plant community dominated by broadleaf shrubs. The alga resembles morphologically *Chloromonas* sp. B cysts reported from ski slopes in New England, USA (Hoham et al. 1993, Duval & Hoham 2000).

10:00. ***MOJAVIA AGUILERAE*** **AND** ***MOJAVIA DOLOMITESTRIS*** **- TWO NEW SPECIES OF** ***MOJAVIA*** **(NOSTOCACEAE, CYANOBACTERIA).**

Jeffrey R. Johansen[1], Nicole Pietrasiak[2], Lauren M. Baldarelli[3] & Karina Osorio-Santos[4].
[1]Department of Biology, John Carroll University, University Heights, OH 44118 U.S.A.; [2]Plant and Environmental Sciences Department, New Mexico State University, Las Cruces, NM 88003 U.S.A.; [3]Department of Biological Sciences, Kent State University, Kent, OH 44242 U.S.A.; [4]Departamento de Biología Comparada, Universidad Nacional Autónoma de México, Ciudad de México, México.

While Nostocacean cyanobacteria are ubiquitous and play critical roles in terrestrial ecosystems, their taxonomy and biogeography still entail many mysteries. We isolated two *Nostoc*-like cyanobacteria from biological soil crusts of the Atacama (Chile) and Mojave (USA) Deserts. Initial 16S rRNA gene phylogeny placed both in monophyly with *Mojavia pulchra*. We are describing these strains as two new species of *Mojavia* using a polyphasic approach including morphology, 16S rRNA phylogenies, secondary structure and percent similarity of the 16S-23S ITS region. Like *M. pulchra,* both new species produce compact microcolonies, arthrospore-like akinetes, and monocytes representing traits characteristic for the genus. *M. aguilerae* is morphologically distinct from both others in producing bluntly conical end cells, abundant enlarged akinetes in multiseriate filaments, and gold-colored cells during senescence. *M. dolomitestris* exhibited distinctly firm, colored, compartmentalized mucilage. *M. dolomitestris* is somewhat cryptic to *M. pulchra*, but with more densely packed microcolonies and an absence of dark brownish sheath pigmentation. The two new species strengthened *Mojavia*'s position as a robust phylogenetic sister to *Nostoc.* However, 16S rRNA data could not separate the *Mojavia* species from each other. In contrast, the three *Mojavia* species showed distinct dissimilarities in secondary ITS structure and differed greatly from *Nostoc sensu stricto.* The high dissimilarities between their 16S-23S ITS regions suggest a long evolutionary history of the three species as separate lineages. In summary, we provide evidence that *Mojavia* is an evolutionary and ecologically unique Nostocaceaen genus. The rarity of *Mojavia* records and restriction in habitat point to an urgent need of recognition and protection.

Oral Session V

10:30. **THE EVOLUTION OF AN UNUSUAL NA-ATPASE IMPORTANT FOR SALT TOLERANCE IN *CHARA:* THE POSSIBLE ROLE OF WHOLE GENOMIC DUPLICATION.**

Shaunna Phipps[1], Charles F. Delwiche[2], **Mary A Bisson[1]** [1]Department of Biological Sciences, University at Buffalo, NY [2]Department of Cell Biology & Molecular Genetics, University of Maryland, College Park, MD

Chara spp. are green macrophytes, more closely related to Embryophytes (higher plants) than to Chlorophytes [1]. They are primarily a freshwater group, but salt tolerance has evolved, apparently more than once [2]. We study two species, the freshwater and salt sensitive *Chara australis* (R.Br) and the salt tolerant *C. longifolia* (C.B.Robinson) [3]. A vital component of salt tolerance is the ability to maintain a low cytoplasmic Na^+ concentration in the face of a large electrochemical force driving its entry. The consensus model for Na^+ export in green plants is efflux via a Na^+-proton exchange (Na/H antiport), with a large H^+ gradient establish by a H^+-transporting ATPase (H-ATPase) [4]. Both transport systems are known in *Chara* [5]. To determine their significance for salt tolerance, we exposed freshwater-cultured algae to salt conditions, and followed the expression of putative genes for these transporters over 48 h. Neither heat-maps based on RNAseq nor qPCR showed the large, consistent increases that would be expected if they were critical for Na^+ regulation. An alternative mechanism for Na^+ export is an ATPase directly transporting Na^+ (Na-ATPase). Na-ATPases are extremely rare in green plants, known only in a few Chlorophytes and Bryophytes. *C. australis* does not express a Na-ATPase; *C. longifolia* does, and its expression is increased a remarkable 16,000x (qPCR) under salt stress. *C. longifolia* has 28 chromosomes, while *C. australis* has 14. This, and the fact that many genes show more isoforms in *C. longifolia* than *C. australis,* indicates the occurrence of a whole genome duplication (WGD). However, genes for the H-ATPase and Ca-ATPase are not higher in *C. longifolia* than *C. australis,* leading to the hypothesis that Na-ATPase may have arisen from these duplicated ATPases. WGD are common in *Chara* and related genera, and current data suggest that they are more common in salt-tolerant algae than in salt-sensitive [2]. WGD provides many duplicate genes that can provide neofunctionalization, playing a role in evolution to novel environmental stresses.

10:45. **USHERING IN AN ERA OF HIGH-RESOLUTION GENETICS IN PHYCOLOGY: INTRODUCING AN ACCESSIBLE WORKFLOW LEVERAGING WHOLE GENOME SEQUENCING FOR BIODIVERSITY DETECTION AND PHYLOGENETIC ANALYSES.**

Trevor T. Bringloe[1] & Heroen Verbruggen[1]. [1]School of BioSciences, University of Melbourne, Parkville, Melbourne, VIC, 3010, Australia.

The age of DNA barcoding has transformed the field of phycology, revealing remarkable levels of cryptic diversity, unexpected phylogeographic distributions, and novel evolutionary insights. Sequencing whole genomes, that is all the genomic information present in a set of specimens/samples, represents the next major step in species detection and inferring evolutionary relationships, yet only a handful of recent phycological studies have leveraged this approach for these purposes. Steep learning curves and standardization of bioinformatic workflows present major barriers for the uptake of whole genome sequencing in phycology. Here, we introduce a workflow that inputs sequence data and a reference genome, and outputs fully assembled mitochondrial and chloroplast genomes as well as nuclear genome-wide variant positions across samples (Single Nucleotide Polymorphisms and indels). The workflow operates through the command-line interface, wherein users specify a set of key parameters related to assembly, read mapping, and quality control for the retention of nuclear variant positions (e.g. min/max coverage, r^2 values for linkage disequilibrium, ect). Among the key outputs are organellar and nuclear phylogenies, a phylogenetic network of nuclear variant positions, admixture and PCA plots, and basic population statistics such as levels of diversity and inbreeding coefficients. The workflow has been used to detect 100,000s to 1,000,000s of variant positions in global kelp *Alaria* datasets, several orders of magnitude greater than current sanger sequencing and reduced genomic capture methods (e.g. RADseq). The workflow has revealed species and population level insights, including widespread hybridizations among species, a novel Arctic lineage, and high latitude glacial refugial populations in the North Atlantic. Facilitating the accessibility of bioinformatic workflows will be imperative to the transition to whole genome sequencing in phycology, which in turn promises to reveal new species, holobiome associations, and functional insights.

11:00. **ALGAE FOUNDATION'S ALGAEPRIZE, EDUCATION AND WORKFORCE DEVELOPMENT.**

Ira A. Levine[1.] 1. Natural and Applied Sciences, University of Southern Maine, 04240 USA

The Algae Foundation (AF) has served over 160,000 students and trainees over the past six years. This is the seventh year of the ATEC initiative to develop algal-based bioeconomy workforce development, education and training programs. The newest effort is the US Department of Energy sponsored AlgaePrize 2022-2023. Launched 1/13/2022, the contest attracted 62 registered teams comprised of 234 students from 35 U.S. states and 14 countries. The students come from 33 colleges and universities, 5 community colleges and 13 high schools all competing head to head in three research categories of interest: production, downstream processing, and novel products and analytical tools. U.S. Department of Energy sponsored competition organized and managed by the Algae Foundation and the National Renewable Energy Lab's goal is to support the development of novel algal technologies resulting in gigaton scale algal commercialization endeavors.

11:15. **CHANGES IN THE EPIPHYTIC ALGAL ASSEMBLAGES FOLLOWING MAJOR CHANGES IN THE MACROPHYTE FLORA IN THE COLORADO RIVER.**

John Wehr[1], Mia Wrey[1], and Larry Stevens[2]. 1: Louis Calder Center – Biological Station and Department of Biological Sciences, Fordham University, Armonk, NY, USA; 2: Museum of Northern Arizona, Flagstaff, AZ, USA.

The Colorado River is the sixth-longest river in U.S. (2300 km) with a drainage area of 673,000 km^2 in 7 states, which provides water and hydroelectric power for >35 million people. There are 15 hydroelectric powerplants on river mainstem. Glen Canyon Dam is the largest in the Colorado River Storage Project and forms Lake Powell, which covers about 650 km^2. An extensive study in the 1980s of the riverine foodweb including benthic algae, invertebrates, and fish assemblages in Glen Canyon and Grand Canyon determined that diatoms epiphytic on macrophytic expanses of *Cladophora glomerata* formed the primary food base in the system. In recent decades, with climate warming there has been a severe decline in snow pack in the mountains, resulting in major reductions in river flow, flow variation, and reservoir storage. In 2020 we initiated a study to examine possible changes in the macrophytes and epiphytic algae within Glen Canyon in the face of environmental changes. Our data reveal a major benthic transition, with a decline in the biomass and cover of *Cladophora*, and major increases in *Fontinalis hypnoides, Zanichellia palustris*, *Potamogeton* sp., and *Chara vulgaris.* We document corresponding shifts in the epiphytic diatom flora, with at least 50 previously unrecorded taxa, including the invasive rock-snot species *Didymosphenia geminata*. We also recorded more than 30 soft-bodied algal species previously not seen. Epiphytic diatom composition varied significantly with macrophyte host, although many common species from previous decades were still present. We further conducted colonization experiments on concrete substrata to quantify the biomass and nutrient content of microalgae over a year-long sequence, which showed strong north- vs. south-facing x seasonal differences in algal production and phosphorus storage.

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Poster Abstracts - virtual (Numbered by presenter's last name)

1. DESMID COMMUNITIES AND ENVIRONMENTAL CONDITIONS AT NEW HAMPSHIRE WETLANDS.

Mollie Magner[1], Jenny Call[1] & Karolina Fučíková[1] (*President's Award*) (1) Biological and Physical Sciences, Assumption University, Worcester, MA 01609, U.S.A.

Desmids belong to an order of unicellular, microscopic green algae that live in freshwater habitats. The role of desmids as bioindicators for water quality has been studied due to desmids' narrow ecological ranges, sensitivity to changes in the environment, and morphological diversity. Most desmids prefer habitats with unpolluted, slightly acidic, low nutrient water and an abundance of aquatic plants. In Europe, desmids are used as bioindicators to assess the quality of freshwater habitats. The function of desmids as bioindicators in New England has not been studied thoroughly. This project examined the relationship between the desmid communities and environmental factors of New England wetlands. Desmid samples were collected from fourteen wetlands in New Hampshire. Conductivity, pH, shoreline length, total wetland area, unvegetated open water area, percent vegetation cover were measured for each site. The relationships between the diversity of the desmid communities and the water chemistry measurements at the sites were analyzed. The relations between sites were evaluated with similarity indices based on desmid community composition. Canonical correspondence analysis was also performed to determine which environmental factors explained the greatest amount of variation in the desmid community composition. A total of 241 desmid species belonging to 22 genera were observed across all sites. The highest desmid diversity was observed at Fourth Connecticut Lake, an undisturbed site in Pittsburg, NH, where 109 desmid species were recorded. Although the relationships between the diversity of desmid communities and water chemistry measurements were in the hypothesized direction of higher diversity with lower pH and conductivity, the results of the analyses were not statistically significant. Further research of the desmid communities in New England with a larger sample size and wider range of environmental conditions is necessary to understand the relationship between desmid communities and environmental conditions.

2. COMPARING THE DIVERSITY OF *TREBOUXIA* ASSOCIATED WITH THE *NIEBLA* SPECIES-COMPLEX OF LICHENIZED FUNGI TO THOSE OF SYMPATRIC LICHENS.

Anthony Perugini[1], Zach Muscavitch1, Louise A. Lewis[1] (*President's Award*). (1) EEB, University of Connecticut, Storrs, CT 06269 USA.

Lichens are one of the most successful terrestrial mutualisms on Earth. Lichens comprise a fungus (mycobiont) and cyanobacteria or eukaryotic algae (photobiont). Some lichenized fungi are generalists, forming a lichen with many photobiont species, whereas others are specialists, associating with a single or a few photobionts. This degree of symbiont association likely plays a role in the ecology and geography of the lichen. The fungal genus *Niebla* is endemic to the fog deserts of the western coast of North America. The associated photobiont partners of this lichen

are species of *Trebouxia*, a genus of green algae found worldwide. Recent work demonstrated that *Niebla* is highly specific for only a few closely related molecular species (OTUs) of *Trebouxia*. This project examines the diversity and specificity of algae within lichen-forming genera that are sympatric to *Niebla*. We hypothesize that sympatric lichen genera will have greater diversity of *Trebouxia* than is present in *Niebla*. We collected ITS rDNA sequence data from over 100 specimens of *Niebla* and sympatric lichens collected from a region of California. A variety of *Trebouxia* OTUs were found in the lichens examined, spanning the known phylogenetic diversity of the algal genus. Four closely related *Trebouxia* OTUs were found in *Niebla*. These results support our hypothesis that diverse photobionts are readily available in the environment and that *Niebla* and other genera are selective in its photobionts.

3. CLASSIFICATION OF *STENOMITOS* (LEPTOLYNGBYACEAE, CYANOBACTERIA): RECOGNIZING CRYPTIC DIVERSITY WITH THE DESCRIPTION OF EIGHT NEW SPECIES.

Miranda K. Shetzer[1] **& Jeffrey R. Johansen**[1] **(*President's Award*).** (1) Department of Biology, John Carroll University, University Heights, OH 44118 USA.

Stenomitos is a simple filamentous Cyanobacterial genus described just five years ago from a cave in Kauai. Two additional species were since described, but recent phylogenetic analysis newly sequenced strains as well as strains sequenced many year prior demonstrated much higher diversity. Following phylogenetic analysis of 16S rRNA genes, analysis of the 16S-23S ITS region, and microscopic analysis of strains still viable in culture collections, we have found eight clades (one to four strains per clade) that clearly represent new species, although all new species are either fully cryptic or pseudocryptic based on molecular criteria. Differences in sheath characteristics and minor differences in width of trichomes were the only distinguishing characteristics among strains. The new species and new combinations will include these putatitive taxonomic epithets: *Stenomitos mikhailyukae, Stenomitos vinogradovae, Stenomitos helveticus, Stenomitos kaluanui, Stenomitos frigidus, Stenomitos zionensis, Stenomitos maritimus and Stenomitos turrialbus*.

4. DNA AS A PREDICTOR OF PHYTOPLANKTON CARBON BIOMASS .

Lingjie Zhou[1]**, Senjie Lin**[1] **(*Trainor Award*).** (1) Marine Science Department, University of Connecticut, Groton, CT 06340, U.S.A.

In most phytoplankton studies, species composition and their contribution to the phytoplankton community are essential. However, it is technically challenging to assess individual species' biomass in a phytoplankton assemblage. Fortunately, DNA analysis has the potential to be a proxy for estimating species composition and species-specific biomass simultaneously. This requires an established relationship between carbon biomass and DNA content at the species level using a measurable DNA index, rDNA. To address this shortcoming, species representing major phyla of microalgae are being studied under various growth stages and growth conditions. We used the CTAB method for DNA extraction, qPCR to quantify rDNA abundance, and EPA 440 method for carbon measurement. After statistical analysis, the results from 12 species showed a robust log-log relationship for carbon and DNA content ($R^2=0.93$, $P<0.0001$) as well with DNA and rDNA ($R^2=0.86$, $P<0.0001$) and with Carbon and rDNA ($R^2=0.81$, $P<0.0001$). Meanwhile, this rDNA-to-carbon approach was compared with the widely used method based on

cell size. The anastomotic result further verified the feasibility and advantage of estimating phytoplankton carbon biomass using DNA. Additionally, this rDNA-to-carbon approach was applied to the natural phytoplankton assemblages through the next-generation sequencing technology, which validated the accuracy and efficiency of this method to determine the phytoplankton species composition and species-specific carbon biomass.

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Poster Abstracts - in person (Numbered by presenter's last name)

5. A LABORATORY ASSAY FOR DETECTING GREEN TIDE TOXICITY.

Isabella Ares[1], Danielle Moloney[1], Samantha Parsons[1] & Lindsay Green-Gavrielidis[1]. (*President's Award*). (1)Department of Biology & Biomedical Sciences, Salve Regina University, Newport, RI, U.S.A.

Macroalgal blooms are large aggregations of algae that can affect water quality and negatively impact marine life. Bloom-forming *Ulva* species have been shown to produce and release compounds that impact surrounding organisms. The goal of our research is to determine when macroalgal blooms, specifically green tides, are producing harmful compounds by developing a standard laboratory assay using phytoplankton. In these experiments, phytoplankton (*Dunaliella tertiolecta*) were exposed to water from an artificial *Ulva* algal bloom cultured in the laboratory comprised of *Ulva lacinulata* and *Ulva compressa* at a concentration of 5 g L^{-1} to determine if *Ulva* blooms impact the growth of phytoplankton. Treatment groups included *Ulva* bloom water and pasteurized *Ulva* bloom water (to eliminate impacts of marine viruses), along with a natural seawater control and an artificial seawater control. A spectrophotometer was used to measure the growth of *Dunaliella tertiolecta* via optical density and samples were fixed to quantify cell concentrations. Results showed that the *Ulva* bloom water did not negatively impact the growth of *Dunaliella tertiolecta,* but rather, after 6-7 days *Dunaliella tertiolecta* cultures performed better when grown with *Ulva* bloom water than in the controls. Some discrepancies were observed between trials and further research must be conducted until consistent trends are observed among trials. Research using field-collected *Ulva* bloom water is also necessary to compare to our laboratory results. This research is applicable to coastal cities and towns throughout the United States that rely on beach tourism and local seafood which can be negatively impacted by macroalgal blooms.

6. SYSTEMATICS AND DIVERSITY OF THE FAMILY GALAXAURACEAE (NEMALIALES, RHODOPHYTA) IN AUSTRALIA AND BERMUDA.

Margaret M. Cassidy[1] & Gary W. Saunders[1] (*Trainor Award*). (1) Centre For Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

There are 56 currently accepted species attributed to four genera in the red algal family Galaxauraceae with generally widespread tropical to warm temperate distributions. However, preliminary barcode analyses using COI-5P and rbcL-3P for recent collections from three remote Australian islands, Lord Howe Island, Norfolk Island and the Cocos (Keeling) Islands, have revealed additional species assignable to this family, and potentially novel genera. Similarly, preliminary data also indicate novel Bermudian taxa in need of study. This study will use molecular and morphological/anatomical data to examine species diversity within the Galaxauraceae in the Australian and Bermudian floras to establish the number of known and novel species for each region and describe all new taxa. Cataloging the flora in these regions could be instrumental for conservation efforts given the importance of Galaxauraceae species in warm-water ecosystems as one of the few calcified red algae and the remoteness of the floras studied.

7. CHLOROPLAST GENOMES FOR RESOLVING RELATIONSHIPS AMONG SELECT GENERA (BATRACHOSPERMALES, RHODOPHYTA).

Roseanna M. Crowell[1] & Morgan L. Vis[1] (*Trainor Award*). (1) Environmental and Plant Biology, Ohio University, Athens, Ohio, 45701, U.S.A.

Freshwater red algae are important photosynthetic members of stream communities worldwide and unique as most red algae inhabit marine environments. Although there are freshwater representatives scattered throughout the red algal evolutionary tree, two thirds of the species are in the strictly freshwater order Batrachospermales. Recent systematics research has focused on describing species and defining monophyletic genera. These studies have revealed high statistical support for each genus but little support for how these genera are related to each other. In order to investigate important biological questions such as the evolution of morphological and reproductive characters, a robust or well-supported phylogenetic tree of the genera in the Batrachospermales is essential. Previous research has utilized a few genes to understand the evolutionary relationships at the genus and species level, but a new approach is needed to clarify the relationship among the 21 genera. Within the order, there is a well-supported clade of seven genera that have a variety of morphology and reproductive characters representative of the Batrachospermales as a whole. One species, *Volatus personatus*, has a 180,891bp plastid genome that encodes 226 protein-coding genes, 30 tRNAs, one ncRNA and one tmRNA. Using chloroplast genome data (~190 genes) from 7 species, I will construct phylogenetic trees with high statistical support for relationships among these genera. This phylogeny can serve as a framework to study the evolution of morphological and reproductive characters as well as applying this methodology to clarify the relationships among all genera in the order. These new chloroplast genomes will be useful for broader studies of both freshwater and marine species in the Rhodophyta, a lineage that has few genome data given the rich species diversity.

8. USING MORPHOMETRICS TO DISTINGUISH AMONG MORPHOLOGICALLY SIMILAR POPULATIONS OF *DIDYMOSPHENIA* FROM CONNECTICUT, U.S.A.

Diba Khan-Bureau[1, 2], Saúl Blanco[3], Eduardo A. Morales[4], Luc Ector[5], Michael S. Beauchene[6] & Louise A. Lewis[1]. (1) Department of Ecology & Evolutionary Biology, University of Connecticut, Storrs, Connecticut, 06269, U.S.A. (2) Three Rivers Community College, Norwich, Connecticut, 06360, U.S.A. (3) Departamento de Biodiversidad y Gestión Ambiental, Universidad de León, León, España; (4)Water Laboratory, University of Évora, P.I.T.E. Rua da Barba Rala No. 1, 7005–345 Évora, Portugal; (5) Luxembourg Institute of Science and Technology, Grand-duchy of Luxembourg; (6) Fisheries Division, Department of Energy and Environmental Protection, Connecticut, 06106, U.S.A.

Two morphologically similar populations of *Didymosphenia* were reported in Connecticut, U.S.A. in 2014 and 2016. One was described as a new species, *D. hullii* and the other looked similar to *D. geminata*. Given that the latter, is a worldwide nuisance stalk forming diatom, we wanted to confirm the identification. Thus, we used geometric morphometrics on field-collected samples and images of type materials from the literature to check for phenotypic differences between these two populations and morphologically similar species. Geometric morphometrics

(GM), in combination with features viewed with scanning electron and light microscopy, enhances the ability to distinguish among these morphologically similar species of *Didymosphenia*.

9. THE EFFECTS OF ULVA COMPRESSA AND EUTROPHICATION ON FUCUS.

Sara Labbe[1], Danielle Moloney[1] & Lindsay Green-Gavrielidis[1] (*President's Award*). (1) Department of Biology & Biomedical Sciences, Salve Regina University, Newport, RI 02840, U.S.A.

Rockweeds and specifically *Fucus* spp. are brown seaweeds that grow in rocky intertidal zones and have historically been prevalent in Narragansett Bay. Rockweeds form important ecosystems that provide a home to many organisms, in addition to serving as a food source. The changing ocean environment means that *Fucus* spp. in Narragansett Bay are exposed to more and more excess nutrients from anthropogenic activities, also known as eutrophication. *Ulva compressa* is a green macroalga that has become more prevalent with these excess nutrients. Previous work has shown that *Ulva compressa* produces compounds that can negatively impact the growth of other organisms, including other macroalgae. The first objective of this study was the determine if *U. compressa* inhibited *Fucus* growth in co-culture laboratory assays. We found that *U. compressa* did not significantly impact the growth of *Fucus*. The second objective was to determine if the addition of excess nutrients had any impact on the interaction between *U. compressa* and *Fucus*. There was also no significant impact of *U. compressa* on the growth of *Fucus* under eutrophication. However, we found that *Fucus* grown under eutrophication experienced a significant reduction in growth rate after 3 weeks whether it was grown alone or with *Ulva*. Our findings show that even when *Fucus* is grown with other macroalgae that are presumably taking up some or all the excess nutrients, the growth of *Fucus* was significantly negatively impacted. We also observed degradation in *Fucus* tissue quality and a change in pigmentation under eutrophication. Our results showed that *Ulva* does not impact the growth of *Fucus* with or without the presence of excess nutrients, but eutrophication results in a significant reduction of *Fucus* growth.

10. GLYPHOSATE'S EFFECT ON TOC CONCENTRATIONS IN AQUATIC HABITATS.

Hannah Laird[1], Caitlyn Montross[1] & Sarah Whorley[1]. (1) Natural Sciences, Daemen University, Amherst NY, 14226, U.S.A.

Glyphosate, found in Roundup, has shown to be effective in the management of *Phragmites australis*, an invasive wetland plant that affects biodiversity and nutrient cycling in aquatic habitats. However, the effect of glyphosate on benthic microbial assemblages has not been investigated. Microbes have an important role in the carbon cycle because they use organic carbon for metabolism; therefore, measuring the total organic carbon (TOC) in aqueous samples correlates to the nutrients available for the microbes and the overall health of the ecosystem. This study examined the effect of benthic microbes on TOC processing, with an emphasis on purple sulfur bacteria. We utilized ultraviolet-visible spectroscopy (UV-Vis) to quantify TOC levels in samples of different wetlands habitats and varying concentrations of glyphosate exposure. The quantitative results from the UV-Vis allowed us to look at trends of TOC content. Additionally, a previous study examined the effect of glyphosate on nitrate and phosphate levels in these same

habitats. Therefore, this study will allow for a comparison between TOC trends and the trends of nitrate and phosphate in a wetland environment exposed to glyphosate.

11. IDENTIFICATION AND CHARACTERIZATION OF HAB BLOOM IN ELLICOTT CREEK.

Dylan Normandin[1] & Sarah Whorley. (1) Department of Natural Sciences, Daemen University, Amherst, NY, U.S.A.

Harmful algal blooms (HAB) are characterized by a rapid increase in abundance of a singular algal species and can have important consequences for human health. The increase of climatic shift and global warming have only further exacerbated the frequencies of HAB events observed worldwide. In western New York, a suspected *Euglena* bloom has been observed in Ellicott creek since 2013. *Euglena* blooms have only been reported in Asian fish farms and not in flowing water such as Ellicott creek. Further some *Euglena* can produce euglenophycin, a toxin to fish. Identifying and understanding the factors associated with this bloom is paramount given the proximity to a local dog park where swimming occurs along with human interaction within the water such as kayaking and fishing. Thus, we conduct in-situ stream measurements for stream conditions, algal ash free dry mass, chlorophyll, identification, and cell counting. Generally, increased rainfall resulted in decreased bloom intensity but increased diversity of algal taxa present. Further, bloom intensity increased in periods of sustained high temperatures and pH. Overall, results from this study may be used as a basis for future studies on the ecological impacts of this bloom or water treatment programs.

12. OLDEST KNOWN RECORDS OF THE DIATOM GENUS *EUNOTIA* FROM THE EOCENE, INCLUDING DESCRIPTIONS OF THREE NEW SPECIES.

Erik Oddsund[1], Peter A. Siver[1] & Anne-Marie Lizarralde[1] (*President's Award*). (1) Botany Department, Connecticut College, New London, CT, 06320, U.S.A.

The oldest known records of freshwater diatoms date to the late Cretaceous, including from localities in western Canada, the Canadian Arctic, Mexico and India. The records from these Cretaceous rocks largely include centric and araphid diatoms, but lack species that bear a raphe, the structure that allows the diatom to glide across surfaces. Raphe-bearing taxa begin appearing in the fossil record by the early Eocene, with a large radiation occurring by the end of the Eocene. Members of the Eunotiaceae, of which the genus *Eunotia* is the most diverse, bear a short raphe situated on the mantle rather than the valve face as is the case for most raphid diatoms. Species in the Eunotiales are also unique among raphid diatoms because they possess a structure known as a rimoportula. Because the Eunotiales are believed to represent the earliest raphe-bearing diatoms, information on their geologic origin is central to understanding their evolutionary history. We discovered a large number of eunotioid diatoms from the Giraffe Pipe fossil locality, an extensive deposit found in an ancient freshwater lake that existed within a crater formed by kimberlite emplacement in the Canadian Arctic during the early Eocene. The waterbody existed under a Greenhouse Earth when global temperature was significantly warmer than today, and polar regions lacked a cryosphere. The deposit contains a large diversity of species in 12 m of an extensive core from the site. Collectively, the numerous specimens display many characteristics found on modern species, indicating the lineage was well formed by the early Eocene. We have begun delineating species and present descriptions of three new organisms. Given the diversity and sheer numbers of specimens, coupled with the occurrences of other microfossils, we infer that the waterbody was a shallow, acidic and humic-stained habitat.

13. REPRODUCTIVE PHENOLOGY IN A FREE-FLOATING POPULATION OF *GRACILARIA VERMICULOPHYLLA*.

Stacy A. Krueger-Hadfield[1], Lauren E. Lees[2], Alexis P. Oetterer[1], Jessica Hoffman[1], Erik E. Sotka[3] & Courtney J. Murren[3] (*Trainor Award*). (1) University of Alabama at Birmingham, Birmingham, AL, 35205, U.S.A.; (2) University of California at Irvine[3], College of Charleston, Charleston, SC, 29424, U.S.A.

The timing of recurring biological events has important consequences for ecosystem health and functioning. Phenological changes are expected due to climate change, but the evolutionary consequences of these changes are hard to forecast if we lack a description of phenological patterns. While studies have investigated the phenology of fixed populations of macroalgae, free-floating populations have received less attention. Moreover, free-floating algae are thought to be sterile. The red macroalga *Gracilaria vermiculophylla* has invaded estuaries throughout the Northern Hemisphere. While seasonal patterns of reproduction have been documented in fixed populations in Japan (i.e., native range), few studies have determined phenology in the non-native range or in free-floating populations. In these free-floating populations, thalli are overwhelmingly tetrasporophytes. We characterized reproductive state, fixation status (e.g., free-floating, fixed, or glued to *Diopatra* tubes), and biomass monthly from 2014 to 2015 at one site in Fort Johnson, South Carolina. For all vegetative thalli, we used a recently developed sex-linked marker to determine the life cycle stage. We found that this population is overwhelmingly dominated by tetrasporophytes throughout the year (81-100%), but peak reproduction was in September. We found the largest thalli in the summer and late fall. Free-floating, reproductive tetrasporophytes have the potential to release spores in habitats with hard substratum, facilitating the invasion.

14. IMPACTS OF SEA LETTUCE COMPOUNDS ON SURVIVAL AND GROWTH OF MARINE ISOPODS.

Samantha Parsons[1], Danielle Moloney[1] & Lindsay Green-Gavrielidis[1] (*President's Award*). (1) Department of Biology & Biomedical Sciences, Salve Regina University, Newport, RI 02840, U.S.A.

With the changing climate we have seen an increase in macroalgal blooms locally and globally. Macroalgal blooms occur when there is intense growth in free floating species of macroalgae that is often driven by an abundance of excess nutrients and a reduction of herbivory. Blooms have the potential to alter seawater chemistry as well as harm the communities of organisms that reside in affected waters. These blooms include *Ulva*, a green macroalgae that releases compounds that have been linked to the inhibition of other macroalgal growth, as well as mortality of larval oysters. Based on this previous evidence, we investigated the lethal and sublethal effects of compounds released from both *U. compressa* and *U. lacinulata* on *Idotea balthica*, a marine isopod. *Idotea balthica* is essential to the health of intertidal ecosystems as they are an important prey species for larger invertebrates and fishes. Using divided co-culture mesocosms *I. balthica* was observed for changes in growth and survival over the course of 4 weeks while being exposed to *Ulva* (either 3.5 g/L or 5.0 g/L) or *Gracilaria* (either 3.5 g/L or 5.0 g/L), a red macroalgae that is not known to release inhibitory compounds. Separate trials were conducted with *U. compressa* and *U. lacinulata*. *Idotea balthica* length was measured weekly via photographs and mortality was tracked daily. The standard length of male isopods in the *U. compressa* and *U. lacinulata* trials increased over time in all treatments and we detected no impact of *Ulva* on isopod growth. Additionally, we did not observe significant mortality of isopods in either trial. Our results indicate that isopods have developed a mechanism to tolerate or resist allelopathic chemicals produced and released by *Ulva.* Additional trials will investigate whether juvenile and female isopods respond differently to co-culture with *Ulva.*

15. ASSESSING THE EFFECTS OF POPULATION DENSITY AND CONCENTRATION ON THE EFFECTIVENESS OF HORMONE TREATMENT ON ALGAE CULTURES.

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Many studies have applied various auxins and analogs in order to assess their effects on the growth rates of several algae strains. Among similar strains, several studies have shown varying results while treating a culture with similar auxin concentrations. None of the studies however, state the initial population of the cultures studied. And due to the differences in optical density values caused by variations in apparatus, a population density cannot properly be assessed for reproducibility. The aim of this study is to assess the effects of an algae culture's initial population density and auxin concentration on the growth rate of treated cultures.

The data in this study is part of a long-term research project that aims to study different auxin compounds and analogs, along with different algae strains. This current study is focused on the exogenous administration of Indole-3-acetic acid (IAA) on the population growth rate of *Arthrospira platensis (Spirulina).* The project is using a novel unit of measure that aims to quantify the relationship between auxin administered, culture volume and culture population. A first round of cultures (n=50 variable n=50 control) shows an increase in population across all concentrations tested (between 1.0×10^{-4} M and 1.0×10^{-5} M) and across all populations (between 10,000 trichomes/ml and 50,000 trichomes/ml). However, the rate of increase of population tended to rise with the lowering concentration, regardless of population.

16. AMPLICON SEQUENCING TO DETECT A MICROSCOPIC LIFE CYCLE STAGE.

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Many eukaryotes, including algae, exhibit life cycles with haploid and diploid stages that can prove challenging for biodiversity, systematics, and reproductive biology studies. Freshwater red algae of the order Batrachospermales have heteromorphic diploid and haploid stages. The diploid stage, called "Chantransia", is microscopic and perennial, producing macroscopic, ephemeral haploid gametophytes through vegetative meiosis. Alternatively, Chantransia can produce asexual spores to generate new Chantransia. Systematics and biodiversity studies have focused on the macroscopic gametophytes, largely because they can easily be collected and identified. Yet, this ephemeral stage can be easily missed (i.e., sampling in the wrong season). Studying the Chantransia stage would be more informative of the presence and diversity of Batrachospermalean taxa. To survey Chantransia, we developed primers to amplify a portion of the *rbcL* gene that will differentiate among species in the Batrachospermales using Illumina sequencing. To test their utility, we used these custom primers to amplify and sequence this portion of the *rbcL* gene in gametophytes representing 15 taxa present in the eastern United States. We then collected environmental DNA (eDNA) by scraping rocks from streams and ponds. We verified the presence of Chantransia in the sample through microscopic observations, after which the eDNA was extracted, *rbc*L fragment amplified and amplicons sequenced using Illumina MiSeq. The ability to detect Chantransia of one or multiple species has implications for improved understanding of the distribution of freshwater red algae and environmental conditions under which the life cycle is completed and those where the Chantransia are recycled without gametophytes.

17. DEVELOPING *PORPHYRA UMBILICALIS* AS AN EASY-TO-USE MODEL SYSTEM.

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Developing *Porphyra umbilicalis* into a model system for wide use by scientists requires the ability to mass induce neutral spores (NS) in small blades to produce multiple, sequential generations of blades in the laboratory. Importantly, we discovered small blades (1.3 – 5.5 cm in length) producing NS on the Maine coast in autumn 2021. Each blade had four distinct regions: mature NS, differentiating sporangia, vegetative cells, and rhizoid cells. The mean lengths of each section of the blade (n=13) were 0.60 ± 0.54 (SD) mm for mature NS, 5.21 ± 2.96 mm for differentiating sporangia, 20.0 ± 12.28 mm for vegetative cells, and 3.6 ± 1.64 mm for rhizoid cells. The region with mature NS varied between 0.1 – 2.0 mm in length and was weakly correlated with blade length (R=0.34). Because young blades are producing NS at smaller sizes than previously recognized, small blades could support the establishment of *Porphyra* as a model system. Using this information, we designed an experimental system allowing us to mimic the environmental conditions during autumn (nitrate levels, temperature, photoperiod, and the length of desiccation in the tidal cycle) to attempt to induce NS in young blades in the laboratory. Miniature nori nets were seeded with spores from field-collected blades and cultivated in 6 L transparent cylinders (n=6). A stepper motor-driver shaft controlled by an Arduino is being used to lift the nets out of the seawater for the tidal desiccation cycle. Growing small blades using a simple system to change environmental parameters may make it easier to mass produce NS and blades for laboratory studies. (Supported by NSF MCB2027389 to H.Goodson, J.Kelley, S.Brawley).

18. EFFECTS OF WATER COLUMN MIXING EVENTS ON PHYTOPLANKTON COMMUNITY ASSEMBLY IN MISSISQUOI BAY, LAKE CHAMPLAIN.

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In Lake Champlain and globally, climate change has altered the seasonality of lake physical processes which has cascading impacts on lake ecosystem function. Missisquoi Bay is a small, shallow, eutrophic bay in the northeast arm of Lake Champlain that is projected to be heavily influenced by climate change (surface warming and storm events) due to its shallow depth, isolation from the main lake, and large watershed to lake area ratio. This research assesses the impact of stochastic mixing events on phytoplankton community assembly in Missisquoi Bay and identifies phytoplankton taxa and functional traits that are resilient to these events. We used high-frequency water temperature profile data to calculate Schmidt stability, and collected phytoplankton samples weekly during the ice-free season to assess community turnover in response to water column mixing events. Phytoplankton were identified to species and classified into morpho-functional groups. Preliminary results indicate that small centric diatoms and flagellates (chlorophytes and cryptophytes) dominate in Missisquoi Bay during periods of water column instability, while larger chain-forming or filamentous taxa are correlated with high Schmidt stability. Ongoing research will characterize community turnover in response to duration of stratification. This work will inform predictions of phytoplankton composition and blooms in response to disturbance in shallow lake ecosystems.

19. TAXONOMIC DIVERSITY IN THE FRESHWATER RED ALGAL ORDER BATRACHOSPERMALES (RHODOPHYTA).

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In the book, Freshwater Red Algae: Phylogeny, Taxonomy and Biogeography, we document freshwater taxa throughout the red lineage, but two thirds of the species diversity is within the order Batrachospermales. After the species-rich genus, *Batrachospermum*, was determined to be paraphyletic, researchers have circumscribed monophyletic genera using morphological and molecular tools. Although *Batrachospermum* has almost been rendered monophyletic, two species remain that cannot be placed in *Batrachospermum* sensu stricto and have been described as new monospecific genera. The first, *Notohesperus serendipidus* from Australia, has DNA sequence data showing it to be distinct. It shares the character of pedunculate carposporophytes with *Batrachospermum*, *Sheathia*, *Montagnia*, and *Visia* and loose cortication of the main axis with *Paludicola*; the combination of characters is unique to this genus. The second, *Genadendalia breutelii* from South Africa, has no sequence data but distinctive morphology, zonately septated carposporangia. New species in the genera *Lemanea*, *Paralemanea* and *Torularia* have been described and combinations were proposed in *Kumanoa* (*K. khaoluangensis*), *Paralemanea* (*P. deamii*) and *Torularia* (*T. androinvolucra*). The changes in the genera *Lemanea* and *Paralemanea* clarify taxonomy in North America. *Lemanea occidentalis* is the only species in western North America whereas *L. parva* is one of three species in eastern North America. The new species, *Paralemanea blumii* and *P. deamii* are widespread in eastern North America. *Torularia meridionalis* is a new cryptic species from Australia. These new genera, species and combinations add to the known biodiversity in the order as well as clarify the taxonomy and geographic distributions.

20. EFFECTS OF DISTURBANCE EVENTS ON CYANOBACTERIA BLOOMS IN TWO EUTROPHIC BAYS OF LAKE CHAMPLAIN.

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Missisquoi Bay and St. Albans Bay are two shallow, eutrophic bays in the northeastern arm of Lake Champlain that are known to experience yearly cyanobacterial blooms. Historically, the timing, duration and dominant species of these blooms show interannual variability. In recent years, however, they have been dominated by diverse communities of filamentous nitrogen-fixing taxa including *Dolichospermum flos-aquae* and *Aphanizomenon flos-aquae*, though this varies spatially. Integrating weekly phytoplankton samples, water chemistry, and high-frequency physical and chemical buoy data collected in from 2017-2018, we investigated the effects of disturbance events on cyanobacteria bloom phenology. We predict that cyanobacteria bloom onset, intensity, and senescence will be related to the frequency and intensity of stochastic disturbance events, such as storms and water column mixing events. We predicted that frequent, intense disturbance events in the pre-bloom stage could inhibit cyanobacteria dominance, and lack of frequent disturbance in the summer months will allow stable blooms to develop. In Missisquoi Bay in 2017, a period of stratification was correlated with a stable bloom that was resilient to a large storm event. Rather than decreasing cyanobacteria dominance in the system, the storm increased cyanobacteria abundance through the next week due to a rapid nutrient pulse to a nutrient-limited system. Additionally, it was found that rain disturbance events decreased species diversity initially, leading to dominance of specialist species, such as chain-forming diatoms and filamentous cyanobacteria. Ongoing work will elucidate these relationships in St. Albans Bay, a deeper isolated bay of Lake Champlain with a smaller watershed, and integrate subsequent sampling years (2019-20) from both bays to assess the effect of disturbance events on bloom toxicity and fluctuations in phytoplankton community composition.

21. CHARACTERIZING COMMUNITIES OF ATTACHED CYANOBACTERIA AND THEIR TOXIN PRODUCTION IN NEARSHORE ZONES OF THE FINGER LAKES, NEW YORK.

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Attached and benthic cyanobacteria are far less studied in lakes than their planktonic counterparts, and littoral zones are highly productive yet understudied areas making them important to focus harmful algal bloom (HAB) monitoring efforts. Most of our knowledge of attached and benthic cyanobacteria comes from lotic studies done in New Zealand, Australia, and Europe, but taxonomy and toxin production can vary by geographic location. Very little has been published on these types of cyanobacteria in the United States, especially outside the Laurentian Great Lakes. The Finger Lakes are an ideal location for this work as they range in trophic status, size, and depth, and all eleven Finger Lakes have experienced planktonic HABs in recent years. This work aims to characterize attached cyanobacteria communities in the

nearshore zones of three Finger Lakes through the following studies: 1) develop standard sampling and monitoring methods through the use of artificial substrates and a handheld portable fluorometric tool, the BenthoTorch (bbe Moldaenke), 2) identify explanatory variables of growth and toxin production both spatially and temporally among lakes using measurements of nutrients, pigments, light, and temperature, and 3) develop toxin-taxa relationships and characterize the microbial community with which they interact. The proposed work is primarily focused on attached cyanobacteria with the intention of using sampling and monitoring methods that are accessible and feasible for a wide range of expertise. True benthos samples will also be collected to determine whether artificial substrates deployed in this way are representative of benthic cyanobacteria. This work will inform our understanding of the ecology and toxin production of attached and benthic cyanobacteria in the northeastern United States.

22. METHOD PROPOSAL FOR MOLECULAR IDENTIFICATION OF DIATOMS IN THE COLORADO RIVER BELOW GLEN CANYON DAM.

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Prior research in the Colorado R. below the Glen Canyon Dam in the 1980's and 1990's demonstrated that diatom communities were significantly altered by water release patterns (Hardwick et al., 1992; Blinn et al., 1998; Kegerries et al., 2020). Current data from our laboratory from 2020-2021 indicate that diatom communities have changed further in recent years, likely in response to climate and other environmental changes. I am now building a database to track seasonal diatom communities in real time, through the use of metabarcoding analyses. My aims are to improve monitoring of riverine biodiversity and to detect cryptic and rare species often missed by traditional methods. I have begun the process of designing primers and piloting eDNA extraction and amplification protocols. DNA extraction methods and amplification protocols in the literature vary greatly depending on the sampling method and specific questions of the project. Thoroughly testing these protocols and understanding the limitations of molecular data is a key step towards ensuring that the results of a molecular monitoring effort can be aligned with traditional morphologic taxonomy. I plan to first verify that the method for DNA extraction results in the equal elution of DNA for all species based on starting material. To accomplish this, I will use preparations of artificial communities of diatoms extracted from cultures to generate populations that can be mixed in know concentrations prior to extraction. I plan to test 4 sets of primers, two sets will target the rubisco chloroplast gene, and the other two will target the v4 region of the 18s ribosomal DNA. For each region I will compare established primers against primers have designed to specifically target the most abundant species in the Colorado River.

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