62nd Northeast Algal Symposium, April 5–7, 2024

NEAS

Middletown, RI

• 2024 •

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62nd Northeast Algal Symposium
April 5–7, 2024
Newport Wyndham Hotel, Middletown, RI

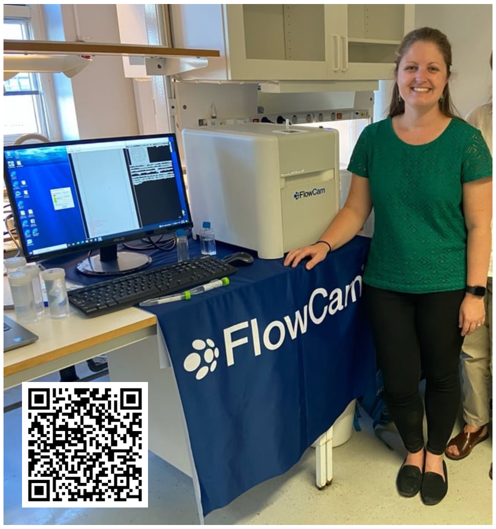
We are pleased to welcome you to the 62nd Annual Northeast Algal Symposium, in Middletown, RI. This year's meeting kicks off with several events that you won't want to miss, so arrive early and stay late because it's phycology without apology and we've got an outstanding line up of talks, posters, a keynote panel featuring Deepwater Phycology, and artists and vendors ready to update your walls, bookshelves and laboratories! We can't wait to see you at several pre-symposium activities on Friday, April 5th that will prime a weekend of rich phycological whimsy:

1. From 5:00 – 8:00 PM, visit Saltwater Studio featuring fabulous phycological works by local artist (and NEAS Vendor), Mary Jameson Chatowsky. Mary's art explores the environment by utilizing seaweed and organic materials collected along New England's coasts. One of her pieces, Sakonnet Tide Pool, was featured in the New Bedford Whaling Museum's 2023 exhibit, A Singularly Marine and Fabulous Produce: The Cultures of Seaweed. Her studio, Saltwater Studio Newport, is located at the corner of [Vernon Avenue and Freeborn Street]() in Newport, just 1.8 miles from the Wyndham. It is directly across from the public tennis courts on Freeborn St. and there is plenty of free parking! Mary's website is: https://saltwaterstudionewport.com/.

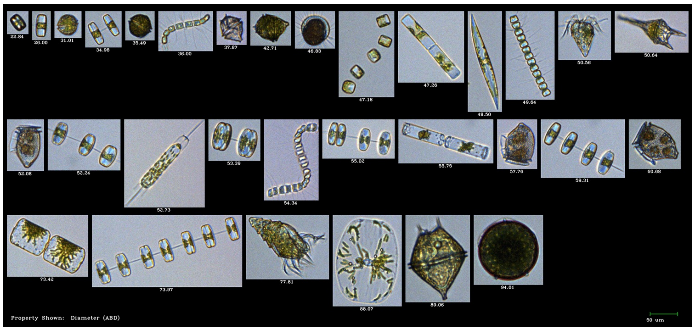
Open Studio:
Friday, 5:00 – 8:00 PM
Sunday, 2:00 – 4:00 PM

saltwater studio™
newport
ART & DESIGN

2. **From 5:30 – 6:30 PM**, NEAS Vendor and Yokagawa Fluid Imaging Microscopy representative, Savannah Judge, will lead a workshop on Flow Microscopy. The purpose of this workshop is to gain a deeper understanding of flow imaging microscopy using FlowCam as a case study. Savannah will provide a 15-minute technology overview, followed by 45 minutes of live FlowCam training. Participants are invited to bring a sample of their own to use during the workshop. Please SIGN UP for the workshop ahead of time, but feel-free to drop-in too. You can indicate your interest in bringing your own sample on the registration form. The workshop will be held in the Mariner Room, adjacent to Johnny's Restaurant.



FlowCam®
Yokogawa Fluid Imaging Technologies, Inc.



Workshop: Friday, 5:30 – 6:30 (Scan QR Code to Register)

3. **From 5:00 – 7:00 PM,** pick up your registration materials and join the NEAS opening reception/social; catch up with old and new friends alike in the reception area at Johnny's Restaurant in the Wyndham Newport Hotel. You can easily drop-in on the FlowCam workshop from the reception.

4. **7:00 PM - ???** Continue to enjoy your time at the Wyndham or experience Newport, RI on your own. Downtown Newport is a short 2.5 mile ride or walk from the Hotel, past famous Easton's Beach (aka: First Beach) and the entrance to the Cliff Walk (1.4 miles away). Restaurants abound along Thames Street and Bowen's Wharf in downtown Newport. If you're looking for something a little closer, may we suggest Diego's Barrio Cantina and Rejects Beer Co., just 0.4 miles from the Wyndham.

5. If you are a runner or walker, it's hard to beat RI's "Phyko-5ks" along First Beach, Second Beach, the Cliff Walk or Sachuest Point National Wildlife Refuge. See Brian Wysor for more details.

Sponsors

This year's meeting and the Deepwater Phycology panel in particular were made possible with the generous support of several organizations, including Rhode Island IDeA Network of Biomedical Research Excellence (RI-INBRE), Connecticut Sea Grant, "FlowCam" by Yokogawa Fluid Imaging Technologies, Rhode Island EPSCoR. Rhode Island Sea Grant, Salve Regina University Office of the Undergraduate Dean, the Dean's office of the School of Social & Natural Sciences at Roger Williams University, and the Narragansett Bay Estuary Program.

NARRAGANSETT BAY
ESTUARY PROGRAM

RHODE ISLAND
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Sea Grant
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RI
C-AIM

Sea Grant
RHODE ISLAND

S R

Roger Williams
University

Land Acknowledgement

Our meeting space sits on the traditional, ancestral, unceded lands of the Pauquunaukit Wampanoag Nation and Mashpee Wampanoag (Wôpanâak) Tribes. It is important for us to acknowledge the history of this space and to acknowledge that although much of the science we will learn about this weekend has a Western focus, there are other ways of knowing and doing science and these are equally important to our field.

Acknowledgements

Many thanks to our judges: Wilce Graduate Oral Presentation Award (Thea Popolizio, Eric Salomaki, Sarah Princiotti & Stacy Krueger-Hadfield), the President's Undergraduate Oral Presentation and Trainor Graduate Poster Award (Diba Khan-Bureau, Dominique Derminio & Hilary McManus), and the President's Undergraduate Poster Award (Brian Teasdale, Heather Spalding, Dion Durnford & Eric Roberts). Many thanks to all who volunteered to judge award presentations!

We also appreciate our session moderators: Karolina Fučíková, Jessica Muhlin & John Wehr, and of course, our well-seasoned auctioneer, Craig Schneider. We are grateful to Nick Bezio for designing our 2024 Deepwater Phycology meeting logo seen on the cover and on NEAS merchandise (see p. 7). We are grateful to our distinguished guests and hope you enjoy the impressive line-up of Deepwater Phycologists, in addition to the many fantastic presentations on our program by students young and old – it should be an exciting meeting!

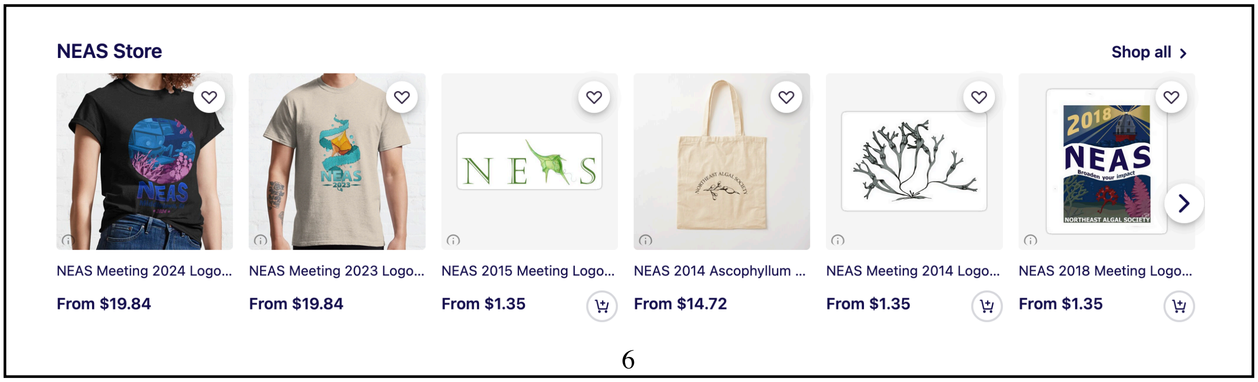
We would also like to thank the following Vendors who support NEAS through auction donations and excellent deals on professional and personal phycology décor and books.

1. Scott Balogh, Balogh International Books
2. Mary Jameson Chatowksy, Saltwater Studio
3. Savannah Judge: FlowCAm, Yokogawa Fluid Imaging Technologies
4. Jordan Chalfant, Maine Natural History Observatory

Finally, we thank the NEAS membership and all the annual symposium participants and guests, whose ideas, fellowship and camaraderie make the Northeast Algal Society and this annual symposium an event to which we all look forward each year.

Your friendly symposium conveners,
Lindsay, Brian & Craig

PS Don't forget: You can get various conference-themed merchandise in the **Northeast Algae Red Bubble** store: https://www.redbubble.com/people/northeastalgae/shop.



Nicholas Bezio, illustrator and marine biologist, designed the meeting logo this year as he has for several of our annual meetings, *e.g.*, 2017, 2018, 2021–2023. Bezio specializes in colored pencil illustrations and wildlife photography, and creates works of art that accurately reflect the behavior, ecology and biodiversity of some of Earth's most beautiful yet strange organisms. His illustrations resonate with an old world feel that evokes the excitement of discovery that early field biologists must have felt when they explored the "new world" for the first time. Unsurprisingly, Bezio derives inspiration from the likes of Ernst Haeckel, a well-known marine scientist and master illustrator famous for some of his stunning drawings featured in ***Kunstformen der Natur*** (known in English as ***Art Forms in Nature***). To see more of Bezio's exceptional drawings and photographs, visit him online at http://www.nickbezio.com/.

Virtual Attendance Directions

Available times, all EST:
Saturday, 8:20 AM-Noon, 1:00–3:30 PM
Sunday, 8:25 –9:45 AM

Join Zoom Meeting
https://salve-edu.zoom.us/j/5657150111?pwd=JC3aChwM39QMPvH6Mw0LxK1AjjIAwE.1

Meeting ID: 565 715 0111
Passcode: NorthAlgae

You can get various conference-themed merchandise in the **Northeast Algae Red Bubble** store: https://www.redbubble.com/people/northeastalgae/shop.

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.

Keynote Panel on Deepwater Phycology

We are really excited to host an in-person keynote panel of phycologists who will speak to their experiences in Deepwater Phycology. Our esteemed guests will share some of their research exploring deep water habitats using submersibles, technical diving and traditional dredging in the western Atlantic, Gulf of Mexico and central Pacific. The 'afterparty' will feature a facilitated panel discussion that we're calling Salty Talk and this will be your chance to ask our speakers about the sordid, scary, mundane and delightful details of deepwater research that won't make it to publication. You can ask your questions in-person or submit them ahead of time (anonymously) using this form. Our featured panel includes: Suzanne Fredericq, Wilson Freshwater, NEAS' very own Craig Schneider and Heather Spalding.

Suzanne Fredericq, Ph.D.

Freeport McMoran & Board of Regents Professor for Coastal Biodiversity Research
Department of Biology, University of Louisiana – Lafayette

Dr. Suzanne Fredericq became interested in seaweeds via the study of marine nematode worms that were always found living around some macroalgae in her native Belgium. She wanted to learn more about the algae to have a better understanding of the worms. During a vacation trip to the Museum of Natural History in Washington D.C. shortly after her zoology studies at the University of Ghent, she spent time in the NMNH Algal Herbarium, Smithsonian Institution, fell in love with the seaweeds from around the world, didn't return home, and hasn't looked at a nematode since. After a M.S. at George Mason University with the research done under the direction of Dr. James Norris at the Smithsonian, she then pursued her Ph.D. with Dr. Max Hommersand at the University of North Carolina at Chapel Hill. After several postdoctoral appointments back to the Smithsonian, UNC-CH, Duke University, Smithsonian again, she accepted her current position at the University of Louisiana at Lafayette due to University's proximity to the wonderful mesophotic habitats of the northwestern Gulf of Mexico. She is currently a Professor of Biology at UL Lafayette.

Suzanne's Deepwater Phycology presentation is entitled, "Rhodoliths and their importance for macroalgal ecology and biodiversity in the NW Gulf of Mexico."

D. Wilson Freshwater, Ph.D.

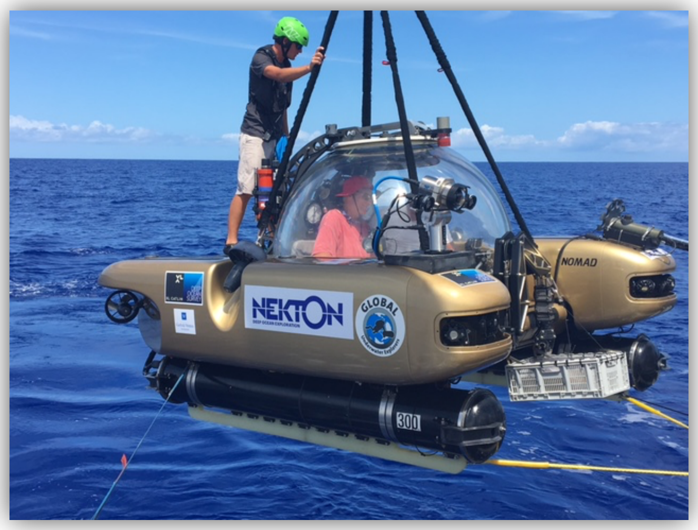
Research Specialist & Core Leader
Center for Marine Science, University of North Carolina - Wilmington

Dr. D. Wilson Freshwater's love affair with the ocean began while growing up in the waters of Carteret County, North Carolina. Initially influenced by his parents' boating and a fifth birthday present of swim fins from Captain Jim Willis, he attended the University of North Carolina Wilmington and began studying marine algae with Donald "Fritz" Kapraun. After graduation he alternated between working as a research technician and pursuing graduate studies under Earnest Seneca (M.S. North Carolina State University) and Max Hommersand (Ph.D. University of North Carolina Chapel Hill), before doing post-docs with Pat Walsh (University of Miami) and Kimon Bird (University of North Carolina Wilmington). Dr. Freshwater joined the Center for Marine Science as a Research Specialist in 1994 and has supervised the Center's DNA Analysis Facility since 2000.

Wilson’s Deepwater Phycology presentation is entitled, “Fumbling towards the ecstasy of the deep: how mistakes lead to a search for understanding community dynamics in a marine transition zone.”

Craig Schneider, Ph.D.

Charles A. Dana Professor of Biology, Emeritus
Trinity College, Hartford



Dr. Craig W. Schneider knew as an undergraduate at Gettysburg College what he wanted to do, study marine algae and teach at a small liberal arts college. He joined Rick Searles’ lab at Duke University where he did a comprehensive study of the deep offshore flora of the Carolinas from Cape Hatteras to Cape Romain. After completing his Ph.D., he moved on to Trinity College, Hartford, where he taught for 45 years and began his study of the Bermuda marine flora, collecting deep samples using surface-supplied air. In 2016, Dr. Schneider and his one and only graduate student, Thea Popolizio of URI, joined the scientific crew of the *Baseline Explorer* where he gathered mesophotic specimens collected using technical divers and submersibles, many of the species representing the first records of the genus in the Atlantic Ocean. After retiring in 2020, he moved his lab home and continues his phylogenetic work with a very short commute.

Craig's Deepwater Phycology presentation is entitled, "Just when you think there's no light and you turn on the floodlights – spectacular macroalgae!"

Heather Spalding, Ph.D.

Associate Professor
Department of Biology, College of Charleston

Dr. Heather Spalding grew up on a small cattle farm in Kentucky but was often found underwater in the murky depths of the farm pond exploring the mud and "moss". She received her undergraduate degree in marine science from Southampton College at Long Island University under the tutelage of Dr. Larry Liddle. This led to an internship on kelp forest ecology at Moss Landing Marine Labs (MLML) with Dr. Mike Foster, where she discovered that being comfortable underwater in low light was a useful skill for a phycologist. After completing her master's degree in marine science at MLML, she was lured to the University of Hawaiʻi to study mesophotic macroalgae with Dr. Isabella Abbott and Dr. Celia Smith. The algae occurred a bit deeper in those clear tropical waters, so she learned how to use technical diving, rebreathers, and submersibles to study mesophotic coral ecosystems in the Hawaiian Archipelago. After several years of post-doctoral fellowships at the University of Hawaiʻi at Mānoa and the Papahānaumokuākea Marine National Monument on algal biodiversity and ecophysiology, Dr. Spalding accepted a position at the College of Charleston in 2019, where the water is still murky but the algae are spectacular.

Heather's Deepwater Phycology presentation will feature "Mesophotic algae in paradise: the interplay of nutrients and light in structuring mesophotic macroalgae in the Hawaiian Archipelago".

NEAS Executive Committee

President: Brian Wysor (2024 – 2026)

Past President: Hilary McManus (2021 – 2024)

Treasurer: Lindsay A. Green-Gavrielidis (2023 – 2027)

Secretary: Sarah Princiotta (2022 – 2026)

Membership Director: Brian Wysor (2022 – 2026)

Nominations: Chris Lane (2022 – 2023)

Members at Large: Ken Karol (2023 – 2025), Anne Lizarralde (2022 – 2024)

Colt Development Committee: Amanda Savoie (chair, 2021 – date), Greg Boyer, Craig Schneider, John Wehr

Publications Committee: vacant

Website: Chris Neefus

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

2024 Convenors: Brian Wysor, Lindsay A. Green-Gavrielidis, Craig Schneider

2025 Convenors: vacant

Candidates for NEAS Executive Committee

We will hold an election during the meeting for certain positions. You can read more about each position in the NEAS Officers Manual: https://northeastalgae.org/organization_docs/NEASofficersmanual.Feb2011.pdf

Program Overview

Friday. April 5

Time	Event	Location
5:00–7:00 PM	Registration & Auction Donations Friday night social	Hallway outside Atlantic Pavilion Johnny’s Restaurant
5:30–6:30 PM 5:00–8:00 PM	FlowCam Workshop Open Studio	Mariner Room Saltwater Studio (15 Vernon Ave Suite 4, Newport)

Saturday, April 6

Time	Event	Location
7:00–8:20 AM	Breakfast & Poster Set-Up & Auction Donations	Atlantic Pavilion
Continental breakfast and coffee will be available		
8:00–10:00 AM	Registration & Auction Donations	Hallway outside Atlantic Pavilion
8:20–8:30 AM	Presentation Upload Welcoming Remarks	Atlantic Pavilion Atlantic Pavilion
8:30–10:00 AM 10:00–10:30 AM 10:30–12:00 PM	Student Award Talks 1 Break Student Award Talks 2	Atlantic Pavilion Atlantic Pavilion Atlantic Pavilion
12:00–1:00 PM	Lunch, EC meeting A buffet will be available	Atlantic Pavilion, Mariner Room (EC)
1:00–3:30 PM	Special Symposium: Deepwater Phycology	Atlantic Pavilion
3:30–3:45 PM 3:45–5:45 PM	Break Poster Session I	Atlantic Pavilion Atlantic Pavilion
7:00–10:00 PM	NEAS Annual Banquet & Student Benefit Auction A buffet meal with begin being served at 7:00 PM. There will be a cash bar available.	Atlantic Pavilion

Sunday, April 7

Time	Event	Location
7:00–8:20 AM	Breakfast & Poster Set-Up	Atlantic Pavilion
	Continental breakfast and coffee will be available	
8:00–10:00 AM	Registration	Hallway outside Atlantic Pavilion
8:25–8:30 AM	Presentation Upload Morning Announcements	Atlantic Pavilion Atlantic Pavilion
8:30–9:45 AM 9:45–10:00 AM 10:00–10:30 AM 10:30 AM–12:00 PM	Contributed Talks 1 Break Lightning Talks Contributed Posters	Atlantic Pavilion Atlantic Pavilion Atlantic Pavilion Atlantic Pavilion
12:00–1:00 PM	Business Meeting	Atlantic Pavilion
	Boxed lunches will be available	Atlantic Pavilion

Departure: See you all next year!

If you’re hanging around Newport for a while, stop by Saltwater Studios (15 Vernon Avenue Suite 4, Newport) between 2:00–4:00 PM to enjoy more seaweed art!

General Program: 62nd Northeast Algal Symposium, Middletown, Rhode Island

Friday, April 5, 2024

5:00 – 7:00 PM	***Evening Registration & Friday Night Social*** **Johnny's Lounge, Wyndham Hotel**
5:30 – 6:30 PM	***FlowCam Demonstration*** Mariner Room, Wyndham Hotel

Saturday, April 6, 2024

7:00 – 8:20 AM	***Breakfast & Poster Set-up*** Atlantic Pavilion *Poster setup for Student Awards Competition, Atlantic Pavilion* *Session I speakers load ppts, Atlantic Pavilion*
8:00 – 10:00	***Morning Registration*** Hallway outside the Atlantic Pavilion, Wyndham Hotel
8:20 – 8:30	***Welcome and Opening Remarks*** **Lindsay Green-Gavrielidis, Brian Wysor** Atlantic Pavilion, Wyndham Hotel
SESSION I	***Student Award Talks 1*** **– Moderator, Karolina Fučíková**
8:30 – 8:45	*President's Award Candidate* Characterizing the probiotic potential of *Pseudoalteromonas rubra* for the local coral *Astrangia poculata*. **Casidhe Hughes**, Megan Harrington, Sam Ruemmler, Alicia Schickle & Koty Sharp. (Abstract 1, p. 20)
8:45 – 9:00	*President's Award Candidate* Establishing a molecular-informed species inventory of filamentous red algae (order: Ceramiales) in the Narragansett Bay Area. **Thomas Irvine** & Brian Wysor. (Abstract 2, p. 20)
9:00 – 9:15	*President's Award Candidate* Annual spatial and temporal dynamics of *Margalefidinium polykrikoides* in Rhode Island. **Alison J. Whitney**, Abigail K. Scro, Susanna L.H. Osinski, Kristen A. Savastano, Galit Sharon, Timothy F. Scott & Roxanna M. Smolowitz. (Abstract 3, p. 21)
9:15 – 9:30	*Wilce Award Candidate* Two for the price of one: using lichen metagenomic libraries for dual symbiont target capture. **Zachary M. Muscavitch**, Bernard Goffinet & Louise A. Lewis. (Abstract 4, p. 21)
9:30 – 9:45	*Wilce Award Candidate* Heterogeneity of *Chlamydomonas reinhardtii* batch cultures. **Gaganpreet Gill** & Dion G. Durnford. (Abstract 5, p. 22)

9:45 – 10:00	*Wilce Award Candidate* Phylogeographic structure of *Batrachospermum gelatinosum* in the eastern United States. **Roseanna Crowell**, Sarah Shainker-Connelly, Stacy Krueger-Hadfield & Morgan Vis. (Abstract 6, p. 22)
10:00 – 10:30	***Coffee Break*** Atlantic Pavilion *Session II speakers load presentations, Atlantic Pavilion*
SESSION II	***Student Award Talks 2*** **– Moderator, Jessica Muhlin** Atlantic Pavilion
10:30– 10:45	*Wilce Award Candidate* Diversification of New England's macroalgae industry: nursery techniques for *Wildemania amplissima.* **Riplee Mercer** & Christopher Neefus. (Abstract 7, p. 23)
10:45 – 11:00	*Wilce Award Candidate* Mock trial: analyzing the use of mock communities to aid in interpretation and intercomparison of DNA metabarcoding studies. **Fran Webber**, Diana Fontaine, Erin Jones & Tatiana Rynearson. (Abstract 8, p. 23)
11:00 – 11:15	*Wilce Award Candidate* DNA barcoding reveals cryptic diversity within the family Galaxauraceae (Nemaliales, Rhodophyta) in eastern Australia. **Margaret M. Cassidy** & Gary W. Saunders. (Abstract 9, p. 24)
11:15 – 11:30	*Wilce Award Candidate* Ecological storytelling with ArcGIS StoryMap: an application focusing on seaweed ecosystem engineers in Narragansett Bay. **R. Venezia**, C. Thornber, G. Pantoni, L. Green-Gavrielidis, N. Hobbs, G. Cicchetti & D. Taylor. (Abstract 10, p. 24)
11:30 – 11:45	*Wilce Award Candidate* Understanding the cellular and molecular changes of *Choreocolax polysiphoniae* and *Vertebrata lanosa* in response to infection**. Gabrielle M. Kuba**, Jillian M. Freese & Christopher E. Lane. (Abstract 11, p. 24)
11:45 – 12:00	*Wilce Award Candidate* Determinants of longevity in *Chlamydomonas reinhardtii.* **Navpreet Kaur**, Ghaith Zamzam & Dion G. Durnford. (Abstract 12, p. 25)
12:00 – 1:00 PM	***Lunch*** Atlantic Pavilion ***Executive Committee Meeting/Lunch*** Mariner Room *Session III speakers load ppts*
SESSION III	***Special Symposium: Deepwater Phycology*** Atlantic Pavilion
1:00 – 1:10	***Introduction*** **– Moderator, Brian Wysor**

1:10 – 1:35	Rhodoliths and their importance for macroalgal ecology and biodiversity in the NW Gulf of Mexico. **Suzanne Fredericq**, Sherry Krayesky-Self, Thomas Sauvage, Joe Richards, Ronald Kittle, C. Frederico Gurgel, Daniela Gabriel & William E. Schmidt. (Abstract 13, p. 25)
1:35 – 2:00	Fumbling towards the ecstasy of the deep: how mistakes lead to a search for understanding community dynamics in a marine transition zone. **Wilson Freshwater**. (Abstract 14, p. 26)
2:00 – 2:25	Mesophotic algae in paradise: The interplay of nutrients and light in structuring mesophotic macroalgae in the Hawaiian Archipelago. **Heather Spalding**. (Abstract 15, p. 26)
2:25 – 2:50	Just when you think there's no light and you turn on the floodlights – spectacular macroalgae! **Craig Schneider**. (Abstract 16, p. 27)
2:50 – 3:30	**Salty talk panel discussion**
3:30 – 3:45	***Coffee Break*** Atlantic Pavilion
SESSION IV	***Poster Session for Student Awards Competition*** Atlantic Pavilion
3:45 – 5:45	**Poster Session I**
7:00 – 10:00	***Social & Banquet, Awards, Silent & Live Auctions*** Atlantic Pavilion

Sunday, April 7, 2024

7:00 – 8:20 AM	***Breakfast*** Atlantic Pavilion *Session V speakers load ppts* *Poster setup for contributed poster, Atlantic Pavilion*
8:25 – 8:30	**Morning Announcements – Brian Wysor**
SESSION V	***Contributed Papers* – Moderator, John Wehr** Atlantic Pavilion
8:30 – 8:45	Lake mesocosms showing nitrogen as a driver of cyanobacterial bloom development and species composition. **Michael E. Kausch** & John D. Wehr. (Abstract 17, p. 27)
8:45 – 9:00	Iron wars over ligand soup: exploring chemical crosstalk in Symbiodiniaceae – bacteria interactions. **Hannah G. Reich**, MacNeill C. Matthews, Nicole R. Cunningham, Corinne Richard, Cassidy Stadtfeld, Hayden R. Wink, The Students of Siderophore SuperLab, The TAs of Siderophore SuperLab, Kristen E. Whalen & Elizabeth L. Harvey. (Abstract 18, p. 27)

9:00 – 9:15	Tracing the inheritance of bacterial endosymbionts among *Nephromyces* species, using epicPCR. **Marissa Mehlrose** & Christopher E. Lane. (Abstract 19, p. 28)
9:15 – 9:30	Multiple plastid losses within photosynthetic stramenopiles revealed by comprehensive phylogenomics. **Kristina X. Terpis**, Eric D. Salomaki, Dovilė Barcytė, Tomáš Pánek, Heroen Verbruggen, Martin Kolisko, J. Craig Bailey, Marek Eliáš & Christopher E. Lane. (Abstract 20, p. 28)
9:30 – 9:45	Losing histone H1: a critical element in dinoflagellate nuclear drama. **Senjie Lin**. (Abstract 21, p. 29)
9:45 – 10:00	***Coffee Break*** Atlantic Pavilion *Session VI lightening talk load ppts*
SESSION VI	***Contributed Posters & Business Meeting*** Atlantic Pavilion
10:00 – 10:30	Lightening talks
10:30 – 12:00	**Poster session II**
11:00 AM	***Room checkout***
12:00 – 1:00	***Annual NEAS Business Meeting*** **– Brian Wysor, President** Atlantic Pavilion *Boxed-lunches available for the business meeting*

Poster Presentations

President's Award Posters

P1 – Utilizing qPCR to investigate cyanobacteria – viral interactions.
Ava E. Devine, Lily M. Winsten, Michael G. Briggs & Marcia F. Marston. (Abstr. p. 29)

P4 – Investigation into the patchy dispersal of *Choreocolax polysiphoniae* populations.
Emily M. Molino, Gabrielle M. Kuba, Eric D. Salomaki & Christopher E. Lane. (Abstr. p. 31)

P6 – Using stable isotopes to infer interactions between the common intertidal macroalgae *Chondrus crispus* and *Fucus* spp., and an herbivorous snail, *Lacuna vincta***.** **Luke Jensen**, N. Hobbs, A. Oczkowski & C. Thornber. (Abstr. p. 31)

P8 – River macrophytes harbor different epiphytic diatom associations. **Maisie Grogan**, John Wehr, Mia Wrey & Lawrence Stevens. (Abstr. p. 32)

P9 – Invertebrate grazing effects on diatom ecological guilds and species composition. **Olivia Clausen**, Hayden Wilke, John Wehr, Mia Wrey & Lawerence Stevens. (Abstr. p. 33)

P11 – Desmid communities and environmental conditions in selected vermont wetlands.
William Roberts & Karolina Fučíková & Michael Norcia. (Abstr. p. 34)

P13 – Characteristics of Trebouxiophyte organellar genomes. **Colin Brewer** & Karolina Fučíková. (Abstr. p. 34)

P15 – Biodiversity conservation in the face of climate change: fucoid macroalgae dynamics on the Boston Harbor Islands. **Angel Checo Reynoso**, Alysha B. Putnam, Paulette Peckol & Michelle Staudinger. (Abstr. p. 35)

P17 – Molecular characterization of *Bryopsis* species richness from Rhode Island to Panama. **Abigail St. Jean** & Brian Wysor. (Abstr. p. 36)

P19 – Developing a scaled-down assay to screen *Ulva* bloom water for toxicity in real time. **Kaylee Collins**, Danielle Moloney, Ashley Caputo, Sarah Holcomb & Lindsay Green-Gavrielidis. (Abstr. p. 37)

P21 – A laboratory assay for detecting green tide toxicity. **Isabella Ares**, Danielle Moloney, Samantha Parsons & Lindsay Green-Gavrielidis. (Abstr. p. 38)

P23 – The relationship between cell count and optical density in phytoplankton. **Megan Curran**, Kaylee Collins, Isabella Ares & Lindsay Green-Gavrielidis. (Abstr. p. 39)

P25 – Cyanopodoviruses infecting clade I *Synechococcus* spp. possess unique gene sequences. **Michaela L. Johnson**, Michael G. Briggs & Marcia F. Marston. (Abstr. p. 39)

Trainor Award Posters

P18 – The contribution of small eukaryotes to nitrate-based new production in the North Pacific Subtropical Gyre. **Catherine A. Crowley**, Brandon Brenes, Angelicque E. White, Raquel F. Flynn, Adrian Marchetti & Julie Granger. (Abstr. p. 37)

P20 – Siderophore utilization by dinoflagellates as a strategy for iron acquisition. **Sydney McDonald**, Felipe Porto, Xiaoyu Wang, Senjie Lin & Julie Granger. (Abstr. p. 37)

Contributed Posters

P2 – Quantifying coralline algal diversity and assessing its role in community structure in the Gulf of Maine. **Curtis R. Morris** & Jarrett E.K. Byrnes. (Abstr. p. 30)

P3 – A comparative examination of dominant canopy forming macroalgae in southern New England. **Kaleb Boudreaux**. (Abstr. p. 30)

P5 – Selfish elements as a tool for illuminating genetic exchange pathways between green algal chloroplast genomes. **Danielle Arsenault**, J. Peter Gogarten & Louise A. Lewis (Abstr. p. 31)

P7 – Rosette cellulose synthesis complex in *Coleochaete*. **Eric Roberts** & Alison W. Roberts. (Abstr. p. 32)

P10 – Lethal and sublethal impacts of *Ulva* on marine invertebrates. **Danielle Moloney**, Samantha Parsons & Lindsay Green-Gavrielidis. (Abstr. p. 33)

P12 – Placing *Euastropsis* (Sphaeropleales, Chlorophyceae). **Hilary A. McManus**, K.G. Karol & J. Lenarczyk. (Abstr. p. 34)

P14 – Temperature and density effects on interactions between native and introduced macroalgae. Leah Harries, Alysha B. Putnam & **Paulette Peckol**. (Abstr. p. 35)

P16 – Can we find common denominators in freshwater benthic cyanotoxin production? **A.M. Webster**, L.B. Cleckner, G.L. Boyer & N.R. Razavi. (Abstr. p. 36)

P22 – Closely related *Synechococcus* strains from Narragansett Bay, Rhode Island exhibit differences in viral susceptibility. **Michael G. Briggs**, Cammi Mackenzie, Nathan A. Ahlgren & Marcia F. Marston. (Abstr. p. 38)

P24 – Cost effective methods for analyzing nitrate and phosphate in lake samples. **Alana Modugno** & Dominique S. Derminio. (Abstr. p. 39)

P26 – An evaluation of planar waveguide biosensor for detection of cyanotoxins in freshwater systems. **Sydney Hall** & Gregory L. Boyer. (Abstr. p. 40)

ABSTRACTS

Oral Presentation Abstracts

1 – Characterizing the Probiotic Potential of *Pseudoalteromonas rubra* for the Local Coral *Astrangia poculata*. **Casidhe Hughes**, Megan Harrington, Sam Ruemmler, Alicia Schickle & Koty Sharp. Department of Biology, Marine Biology and Environmental Science, Roger Williams University, Bristol, RI 02809, USA. **(President's Award candidate)**

Coral microbiomes play a significant role in coral survival and fitness. *Pseudoalteromonas* is a bacterial genus associated with tropical reefs, and many species are hypothesized to produce protective antimicrobial compounds for their coral host. *Pseudoalteromonas rubra* strains KB1 and CH007, isolated from the RWU Wet Lab temperate coral *Astrangia poculata* systems, both inhibit the growth of the deadly coral and shellfish pathogen, *Vibrio coralliilyticus*. This study located the origin of *P. rubra* in the laboratory and surveyed for it in the wild, via sequence-specific PCR surveys in the RWU Wet Lab and in local coastal habitats. PCR surveys demonstrate that *P. rubra* is likely associated with the surface of CCA in the Wet Lab, but it was not detectable in *A. poculata* itself, or in any of the sampled wild specimens. In an exposure assay, high concentrations (10^8 cells/ml) of *P. rubra* were not lethal to *A. poculata.* High-throughput 16S rRNA amplicon sequence analysis (via QIIME) of the seawater and *A. poculata* mucus microbiomes during the exposures revealed distinct *P. rubra*-induced shifts in microbiome composition. Characterization of these microbiome shifts will lay the groundwork for developing *P. rubra* as a probiotic treatment and understanding microbial mechanisms for coral benefits.

2 – Establishing a Molecular-Informed Species Inventory of Filamentous Red Algae (Order: Ceramiales) in the Narragansett Bay Area. **Thomas Irvine** & Brian Wysor. Department of Biology, Marine Biology and Environmental Science, Roger Williams University, Bristol, RI 02809, USA. **(President's Award candidate)**

The Narragansett Bay Area (NBA) is an estuarine system that harbors a diverse marine flora that provide structure, habitat, and food for native biodiversity. This area has been the center of numerous environmental, biological, ecological, and oceanographic studies, however marine macroalgae have not been thoroughly examined through the lens of molecular work here. As a result of decades of anthropogenic disturbances including climate change, pollution, coastal development, and the introduction of alien and invasive species, the marine flora in the NBA is changing. However, visually monitoring for changes in species composition of RI macroalgae is difficult because many species closely resemble each other. Utilizing two chloroplast-encoded genes, the 3' end of the RuBisCo large subunit (*rbc*L-3P) and the universal plastid amplicon (UPA), red algae of the order Ceramiales were barcoded. Thirty-seven distinct species of this order were identified and validated with molecular data, including five new species reports and at least one new report of an alien species in the NBA. Novel sequence data were generated for numerous species and it was determined that the UPA marker, which has not been extensively used in red algal floristics, is just as effective as the traditionally used *rbc*L-3P marker at differentiating between red algae species of the order Ceramiales.

3 – Annual Spatial and Temporal Dynamics of *Margalefidinium polykrikoides* in Rhode Island. **Alison J. Whitney**[1], Abigail K. Scro[1], Susanna L.H. Osinski[2], Kristen A. Savastano[2], Galit Sharon[1], Timothy F. Scott[2] & Roxanna M. Smolowitz[1]. [1]Aquatic Diagnostic Laboratory, Center for Economic and Environmental Development, Roger Williams University, Bristol, RI 02809; [2]Shellfish Program, Center for Economic and Environmental Development, Roger Williams University, Bristol, RI 02809, USA. **(President's Award candidate)**

Estuaries and saltwater ponds in the Northeast United States have observed frequent rust tide blooms over the past few decades caused by the dinoflagellate, *Margalefidinium polykrikoides* (Mp). Blooms are described by their rusty color, high cell densities ($>10^3$ cells/mL), and large area of affected water (10–100 km). The blooms create mortality events and lead to decreased growth rates of shellfish with inflammation and necrosis of the gills. This study developed a sensitive Mp monitoring method and characterized the spatial and temporal trends of Mp in Ninigret Pond, Charlestown, Rhode Island, over the course of a year. Samples were collected from three locations in the pond from December 2022 through December 2023. An eDNA diagnostic qPCR assay was utilized to track Mp cell concentrations and compare them with environmental factors such as water temperature, depth, dissolved oxygen, and salinity to explore trends. While a bloom did not occur, Mp was observed in lower levels throughout the year which spoke to the sensitivity of the developed method and appeared to correlate with water temperature. This study provided insight into the annual dynamics of Mp and develop a bloom monitoring method.

4 – Two for the Price of One: Using Lichen Metagenomic Libraries for Dual Symbiont Target Capture. **Zachary M. Muscavitch**, Bernard Goffinet & Louise A. Lewis. Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269, USA. **(Wilce Award candidate)**

Despite the inherent duality of lichens, much more is known about the diversity of the fungal (mycobiont) partners than of the corresponding algae (photobionts). The systematics of *Trebouxia*, the most common lichen photobiont, is challenged by the need for culturing and interpretation of cryptic morphological variation, which has led to a widescale adoption of molecular tools for systematic studies of these algae. Recent 1 or 2 locus molecular analyses suggest the existence of at least 100 new *Trebouxia* species, and increased diversity may be detected with phylogenomic approaches. However, due to the low algal biomass in lichens and lack of cultures, the phylogenomic tools available to study photobiont diversity are limited.

To address these challenges and explore the hypothesis of cryptic diversity in lichen photobionts, we developed 564 custom target capture baits for lichen symbionts (260 algal, 304 fungal), using available genomic and transcriptomic data. We tested lichen derived metagenomic libraries for parallel target capture of fungal and algal loci; simultaneously decreasing library preparation costs by at least 50% and allowing for phylogenomic-scale resolution of both symbionts. The success in using parallel capture to identify less abundant symbionts implies this technique could be extended to other symbiotic associations, particularly in cases like corals or anemones where photobiont cells are less numerous than their metazoan host.

5 – Heterogeneity of *Chlamydomonas reinhardtii* Batch Cultures. **Gaganpreet Gill** & Dion G. Durnford. Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada. **(Wilce Award candidate)**

Heterogeneity within natural populations of microalgae is expected based on genetic differences, but there is increasing evidence that in genetically identical lines, there exists an unexpected phenotypic heterogeneity. There is growing evidence for different subpopulations in cultures of different microorganisms, including bacteria and yeast, and these differences may offer an advantage when acclimating to different environmental stressors. In *Chlamydomonas* batch cultures, there is little known about the phenotypic diversity of cells. Recently, subpopulations of an isogenic *Chlamydomonas* culture have been identified based on slow and fast-growing phenotypes. Using Percoll density gradients, we were able to isolate two subpopulations of *C. reinhardtii* grown in batch culture. While both populations were of a similar size and internal complexity, the least dense subpopulation made up 89.5% of the cells, and these cells had a greater chlorophyll and protein content. When supplemented with fresh media to evaluate their growth-rate over time, this subpopulation also had a faster yield rate and shorter lag time. The second, denser subpopulation had 10.5% of the cells and greater capacity for dissipating excess light energy. Our preliminary experiments suggest that the second subpopulation was more resistant to high-light stress, suggesting that the culture produced distinct phenotypic variants that may be part of a "hedging your bet" strategy to give a selective advantage under different stress conditions.

6 – Phylogeographic Structure of *Batrachospermum gelatinosum* in the Eastern United States. **Roseanna Crowell**[1], Sarah Shainker-Connelly[2], Stacy Krueger-Hadfield[2,3] & Morgan Vis[1]. [1]Environmental and Plant Biology, Ohio University, Athens, OH 45701, USA; [2]Department of Biology, University of Alabama at Birmingham, Birmingham, AL 35294, USA; [3]Virginia Institute of Marine Science Eastern Shore Laboratory, Wachapreague, VA 23480, USA. **(Wilce Award candidate)**

The freshwater red alga *Batrachospermum gelatinosum* has a well-documented distribution from Alabama to Newfoundland, spanning historically glaciated and unglaciated eastern North America. This alga has no known desiccation-resistant propagule, thus long-distance dispersal events are potentially rare with little subsequent migration. We used 10 microsatellite loci to investigate genetic diversity sampling 311 gametophytes from 18 sites in five major drainage basins, South Atlantic Gulf, Mid Atlantic, Ohio River, Great Lakes and Northeast. We predicted: (1) strong genetic structure among drainage basins and admixture among sites within basins and (2) higher latitude sites are characterized by lower genetic diversity than lower latitude sites as the southernmost sites were likely found in refugia that served as the origin of post-Pleistocene dispersal. Our data showed strong genetic partitioning among drainage basins and among sites within basins. The highest genetic diversity was observed in the Great Lakes, contrary to our prediction. Simulations of migration from southern refugia suggested dispersal from the Mid Atlantic to Ohio River and then to the Great Lakes and Northeast. The results for *B. gelatinosum* provide strong support that streams are distinct genetic units due to limited dispersal and potentially applicable to dispersal of other freshwater red algae.

7 – Diversification of New England's Macroalgae Industry: Nursery Techniques for *Wildemania amplissima*. **Riplee Mercer** & Christopher Neefus. Department of Biological Sciences, University of New Hampshire, Durham, NH 03824, USA. **(Wilce Award candidate)**

Although the New England macroalgae aquaculture industry has been expanding, it is based almost entirely on longline production of kelp. The goal of our research is to facilitate diversification by developing nursery and grow-out methods for longline production of *Wildemania amplissima,* a local nori species. Although conditions for nursery production of Asian nori species are well established, the optimal conditions for *W. amplissima* have yet to be established. Experiments were performed 1) to compare culture initiation methods, 2) to optimize culture conditions for vegetative conchocelis growth, and 3) to determine changes in conditions required to trigger conchospore development and release. Fertile blade maceration was found to be an effective method for inoculation of conchocelis cultures on oyster shells. Conchocelis growth experiments were carried out in culture chambers to determine the effect of temperature (10, 14, 18˚C), photoperiod (12L:12D, 16L:8D), and light level (30 and 60μM/m^2/s). Maximum growth rate occurred at 14˚C regardless of photoperiod and light level. An additional experiment was completed to test the effects of changes in temperature, photoperiod, and light levels on triggering progression through the life history stages ov *W. amplissima*. Conchosporangial development and conchospore release occurred 6 to 13 weeks after a shift from 14˚C short-day (8L:16D) to 8˚C short-day conditions.

8 – Mock Trial: Analyzing the Use of Mock Communities to Aid in Interpretation and Intercomparison of DNA metabarcoding studies. **Fran Webber**, Diana Fontaine, Erin Jones & Tatiana Rynearson. Graduate School of Oceanography, University of Rhode Island, Narragansett, RI 02882, USA. **(Wilce Award candidate)**

The ease and power of high throughput sequencing methods have led to a blossoming of their use in recent years. However, given the relative nature of amplicon sequencing as well as the existence of multiple points where bias can be introduced—via DNA extraction, PCR, and sequencing—interpreting and comparing results among sequencing runs, labs, and studies is fraught. The use of mock communities may allow us to move towards more confident intercomparison of amplicon sequencing data and enhance our interpretation of microbial community sequencing results. Here, we used amplicon sequencing to examine the performance of multiple mock communities, generated using both plasmids and whole cells across multiple studies and several labs. Mock community sequencing alongside sequencing of environmental samples sets a known baseline against which we can determine if error has been introduced at some point in the sequencing process. It also allows us to identify contaminants and set quantitative, rational thresholds for excluding contaminant and other spurious results from sample analysis. This examination of mock community results will aid in the understanding of appropriate use of mock communities to understand, and correct for, biases potentially introduced in the sequencing process.

9 – DNA Barcoding Reveals Cryptic Diversity within the Family Galaxauraceae (Nemaliales, Rhodophyta) in Eastern Australia. **Margaret M. Cassidy** & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada. **(Wilce Award candidate)**

Most reports of Galaxauraceae in eastern Australia occurred before the widespread use of molecular data, therefore a MAAT study is necessary to understand the true species diversity in this region. A total of five species in this family have been reported for the state of New South Wales, including Lord Howe Island, and Norfolk Island. Only one species, *Dichotomaria australis*, has been confirmed with DNA sequencing. The remaining species, *D. marginata*, *D. obtusata*, *Galaxaura rugosa* and *Tricleocarpa cylindrica*, lack molecular support for their reported pantropical distributions. DNA barcode analyses using COI-5P and *rbc*L-3P for recent collections from this region compared to topotype material (when possible) have revealed additional cryptic species in these growing complexes. Morphological and anatomical data support five novel species previously confused with one of the four "pantropical" species above, as well as a new record of Korean *T. jejuensis*. Using both molecular and morphological/ anatomical tools to study these species will help elucidate patterns of biogeography, specifically how the flora of these two remote islands (Lord Howe and Norfolk) relate to each other and the mainland, in addition to potential species introduction events.

10 – Ecological Storytelling with ArcGIS StoryMap: An Application Focusing on Seaweed Ecosystem Engineers in Narragansett Bay. **R. Venezia**[1], C. Thornber[1], G. Pantoni[2], L. Green-Gavrielidis[3], N. Hobbs[1], G. Cicchetti[4] & D. Taylor[5]. [1]University of Rhode Island, Kingston, RI, USA; [2]Florida Atlantic University, Boca Raton, FL, USA; [3]Salve Regina University, Newport, RI, USA; [4]US Environmental Protection Agency, Narragansett, RI, USA; [5]Roger Williams University, Bristol, RI, USA. **(Wilce Award candidate)**

Science storytelling, a vital form of science communication, can be a novel approach for sharing research findings with local human communities. One such storytelling tool is the program ArcGIS StoryMap, which incorporates interactive maps, photographs, videos, graphs, and tables to guide the viewers through the topic in an organized manner via a slide bar of images or map with guided points. I have developed an ArcGIS StoryMap to share the story of how ecostyems engineers in Narragansett Bay have changed from the 1960s to today. Rockweed, *Ascophyllum* and *Fucus*, and kelp, *Saccharina*, are ecosystem engineers that provide the foundation of benthic habitats as well as many essential ecosystem services in subtidal and rocky intertidal zones. This StoryMap incorporates underwater videos, maps, figures and images, which show species distribution and percent cover in subtidal habitats to illustrate how these species have changed in abundance. By providing information in an interactive format, this visually conveys how these ecosystem engineers and their habitats have changed from the 1960s to today.

11 – Understanding the Cellular and Molecular Changes of *Choreocolax polysiphoniae* and *Vertebrata lanosa* in Response to Infection. **Gabrielle M. Kuba**[1], Jillian M. Freese[2] & Christopher E. Lane[1]. [1]Biological Sciences, University of Rhode Island, Kingston, RI 02881, USA; [2]Craig Venter Institute, La Jolla, CA 92037, USA. **(Wilce Award candidate)**

Florideophyceaen red algae offer a unique model to investigate the genetic relationships between host and parasite lifestyles. Common traits of red algal parasites include the lack of, or lessened pigmentation, reduced morphologies, and secondary pit connections that connect host and parasite cells. Although the ecology and morphology of *Choreocolax polysiphoniae* has been well studied, the molecular factors involved in parasite development and subsequent host response are not well understood. Three-dimensional reconstructive histology and single cell transcriptomics were applied to better understand the cellular and molecular development across infection of *Vertebrata lanosa* by *C. polysiphoniae.* Transcriptomes were obtained from host and parasite across eight time points of parasite development and uninfected tissue. Differential gene expression analysis was applied to identify differentially expressed genes during parasite development and in response to infection. Gene expression profiles only represent a snapshot of cellular activity, but changes in gene expression can dramatically influence biological processes. Changes in gene expression in *C. polysiphoniae* correspond to growth and lifestyle, whereas gene expression in *V. lanosa* correspond to infection response. Transcriptomic data show higher upregulation of Glycolysis, Citric Acid Cycle, and carbohydrate metabolism pathway in the parasite across infection. These data also suggest alternations between *C. polysiphoniae* growth and *V. lanosa* infection response. Combining transcriptomic and morphological data allows for a more thorough assessment of significant pathways involved with or impacted by parasite infection. This study highlights manipulations of the host by parasite transmission and growth, highlighting the evolutionary history of host/parasite relationships.

12 – Determinants of Longevity in *Chlamydomonas reinhardtii.* **Navpreet Kaur**, Ghaith Zamzam & Dion G. Durnford. Department of Biology, University of New Brunswick, Fredericton NB E3B 5A3, Canada. **(Wilce Award candidate)**

While aging is a well-studied phenomenon in multicellular organisms, in microalgae how and under what circumstances they age is not well understood. Under ideal conditions, microalgae are immortal, but when nutrients are limited, conditional senescence occurs. *Chlamydomonas reinhardtii* is a single-celled, mixotrophic alga; its nutritional flexibility and ease of culturing make it an ideal organism for studying aging. Calorie restriction (CR) is a robust environmental intervention to increase lifespan in animals. In *Chlamydomonas,* the determinants of longevity were explored through CR using varying acetate concentrations. Higher acetate concentrations in batch cultures were found to decrease longevity, aligning with the CR hypothesis. Interestingly, Starch-deficient strains exhibited prolonged viability in high-acetate media, indicating a link between starch accumulation and lifespan. We hypothesized that elevated acetate leads to increased chloroplast metabolic activity, promoting starch accumulation and subsequent reactive oxygen species (ROS) production, causing damage, and reducing lifespan. ROS estimation using DCFH-DA (2,7-dichlorodihydrofluorescein diacetate) confirmed higher ROS levels in high-acetate cultures, correlating well with reduce longevity. However, in the starch-deficient mutant, ROS levels were also high indicating that a direct-connection between ROS production through metabolism and longevity was not the sole determining factor. This study sheds light on conditions influencing microalgal survival during conditional senescence and emphasizes the role of ROS production in lifespan regulation which will be helpful to study other species senescence as well.

13 – Rhodoliths and their Importance for Macroalgal Ecology and Biodiversity in the NW Gulf of Mexico. **Suzanne Fredericq**[1], Sherry Krayesky-Self[1], Thomas Sauvage[2], Joe Richards[1], Ronald Kittle[1], C. Frederico Gurgel[3], Daniela Gabriel[4] & William E. Schmidt[1]. [1]Biology, University of Louisiana, Lafayette, LA 70504-3604, USA*;* [2]Ifremer Centre Atlantique Nantes, France; [3]Botânica, Universidade Federal de Rio de Janeiro, Brazil; [4]Research Center in Biodiversity and Genetic Resources, University of the Azores, Portugal.

Understanding the ecology and biodiversity of deep-water communities is a major challenge. In the NW Gulf of Mexico, unique deep bank habitats associated with salt domes occur at ~50-90m on the continental shelf offshore Louisiana and Texas. In these mesophotic rubble habitats rhodoliths are the main hard substrata for the attachment of macroalgae. Metabarcoding of environmental DNA using molecular markers for rhodolith's endolithic portions has revealed hidden cryptic algal diversity including spores, propagules, and unsuspected life history stages. We explored cryo-SEM in the study of endolithic cell inclusions which brought to light a suite of microalgal stages. We were able to differentiate floridean starch from cellular inclusions. Analyses of combined 16S V4 metabarcodes and 16S Sanger sequences of several macroalgal orders increased the established record of diversity in the region. Progress is underway to link the eukaryotic component of the rhodolith holobiont ("total organism") with its co-occurring prokaryotic component. Rhodoliths are marine biodiversity hotspots that may function as seedbanks, temporary reservoirs for life history stages of ecologically important eukaryotic microalgae, or as refugia for ecosystem resilience following environmental stress.

14 – Fumbling Towards the Ecstasy of the Deep: How Mistakes Lead to a Search for Understanding Community Dynamics in a Marine Transition Zone. **D. Wilson Freshwater**. Center for Marine Science, UNCW, Wilmington, NC 28409, USA.

Through a series of unwitting mistakes, the author received decompression and technical dive training, which lead to a series of studies on epibenthic community dynamics along North Carolina's coast. An initial study of hard bottoms ranging from 18–42 m depths found depth was the most important factor structuring the epibenthic communities. The largest difference was found between depths ≤31 m and ≥32.5 m where there was a shift from macroalgae dominance to shared macroalgae and sessile invertebrate dominance. A subsequent study assessed the seasonal epibenthic communities on five hard bottoms along a 17–36 m depth gradient and found seasonal development and community composition was determined primarily by depth and proximity to the Gulf Stream. Although the studied depth zones were different, community composition converged in 'winter' and diverged during the growing and peak algal coverage seasons. Multiple sites on a single hard bottom were then surveyed over 16 months at a frequency to allow a better understanding of intra-annual and short term inter-annual change. Temporal communities were allowed to define themselves by grouping sampling days that did not differ. Community composition was significantly different between these communities, but a consistent intra-annual cycle did not occur. The cause for this (probably light), our current work, and other cool findings will be discussed.

15 – Mesophotic Algae in Paradise: The Interplay of Nutrients and Light in Structuring Mesophotic Macroalgae in the Hawaiian Archipelago. **Heather Spalding**, Department of Biology, College of Charleston, Charleston, SC 29424, USA.

The Mesophotic Coral Ecosystem (MCE) in the Hawaiian Archipelago is a low-light and presumably oligotrophic environment, yet it contains a high diversity and abundance of macroalgae. What processes are driving the high abundance and diversity of these algae? Measurements of macroalgal tissue nutrients, stable isotopes, and irradiance profiles in the water column were conducted across a gradient of anthropogenic impact in the Hawaiian Archipelago to determine how bottom-up processes may be influencing macroalgal abundance. Invasive macroalgae were abundant at mesophotic depths in areas offshore of densely populated areas and contained elevated tissue nutrients, suggesting that eutrophication may be impacting some MCEs via hypothesized submarine groundwater discharge. Several different genera of native and invasive psammophytic, bryopsidalean algae were observed to 90 m depths, and appeared to compete for available space. These data suggest that some macroalgae have evolved to thrive in these low-light habitats and have created islands of biodiversity that may be under threat from invasive species influenced by anthropogenic nutrients.

16 – Just When You Think There's No Light and You Turn on the Floodlights – Spectacular Macroalgae! **Craig Schneider**. Department of Biology, Trinity College, Hartford, CT 06106, USA.

The mesophotic (or 'twilight') zone is a magical place where most macroalgae are incapable of surviving in what appears to the human eye to be near total darkness. But some do. Such extreme light conditions clearly limit the species that can survive in the mesophotic, as well as their cover on these deep reefs, but what is found is often a collection of previously unknown species, many in genera that are found in distant oceans. Several of the species encountered in the mesophotic zone off Bermuda have congeners in Australasia or Hawaii, some of these as well being restricted to low-light environments. Examples of such geographically distant evolved species in the same genus will be highlighted using a list of the new species discovered on an expedition to the mesophotic in Bermuda including the red algae *Galene*, *Nothokallymenia* and *Psaromenia*. Others discussed include species with disjunct populations of Bermuda and the Gulf of Mexico (*e.g.*, *Halarachnion*), and unique species surviving severe light limitation when multiple sister taxa live a stone's throw away the in the euphotic zone off Bermuda (*e.g.*, *Cryptonemia*, *Dasya, Wrangelia*).

17 – Lake Mesocosms Showing Nitrogen as a Driver of Cyanobacterial Bloom Development and Species Composition. **Michael E. Kausch** & John D. Wehr. Louis Calder Center - Biological Station and Department of Biological Sciences, Fordham University, Armonk, NY, USA.

Nitrogen loading has become a focus of studies investigating the drivers of cyanobacterial bloom development, composition, and toxicity. We tested the effects of nitrogen additions in 24 large-scale outdoor mesocosms at the Louis Calder Center Experimental Lake Facility. Replicated mesocosms replete with phosphorus were treated with different forms (nitrate, ammonium nitrate, urea) and concentrations (0, +15, +50 uM) of nitrogen in a randomized block design. Blooms of *Aphanizomenon flos-aquae* co-occurring with other cyanobacterial taxa (*Gomphosphaeria*, *Microcystis*, *Dolichospermum*) were observed in all treatments with nitrogen additions. However, the lower (+15 uM) nitrogen treatment resulted in greater heterocyst abundances. Chl-a concentrations in treatments with only phosphorus added did not differ significantly from controls, suggesting that, at least at the time of our experiment, productivity was not limited by phosphorus alone. Treatments with +50 uM ammonium nitrate produced the highest concentrations of chl-a and cyanobacterial cell density. In all treatments with nitrogen added, cyanobacterial abundance correlated strongly with chl-a concentration. Although blooms were dominated by potentially toxic taxa, microcystins and anatoxins were below minimum detection limits. Our results highlight the importance of nitrogen in cyanobacterial bloom development and composition, and suggest that mitigation strategies should include efforts to reduce nitrogen loading concurrently with the reduction of phosphorus loads.

18 – Iron Wars Over Ligand Soup: Exploring Chemical Crosstalk in Symbiodiniaceae – Bacteria Interactions. **Hannah G. Reich**[1,2,3], MacNeill C. Matthews[1], Nicole R. Cunningham[2], Corinne Richard[1], Cassidy Stadtfeld[1], Hayden R. Wink[1], The Students of Siderophore SuperLab[2], The TAs of Siderophore SuperLab[2], Kristen E. Whalen[2] & Elizabeth L. Harvey[1.] [1]Department of

Biological Sciences, University of New Hampshire, Durham, NH 03824, USA; [2]Department of Biology, Haverford College, Haverford, PA 19041, USA; [3]Department of Environmental Biology, SUNY College of Environmental Science & Forestry, Syracuse, NY 13210, USA.

Nutritional exchanges among cnidarians, endosymbiotic dinoflagellates (Family: Symbiodiniaceae), and bacteria enable the ecological dominance reef-building corals in oligotrophic oceans. In some instances, bacteria can acquire forms of trace elements otherwise inaccessible to their eukaryotic partners. For example, bacterial siderophore (Gr., iron carrier) production of small, low-molecular weight ligands with high Fe^{3+} affinity can facilitate the uptake of insoluble iron. To ascertain the presence of siderophore production in Symbiodiniaceae-associated bacteria, we isolated ~150 strains of bacteria (spanning 25+ genera) from key Symbiodiniaceae cultures and observed widespread siderophore production via a colorimetric Chrome Azurol S (CAS) assay. To evaluate the sensitivity of bacterial growth to host iron stress, isolates of two 'core' bacterial genera (*Marinobacter, Labrenzia*) were grown on 'spent' media (algal filtrate) from algal hosts with symbiotic (*Symbiodinium microadriaticum*) and free-living ecologies (*S. natans*) reared in either iron deplete or replete conditions. Bacteria were grown on the spent *Symbiodinium* media for 12 da. and assayed for siderophore production every 4 da. These experiments elucidate a biotic route of iron exchange as well as the abiotic triggers for its activation. Attaining a multidisciplinary understanding of iron exchanges within the coral holobiont is a critical for identifying biogeochemical scenarios that exacerbate coral bleaching responses.

19 – Tracing the inheritance of bacterial endosymbionts among *Nephromyces* species, using epicPCR. **Marissa Mehlrose** & Christopher E. Lane. College of Environment and Life Sciences, University of Rhode Island, Kingston, RI 02881, USA.

Despite being members of the largely parasitic clade, Apicomplexa, species in the genus Nephromyces have an extracellular life and are reportedly commensal with their hosts. An additional unusual feature of *Nephromyces* spp. is that they all host one of three different types of bacterial endosymbionts. These bacteria compensate for the fact that apicomplexans have lost the ability to produce many amino acids and cofactors, by providing these important resources *for Nephromyces*. However, previous work has demonstrated that each individual bacterial species does not encode the genes for all essential amino acids that have been lost by *Nephromyces*. Because of this, *Nephromyces* spp. with different bacterial symbionts have to co-infect a host and exchange metabolites to survive. It is unknown whether the bacteria are inherited vertically within *Nephromyces* species, or if bacteria can be passed horizontally between them. Using "emulsion, paired isolation, and concatenation PCR" (epicPCR), single cells were trapped in polyacrylamide beads and successive PCRs were performed to link the 16S gene from the bacterial endosymbiont to the COI gene of the *Nephromyces* host. This will allow for the identification of which bacteria live inside which *Nephromyces* and to determine whether there is strict vertical inheritance.

20 – Multiple Plastid Losses Within Photosynthetic Stramenopiles Revealed by Comprehensive Phylogenomics. **Kristina X. Terpis**[1], Eric D. Salomaki[2,3], Dovilė Barcytė[4], Tomáš Pánek[4,5], Heroen Verbruggen[6], Martin Kolisko[2], J. Craig Bailey[7], Marek Eliáš[4] & Christopher E Lane[1]. [1]Department of Biological Sciences, University of Rhode Island, Kingston RI, USA; [2]Biology Centre, Czech Academy of Sciences, České Budějovice, Czech Republic; [3]Center for Computational Biology of Human Disease and Center for Computation and Visualization, Brown University, Providence, RI, USA; [4]Department of Biology and Ecology, Faculty of

Science, University of Ostrava, Czech Republic; [5]Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic; [6]School of BioSciences, University of Melbourne, Victoria 3010, Australia; [7]Department of Biology and Marine Biology, University of North Carolina, Wilmington, NC, USA.

Ochrophyta is a vast and morphologically diverse group of algae with complex plastids, including familiar taxa with fundamental ecological importance, and a wealth of lesser-known and obscure organisms. The sheer diversity of ochrophytes poses a challenge for reconstructing their phylogeny, with major gaps in sampling and the placement of certain taxa yet to be tackled. We sequenced transcriptomes from 25 strategically selected representatives and used these data to build the most taxonomically comprehensive ochrophyte phylogenomic supermatrix to date. While generally congruent with previous analyses, the updated ochrophyte phylogenomic tree resolved the position of several taxa with previously uncertain placement. Our results indicated that the heterotrophic plastid-lacking heliozoan *Actinophrys sol* is not a sister lineage of ochrophytes, as proposed recently, but rather phylogenetically nested among them, implying that it lacks a plastid due to loss. In addition, we found *Picophagus flagellatus* to be a secondarily heterotrophic ochrophyte lacking all hallmark plastid genes, yet exhibiting mitochondrial proteins that seem to be genetic footprints of lost plastid organelle. We thus document, for the first time, complete plastid loss in two separate ochrophyte lineages. Altogether, our study provides a new framework for reconstructing trait evolution in ochrophytes and demonstrates that plastid loss is more common than previously thought.

21 – Losing Histone H1: A Critical Element in Dinoflagellate Nuclear Drama. **Senjie Lin**. Department of Marine Sciences, University of Connecticut, Groton, CT 06340, USA.

About ten years ago dinoflagellate/viral nucleoprotein (DVNP) was discovered in dinoflagellates, an ecologically important and evolutionarily enigmatic group of aquatic protists. Apparently acquired from a viral origin, the appearance of DVNP coincided with the loss of nucleosome, a rare event in eukaryote evolution. Despite the potential importance of DVNP as the substitute of histones, its evolutionary trajectory remains elusive. Here, we conducted comparative analyses using existing dinoflagellate genomes and transcriptomes from 26 species ranging from ancestral to later-diverging lineages to investigate the pattern of sequence and structural divergence. Results showed that the functional domestication of DVNP in ancestral dinoflagellates coincided with the loss of histone H1, while subsequent DVNP differentiation was accompanied by the yet another genomic innovation: acquisition of bacterial-originated histone-like protein. The adaptive significance and ecological implications of these remarkable nuclear reconfiguration will be discussed.

Poster Abstracts

P1 – Utilizing qPCR to Investigate Cyanobacteria – Viral Interactions. **Ava E. Devine**, Lily M. Winsten, Michael G. Briggs & Marcia F. Marston. Biology and Marine Biology, Roger Williams University, Bristol, RI 02809, USA. **(President's Award candidate)**

Synechococcus spp. are unicellular cyanobacteria that form the base of the food web in coastal ecosystems. Significant proportions of *Synechococcus* communities can be lysed daily by viruses. These viruses can influence the evolution and diversification of *Synechococcus* by applying selective pressure on populations for viral resistance. In this study, a qPCR assay was used to examine interactions between co-occurring *Synechococcus* strains and viruses from Narragansett Bay, Rhode Island. Pairwise infectivity assays were performed to evaluate whether *Synechococcus* strains were susceptible or resistant to viruses. In these experiments, viruses were added to host cells and multiple samples were collected over a 48-hour period. Viral attachment to *Synechococcus* cells and replication within the cells were quantified using qPCR. Preliminary data show that rates of viral attachment and replication can vary significantly even among *Synechococcus* strains with identical ITS sequences. These infection experiments will lead to a better understanding of how genetic variation among closely related *Synechococcus* strains can influence susceptibility to viral infection.

P2 – Quantifying Coralline Algal Diversity and Assessing its Role in Community Structure in the Gulf of Maine. **Curtis R. Morris** & Jarrett E.K. Byrnes. University of Massachusetts, Boston, MA, USA.

Coralline algae are an understudied taxon which may play a critical role in determining ecosystem structure and resilience in kelp forests in the Gulf of Maine (GoM). These calcifying algae potentially contribute to kelp recruitment and development and thus may be a foundational component of benthic ecology in our region; however, relatively little is known of their ecology outside of the tropics. One challenge preventing the assessment of ecosystem services provided by coralline algae is the difficulty of assigning species-level identification as a result of cryptic morphology. This represents a potential gap in our understanding of benthic ecology in the GoM as without a baseline understanding of the species assemblage present it is difficult to assess ecosystem roles. Though evidence suggests that coralline algae do contribute to kelp settlement and development, that role likely varies across different coralline species as well as among different kelp species. However, with our current knowledge of coralline diversity in the GoM, a species-specific investigation is impossible to carry out. Here we outline a future study which has three objectives: (1) identify the baseline species assemblage of coralline algae present in the in the GoM using DNA sequencing to overcome cryptic morphology; (2) compare sequencing results with morphological identification to groundtruth methods currently and historically used; and (3) identify associational trends between coralline algae and overgrowth taxa.

P3 – A Comparative Examination of Dominant Canopy Forming Macroalgae in Southern New England. **Kaleb Boudreaux**. Department of Biology, Southern Connecticut State University, New Haven, CT 06516, USA.

Climate change has directly affected the various species of macroalgae in Southern New England via marine heatwaves. A marine heatwave is a period where the ocean's surface temperature is two or three degrees (Celsius) higher than the average. We will look at two macroalga, *Saccharina latissima* and *Sargassum filipendula*, to see which species dominates the intertidal zone. At three sites in Rhode Island, *S. filipendula* and *S. latissima* will be examined around 20 ft for 30 minutes by a Go-pro video recorder which will be analyzed in a lab. Additionally, the height will be measured using a measuring tape. Biodiversity around both macroalgae will be examined using a plankton tow and a fish count. This process will be repeated throughout the year as well as light and temperature levels. Results will vary by seasonal patterns as *Saccharina* degrades in warmer temperatures and *Sargassum* will degrade in colder temperatures reducing their overall canopy size. However, because marine heatwaves continue to be more common, we hypothesize that *Sargassum* will become the new dominant canopy in Southern New England. This study is important because the ecological changes caused by climate change needs to be examined in our oceans for us to understand the new biodiversity that will inhabit southern New England.

P4 – Investigation into the Patchy Dispersal of *Choreocolax polysiphoniae* Populations
Emily M. Molino[1], Gabrielle M. Kuba[1], Eric D. Salomaki[2] & Christopher E. Lane[1]. [1]Biological Sciences, University of Rhode Island, Kingston, RI, 02881 USA; [2]Center for Computational Biology of Human Disease and Center for Computation and Visualization, Brown University, Providence, RI 02912, USA. **(President's Award candidate)**

Parasites have independently evolved within the Florideophyceae (Rhodophyta) over 100 times. The relationship between host and parasite offers a unique model to study the evolution of parasitism. One well studied host/parasite relationship includes that of *Vertebrata lanosa* and the parasite *Choreocolax polysiphoniae.* Although the ecology and morphology of *C. polysiphoniae* is understood, the dispersal of this parasite is not well studied. *Choreocolax polysiphoniae* population distribution has been identified as non-random, however the role of the host in this distribution is unknown. Samples of uninfected and infected *V. lanosa* were collected from multiple locations around Rhode Island (USA), Maine (USA), and Roscoff (France). The Internal Transcribed Spacer (ITS) region of the nuclear ribosomal operon was amplified via PCR and Sanger Sequencing was performed. These results will allow us to determine whether the distribution of red algal parasites has underlying genetic factors of the host, influencing these relationships. Red algal parasite population genetics has never been explored, despite notoriously patchy distributions. Our study is the first to take this topic on.

P5 – Selfish Elements as a Tool for Illuminating Genetic Exchange Pathways Between Green Algal Chloroplast Genomes. **Danielle Arsenault**[1], J. Peter Gogarten[1] & Louise A. Lewis[2]. [1]Department of Molecular and Cell Biology, University of Connecticut, Storrs, CT 06269, USA; [2]Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269, USA.

Chloroplast genome rearrangement, expansion, and shrinkage have occurred frequently throughout the evolution of green algae (Chlorophyta), leading to significant variation in genome architecture and size. A key driver of observed size diversity is the frequent gain and loss of organellar introns (group I and II). Many contain open reading frames that encode selfish elements called homing endonucleases (HEs). The wide and sporadic distribution of these introns paired with the need of HEs to be frequently transferred to maintain their function makes HE-encoding introns a powerful tool for tracing the pathways available for horizontal transfer across Chlorophyta chloroplast genomes. By comparing the evolutionary histories of HE-encoding introns to those of their host genes, we can use topological conflicts to identify potential intron transfer events to be further investigated. Chloroplast gene *psbA,* which encodes the D1 subunit of photosystem II, is riddled with these introns. We characterized *psbA* intron distribution across 192 completely sequenced Chlorophyta chloroplast genomes and found over 50 distinct intron insertion sites in *psbA*, with some organisms containing up to 11 *psbA* introns. We found highly similar HE-encoding introns occupying identical insertion sites spanning three classes of Chlorophyta with sporadic distribution within each class, indicating potential transfer between divergent species.

P6 – Using stable isotopes to infer interactions between the common intertidal macroalgae *Chondrus crispus* and *Fucus* spp., and an herbivorous snail, *Lacuna vincta***.** **L. Jensen**[1], N.-V-.

Hobbs[1], A. Oczkowski[2] & C. Thornber[1]. [1]University of Rhode Island, Kingston, RI, USA; [2]US Environmental Protection Agency, Narragansett, RI, USA. **(President's Award candidate)**

In temperate marine ecosystems, some benthic macroalgal species have perennial life cycles, while others are only present seasonally. Understanding the nutrient content in perennial macroalgae and associated invertebrates can yield valuable insights into seasonal and/or annual nutrient dynamics in estuarine systems, which receive nutrient inputs via several sources. Here, we collected *Chondrus crispus* and *Fucus* spp. individuals from the rocky shore at the URI Narragansett Bay Campus in Rhode Island seasonally from Fall 2022- Spring 2023. In the laboratory, we separated the common small herbivorous snail, *Lacuna vincta*, from each algal thallus. All snails and algae were dried in a drying oven, ground into a powder, and prepared for nutrient analysis via mass spectrometry at the US EPA facility in Narragansett, RI. We analyzed all samples for % nitrogen, % carbon, $\delta^{15}N$, and $\delta^{13}C$, and we found significant variation in nutrient content across seasonal timescales. We interpret our findings in light of changing nutrient dynamics in Narragansett Bay.

P7 – Rosette Cellulose Synthesis Complex in *Coleochaete*. **Eric Roberts**[1] & Alison W. Roberts[2]. [1]Biology, Rhode Island College, Providence, RI, 02908, USA; [2]Biological Sciences, University of Rhode Island, Kingston, RI 02881, USA.

Cellulose Synthase (CESA) enzymes in land plants form hexagonal plasma membrane structures called Cellulose Synthesis Complexes (CSCs or rosettes), which produce cellulose microfibrils. Rosette CSCs occur in land plants but also in charophyte green algae in the Zygnematales and Charales. CESA is just one family in a larger Cellulose Synthase superfamily. Other members of this superfamily, the Cellulose Synthase-Like D (CSLD) proteins, have been associated with cellulose biosynthesis in tip-growing cells and during cell division. However, it is unknown whether CSLDs form rosette CSCs and produce microfibrillar cellulose. Understanding CSLD function is challenging due to the simultaneous activity of CESAs in most plants. Surprisingly, several transcriptome projects have shown that the charophycean green alga *Coleochaete* possesses CSLDs, but no CESAs have been identified. Previous studies suggested that *Coleochaete* does not form rosette CSCs, but instead has distinctive CSCs and makes cellulose microfibrils that differ morphologically from those of land plants. These differences could be explained by CSLDs forming unique CSCs that, in turn, synthesize microfibrils with unusual physical structures. Contrary to these hypotheses, we have used freeze-fracture transmission electron microscopy to show that *Coleochaete* does, indeed, have hexagonal rosette CSCs which we propose are composed of CSLDs. If so, this discovery would provide an opportunity to further investigate the function of CSLDs in cellulose synthesis independently of CESA activity.

P8 – River Macrophytes Harbor Different Epiphytic Diatom Associations. **Maisie Grogan**[1], John Wehr[1], Mia Wrey[1] & Lawrence Stevens[2]. [1]The Louis Calder Center, Fordham University, Bronx, NY 10458, USA; [2]Springs Stewardship Institute, Flagstaff, AZ 86001, USA. **(President's Award candidate)**

Aquatic macrophytes and epiphytic diatoms form the base of the Colorado River food web. Our study examined species composition and ecological guilds (high- vs low-profile) of diatoms attached to different macrophyte hosts. Previously, *Cladophora* was the dominant river macrophyte, but altered water release patterns from Glen Canyon Dam transformed a turbulent system into a more stable flow system, allowing other macrophytes to proliferate: *Chara vulgaris*, *Fontinalis hypnoides*, and *Potamogeton* spp. We predicted the new macrophyte assemblage would alter diatom species composition. Proportions of the two most abundant species were compared: high-profile *Gomphonema pumilum* and *Rhoicosphenia abbreviata* were more abundant on *Chara* and *Fontinalis*, respectively. Low-profile *Cocconeis pediculus* and *Cocconeis placentula* were more abundant on *Fontinalis* and *Potamogeton.* We tested the hypothesis that the ratios of two guilds among 10 major species were equal (H:L = 1.0) or suggested a preference (H:L > or < 1.0). Average H:L on moss (0.202) and *Potamogeton* (0.207) averaged significantly less than 1.0, suggesting low-profile diatoms were more common on these plants. Pairwise comparisons identified significantly different epiphyte compositions between *Chara* vs moss (t = 2.397, p = 0.050) and *Chara* vs *Potamogeton* (t = 2.471, p = 0.044). Our data suggest the diatom food base changed in response to a new macrophyte composition, with implications for the food web.

P9 – Invertebrate Grazing Effects on Diatom Ecological Guilds and Species Composition. **Olivia Clausen**[1], Hayden Wilke[1], John Wehr[1], Mia Wrey[1] & Lawerence Stevens[2]. [1]The Louis Calder Center, Fordham University, Bronx, NY 10458, USA; [2]Springs Stewardship Institute, Flagstaff, AZ 86001, USA. **(President's Award candidate)**

Our study assessed impacts of invertebrate grazing on diatom species composition and ecological guilds in the Colorado River below Glen Canyon Dam, Arizona, USA. We analyzed gut contents of two invertebrate taxa, the invasive New Zealand Mudsnail (*Potamopyrgus antipodarum*) and the amphipod *Gammarus lacustris* collected in 2021. Goals were to assess whether invertebrates selectively consumed diatom growth forms or guilds and contrast the impacts of two major consumers. Mudsnails consumed significantly more low-profile than high-profile diatoms at two river locations (RM-2: U = 599, $p < 0.001$; RM-12: U = 413, $p < 0.001$), with slightly greater consumption of high-profile species downstream (U = 518, $p < 0.001$). Species proportions in snail guts were similar to *in situ* numbers recorded in the river 2020 downstream (RM-2) but differed significantly from abundances upstream (RM-12), suggesting possible shifts in selectivity with habitat. In contrast, amphipods consumed more high-profile vs low-profile diatoms (U =1134, p < 0.05) in these same habitats, but no significant difference was found in their consumption of low-profile species. Our results likely reflect differences in feeding morphology of the two species, and differential impacts on the epiphytic diatom flora of the river. Our data also suggest that the recent invasion of NZ mudsnails colonization may accelerate the consumption of low-profile diatoms.

P10 – Lethal and Sublethal Impacts of *Ulva* on Marine Invertebrates. **Danielle Moloney**, Samantha Parsons & Lindsay Green-Gavrielidis. Department of Biology & Biomedical Sciences, Salve Regina University, Newport, RI 02840, USA.

Harmful algal bloom research has largely focused on microalgal blooms, but there is growing interest in macroalgal blooms, commonly consisting of *Ulva*, as they expand on a global scale. *Ulva* produces chemicals for competition that may be offensive, defensive, or both, and these chemicals can inhibit co-occurring macroalgae and marine invertebrates. This study assessed the impact of *Ulva compressa, Ulva lacinulata*, and tubular *Ulva* on three marine invertebrates: *Idotea balthica*, *Mytilus edulis*, and *Palaemon pugio.* We used bloom densities of 3.5 g/L and 5.0 g/L in four-week mesocosm experiments that tracked invertebrate growth and mortality, as well as pleopod beating in *P. pugio*. Exposure to *Ulva* did not significantly affect growth or mortality of shrimp or isopods. Mussels grew significantly less when exposed to 5.0 g/L of *U. compressa* than they did in mesocosms with no algae present. Mussel mortality was higher across all experiments, and slightly higher in mesocosms containing *Ulva*, which may be partially attributed to fluctuating pH in mesocosms. Pleopod beating in *P. pugio* varied widely by treatment and week. Lethal and sublethal characteristics of these species can have wide ranging impacts on the ecosystem. These findings may help to discern the conditions under which *Ulva* produces toxins, a key step for macroalgal bloom research as climate change continues to increase bloom size and frequency worldwide.

P11 – Desmid Communities and Environmental Conditions in Selected Vermont Wetlands. **William Roberts** & Karolina Fučíková & Michael Norcia. Biological and Physical Sciences, Assumption University, Worcester, MA 01609, USA. **(President's Award candidate)**

Desmids are an order of unicellular green algae that have been used as bioindicators of freshwater wetland health based on their narrow ecological ranges and sensitivity to changes in environmental conditions. Human activities threaten wetland health, and the monitoring of bioindicators and water chemistry is essential for wetland conservation. Desmids have not been previously monitored in Vermont, so the purpose of this study was to analyze desmid communities and water chemistry from various Vermont wetlands. Twelve Vermont wetland sites were analyzed by assessing temperature, pH, water hardness, and conductivity, and collecting plankton, periphyton, and sediment samples at each site. Desmids from each sample were microscopically analyzed and photographed, and then identified and recorded in iNaturalist. Data analysis was then performed to determine the relationships among desmid diversity, community composition, microhabitat, and water chemistry variables. A total of 175 species and 16 genera of desmids were observed. The sites that desmid communities were collected from shared more similarities in community composition than microhabitats, and on average, there were fewer species and genera in plankton and sediment samples than in periphyton. There was also a slight, nonsignificant negative correlation between genus richness and water hardness ($r(10) = -.25$, $p = .424$). In conclusion, desmid community composition was found to be most influenced by site, periphyton was determined to be the richest harbor of desmid communities, and genus richness decreased as water hardness increased. Further studies could focus on adding data from localities with a wider range of pH and/or conductivity values.

P12 – Placing *Euastropsis* (Sphaeropleales, Chlorophyceae). **Hilary A. McManus**[1], K.G. Karol[2] & J. Lenarczyk[3]. [1]Biological and Environmental Sciences at Le Moyne College, Syracuse, NY, USA; [2]New York Botanical Garden, Bronx, NY, USA; [3]Department of Phycology, W. Szafer Institute of Botany, Polish Academy of Sciences, Lubicz 46, PL-31-512 Kraków, Poland.

Molecular studies of the green algal family Hydrodictyaceae (Sphaeropleales) over the last two decades have revealed new lineages, a diversity of chloroplast and mitochondrial genomes in size and architecture, and aided in resolving evolutionary relationships. Representatives of all genera within Hydrodictyaceae have been included with the exception of *Euastropsis* Lagerheim 1895. This study incorporates *Euastropsis* after isolating it from a pond in Drawa National Park in Poland. Phylogenetic analyses place *Euastropsis* as a sister lineage to *Stauridium* spp., and its plastome architecture is characteristic of Hydrodictyaceae. The addition of *Euastropsis* offers insight into the trends of plastome and morphological evolutionary patterns in the family.

P13 – Characteristics of Trebouxiophyte Organellar Genomes. **Colin Brewer** & Karolina Fučíková. Biological and Physical Sciences, Assumption University, Worcester, MA 01609, USA. **(President's Award candidate)**

Trebouxiophyceae is a class of green algae that belongs to the phylum Chlorophyta. This class includes a diverse range of microorganisms. They are generally found in freshwater or terrestrial habitats. Like many other microorganismal groups, they are severely under-researched, although recent studies have provided insights into their biodiversity and evolution. Trebouxiophyte organellar genomes vary considerably in size (94,206–306,152 for plastomes and 78,500–123,371 for mitogenomes). Trebouxiophyte chloroplast genomes have been studied more intensively than their mitochondrial genomes. In this study, we compiled data from available organellar genomes as well as nuclear ribosomal gene data and environmental data for the algae's localities of origin across Chlorophyta. We focused on GC content, genome size and coding content. In addition, we contributed four newly sequenced trebouxiophyte chloroplast genomes (*Eremochloris sphaerica*, *Kalinella apyrenoidosa*, *Leptochlorella* sp., *Muriella* sp., *Viridiella fridericiana*, and *Xerochlorella olmae*), as well as two new mitogenomes (*Leptochlorella* sp. and *Xerochlorella olmae*). The new genomes fell within the expected size ranges and their GC varied from 28–39% for plastomes and 29–30% for mitogenomes. Trebouxiophyceae appeared to have a broad range of chloroplast GC content, on average higher than that of Chlorophyceae and Ulvophyceae

P14 – Temperature and Density Effects on Interactions Between Native and Introduced Macroalgae. Leah Harries[1], Alysha B. Putnam[2] & **Paulette Peckol**[1]. [1]Biological Sciences, Smith College, Northampton, MA, 01060, U.S.A.; [2]Environmental Conservation, University of Massachusetts Amherst, Amherst, MA 01003, USA.

The Gulf of Maine is one of the most rapidly warming bodies of water in the world. Interactions among native and introduced macroalgae will be affected by this warming; thus, their importance as food and habitat may shift with rising temperatures. Native *Fucus vesiculosus* has been under threat of displacement by an introduced red alga, *Gracilaria vermiculophylla*, in some locations. We investigated inter- and intraspecific interactions of *F. vesiculosus* and *G. vermiculophylla* at 15°C and 25°C and two densities. We measured growth rates under various treatment conditions (ambient, +nutrient (+N) enrichment, and +nutrients (+N)/+dissolved inorganic carbon (DIC) enrichment). Both species showed higher growth rates under 25°C and lower densities, and *G. vermiculophylla* grew faster than *F. vesiculosus* across all treatments. Growth did not vary between the ambient and +N treatments; only +N/+DIC resulted in consistently enhanced growth. *F. vesiculosus* demonstrated a clear density effect under both intra- and interspecific conditions. In contrast, *G. vermiculophylla* showed significantly lower growth rates under interspecific pairings, suggesting negative effects of *F. vesiculosus*. Dominant gastropods showed 2X higher combined grazing rates on *F. vesiculosus*. Thus, while both species may survive under warming temperatures, higher growth rates by *G. vermiculophylla* coupled with lower grazing pressure may result in greater success of this introduced species, particularly in dense mats.

P15 – Biodiversity Conservation in the Face of Climate Change: Fucoid Macroalgal Dynamics on the Boston Harbor Islands. **Angel Checo Reynoso**[1], Alysha B. Putnam[1], Paulette Peckol[2] & Michelle Staudinger[1,3]. [1]Environmental Conservation, University of Massachusetts, Amherst, MA 01003, USA; [2]Biological Sciences, Smith College, Northampton, MA 01060, USA; [3]School of Marine Sciences, Darling Marine Center, University of Maine, Walpole, ME 04573, USA. **(President's Award candidate)**

In 2022, the Boston Harbor Islands were included among the 11 most endangered historic places in the U.S. due to climate change. *Ascophyllum nodosum* and *Fucus* spp. are dominant macroalgae in this area and due to the region's climate vulnerability, assessing fucoid distribution, abundance, and associated biodiversity is crucial. We surveyed intertidal regions of five key islands in Boston Harbor: Gallops, Georges, Peddocks, Lovells, and Thompson, hypothesizing that islands with higher fucoid abundances would be associated with higher biodiversity of invertebrate and attached algal species. Study sites were gridded into 48 m wide areas with 9 quadrants spanning from upper shore to low mean water. Quadrats (~35, 0.5m^2) were randomly placed per sampling area, evaluating total counts of mobile invertebrates and percent cover of sessile invertebrates/macroalgae. Gallops and Georges Islands exhibited high fucoid frequency and diversity (5 spp.), including the exclusive presence of *A. nodosum*. Thompson Island exhibited the least representation, with only two fucoid species present, *F. vesiculosus* and *F. spiralis*. Quadrats with fucoid species generally exhibited significantly higher species richness than those without on four of the five islands. Given these abundance and biodiversity patterns, prioritizing conservation efforts for fucoid-rich islands is pivotal in the face of climate change.

P16 – Can We Find Common Denominators in Freshwater Benthic Cyanotoxin Production?
A.M. Webster[1], L.B. Cleckner[2], G.L. Boyer[1] & N.R. Razavi[1]. [1]State University of New York, College of Environmental Science and Forestry, Syracuse, New York, USA; [2]Finger Lakes Institute, Hobart and William Smith Colleges, Geneva, New York, USA.

Benthic cyanobacteria are an understudied yet important component to cyanobacterial harmful algal blooms (cHABs) research. Because cHAB research has been centered around planktonic cyanobacteria, we lack confidence and data on the conditions that promote benthic blooms and toxicity. In 2022 and 2023, we surveyed nearshore zones in the Lake Ontario watershed for benthic cyanobacteria and cyanotoxins. Populations of benthic cyanobacteria were found in the three Finger Lakes studied and in Lake Ontario embayments, but they were not found along either Lake Ontario shoreline surveyed. Cyanotoxins were detected in 45% of all samples analyzed, with no detections from Lake Ontario. In both years, we detected nodularin in colonies of a re-occurring population of *Nostochopsis* from a small eutrophic Finger Lake. Here, we present our observations of toxic and non-toxic benthic cyanobacteria in New York State lakes in relation to their environmental conditions (i.e., water temperature, nutrient availability, and light intensity) and suggest methods for future toxicity experiments using *Nostochopsis*. These observations are, to our knowledge, the first reports of cyanotoxin production by *Nostochopsis*. We are taking a whole genome approach to this work in effort to resolve toxin biosynthesis gene clusters and invite feedback from those who have performed toxicity experiments or have isolated benthic cyanobacteria.

P17 – Molecular characterization of *Bryopsis* species richness from Rhode Island to Panama. **Abigail St. Jean** & Brian Wysor. Department of Biology, Roger Williams University, Bristol, RI 02809, USA. **(President's Award candidate)**

Bryopsis is a species-rich genus of siphonous green algae known for its feathery and sometimes iridescent appearance. There are two species of *Bryopsis* in Rhode Island (*Bryopsis plumosa, B. hypnoides*) but preliminary DNA barcoding data suggest at least three species are present. Given their potential for causing environmental problems through biological invasion, and their pharmacological potential, being able to identify species is critically important. My project attempts to clarify *Bryopsis* species richness by assessing DNA sequence variation from 46 specimens from throughout its western hemisphere range including Rhode Island and Caribbean and Pacific Panama.

P18 – The Contribution of Small Eukaryotes to Nitrate-Based New Production in the North Pacific Subtropical Gyre. **Catherine A. Crowley**[1], Brandon Brenes[2], Angelicque E. White[2], Raquel F. Flynn[3], Adrian Marchetti[3] & Julie Granger[1]. [1]Department of Marine Sciences, University of Connecticut, Groton, CT 06442, USA; [2]School of Ocean and Earth Sciences, University of Hawaii at Manoa, Honolulu, HI 96822, USA; [3]Earth, Marine and Environmental Sciences Department, University of North Carolina, Chapel Hill, NC 27514, USA. **(Trainor Award candidate)**

Anthropogenic climate change is expected to result in the expansion of subtropical gyres and increased stratification of the surface ocean. It is anticipated that these changes will cause decreased nutrient transport to the sunlit surface waters, potentially weakening carbon storage in the ocean's interior. To understand and anticipate how climate change will impact the nutrient cycling of subtropical gyres, their biogeochemistry and ecology need to be investigated. In the North Pacific Subtropical Gyre (NPSG), the supply of nutrients to the surface waters is low, and primary production is predominantly fueled by recycled nutrients. However, in the Sargasso Sea, an analogous ocean region, recent evidence suggests that nitrate assimilation occurs throughout the euphotic zone in summer, despite surface stratification. This nitrate assimilation is conducted by small eukaryotic phytoplankton, whereas recycled production is dominated by prokaryotic phytoplankton. This dynamic suggests that some portion of subsurface nutrients are supplied to the strongly stratified surface waters by mechanisms not yet understood. Our aim is two-fold: 1) to study the extent to which primary production at station ALOHA in the NPSG is fueled by nitrate-based new production and 2) to determine where small eukaryotes account for most new production, similarly to in the Sargasso Sea. To investigate these aims, we measured the $^{15}N/^{14}N$ of four flow-sorted phytoplankton populations (*Prochlorococcus, Synechococcus,* pico- and nanoeukaryotes) to determine whether they relied predominantly on nitrate or regenerated nitrogen sources.

P19 –Developing a scaled-down assay to screen *Ulva* bloom water for toxicity in real time. **Kaylee Collins**, Danielle Moloney, Ashley Caputo, Sarah Holcomb & Lindsay Green-Gavrielidis. Department of Biology and Biomedical Sciences, Salve Regina University, Newport, RI 02840, USA. **(President's Award candidate)**

The green algae *Ulva* are ubiquitous throughout Narragansett Bay, where they provide habitat and food for marine life. Large blooms of *Ulva* grow due to excess nutrients, leading to impacts on marine life and water quality. *Ulva* also releases allelopathic chemicals that impact marine species, including phytoplankton. Phytoplankton are a proxy that can indicate toxicity of water. Using water samples from *Ulva* blooms, we grew *Skeletonema costatum* to assess whether bloom water was toxic. This study evaluated if our larger, previously established test tube assay, could be scaled down to well plates. Our results indicated that 60% of well plate trials (n=5) showed consistency with test tube trials. In these trials, we recorded one trial each with a positive effect and a negative effect of green tide on *S. costatum* growth. We also found that 40% of well plate trials showed no effect of green tide toxins and no consistency between well plate and test tube trials. For example, one trial showed a negative effect on *S. costatum* in well plates, but a positive effect in test tubes. Additional modifications (e.g., better mixing protocol) are needed to successfully scale down to well plates. If successful, organizations can use this easily managed method to determine whether action should be taken to remove green tides.

P20 – Siderophore Utilization by Dinoflagellates as a Strategy for Iron Acquisition. **Sydney McDonald**[1], Felipe Porto[1], Xiaoyu Wang[2], Senjie Lin[1] & Julie Granger[1]. [1]Department of Marine

Sciences, University of Connecticut, Groton, CT 06340, USA; [2]College of Ocean and Earth Sciences, Xiamen University, China. **(Trainor Award candidate)**

Iron is a limiting nutrient for primary production in 30% of the global ocean. Dinoflagellates thrive in a wide variety of coastal and oceanic environments, including iron-limited regions. As iron is a biologically essential element for the growth and proliferation of marine algae, dinoflagellates may have evolved strategic mechanisms to combat iron limitation. Presently, these mechanisms have been scantly investigated in dinoflagellates. Here, we compare the growth response of the well-studied diatom *Thalasiossira weissflogii* to that of dinoflagellates *Amphidinium carterae, Heterocapsa triquetra,* and *Symbiodinium tridacnidorum* to different iron conditions: (a) iron-replete medium, (b) iron-limited medium, and (c) iron-limited medium supplemented with the siderophore Deferoxamine B (DFB). Preliminary observations suggest that *A. carterae* is able to assimilate iron bound to DFB, in contrast to *T. weissflogii, H. triquetra,* and *S. tridacnidorum*. A survey of the transcriptome of *A. carterae* suggests that it possess genes analogous to the TonB-dependent receptors (TBDRs) associated with iron-siderophore transport in prokaryotes. Additional species of dinoflagellates will be observed to investigate the ubiquity of this strategy in dinoflagellates. A more comprehensive understanding of dinoflagellate acclimation to low iron conditions is key to understanding their ecophysiology and the biogeochemical dynamics of iron-limited regions.

P21 – A Laboratory Assay for Detecting Green Tide Toxicity. **Isabella Ares,** Danielle Moloney, Samantha Parsons & Lindsay Green-Gavrielidis. Department of Biology & Biomedical Sciences, Salve Regina University, Newport, RI 02840, USA. **(President's Award candidate)**

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 are producing harmful compounds by developing a standard laboratory assay using phytoplankton. This research is applicable to coastal cities throughout the United States that rely on beach tourism and local seafood which can be negatively impacted by macroalgal blooms. In these experiments, *Dunaliella tertiolecta* and *Skeletonema costatum* were exposed to field-collected *Ulva* bloom water at concentrations of 100% 50% and 20%. The treatment groups included *Ulva* bloom water and pasteurized *Ulva* bloom water (to eliminate marine viruses), along with natural seawater and artificial seawater controls. Spectrophotometry was used to measure the growth of *D. tertiolecta* and *S. costatum* via optical density and samples were fixed to quantify cell concentrations. Results showed that field-collected *Ulva* bloom water had a positive impact on the growth of *S. costatum* compared to controls in most trials. *Ulva* bloom water had a positive impact on the growth of *D. tertiolecta* compared to natural seawater controls, but not compared to the artificial seawater control in some trials.

P22 – Closely Related *Synechococcus* Strains from Narragansett Bay, Rhode Island Exhibit Differences in Viral Susceptibility. **Michael G. Briggs**[1], Cammi Mackenzie[2], Nathan A. Ahlgren[2] & Marcia F. Marston[1]. [1]Biology and Marine Biology, Roger Williams University, Bristol, Rhode Island, 02809 USA; [2]Biology, Clark University, Worcester, MA 01610, USA.

Synechococcus spp. are unicellular cyanobacteria that are important primary producers in Narragansett Bay (NB). During the summer, *Synechococcus* abundance in NB ranges from 10^4 to 10^5 cells/ml. The titer of viruses infecting *Synechococcus* spp. is also between 10^4 to 10^5 viruses/ml. To better understand how viruses influence cyanobacterial mortality, *Synechococcus* and sympatric viruses were isolated from five summer NB seawater samples. Based on ITS sequences, most NB *Synechococcus* strains, isolated via direct pour plating, fall within the CB4 and CB5 clades. Twenty-seven NB *Synechococcus* strains were then used in pairwise cross-infection assays with over 80 NB viral isolates to examine patterns of host susceptibility. For CB4 *Synechococcus*, susceptibility to viruses varied widely, even among isolates with identical ITS sequences. While some CB4 strains were susceptible to approximately 30% of the viruses, other cultures were resistant to all viruses in the assay. In contrast, *Synechococcus* strains in CB5 were generally more susceptible to viruses, capable of being infected by up to 70% of the viruses. Whole genome sequencing of the *Synechococcus* strains is now being conducted to examine how fine-scale genetic variations influence host susceptibility and resistance.

P23 – The Relationship Between Cell Count and Optical Density in Phytoplankton. **Megan Curran**, Kaylee Collins, Isabella Ares & Lindsay Green-Gavrielidis. Department of Biology and Biomedical Sciences, Salve Regina University, Newport, RI 02840, USA. **(President's Award candidate)**

Ulva is green alga that is found throughout Narragansett Bay, RI. Blooms of *Ulva* form due to excess anthropogenic nutrients. Although *Ulva* can be a food source for some animals, when it is in excess it can become toxic causing harmful side effects to marine life. Phytoplankton is a clear indicator of the effect of toxins on marine life. The phytoplankton *Dunaliella* and *Skeletonema* were grown in different concentrations of water samples, some with the presence or absence of *Ulva* blooms, or with lab created seawater in order to determine *Ulva* bloom toxicity. Samples from phytoplankton cultures were taken and individual cells were counted to determine the relationship between count and optimal density (measured via spectrophotometer). We expected cell counts patterns to track growth measured via optical density during the duration of the experiments (14–15 da.). This presentation will discuss our findings for both phytoplankton spp.

P24 – Cost Effective Methods for Analyzing Nitrate and Phosphate in Lake Samples. **Alana Modugno** & Dominique S. Derminio. Division of Natural Sciences and Mathematics, Keuka College, Keuka Park, NY 14478, USA.

Keuka College is a primarily undergraduate institution located on the shore of Keuka Lake. With limited research funding, the College's Center for Aquatic Research is seeking cost-effective nutrient analysis methods to determine nutrient run-off hotspots around the lake. Over the past few decades, Keuka Lake, in the Finger Lakes region of Upstate New York, has changed from an oligotrophic lake to a mesoligotrophic lake. With Keuka Lake becoming mesoligotrophic, more cyanobacterial harmful algal blooms have been identified in recent years. This can lead to ecological imbalances and water quality deterioration affecting Keuka Lake's ecosystem dynamics, lake eutrophication, and economic impacts on local towns. Here, potential cost-effective UV-Spectrophotometry methods were utilized for determining total nitrogen by second-derivative and soluble reactive phosphorus via molybdate blue. Future research will aim to validate the reliability of these methods and expand sampling potential hotspot sites across Keuka Lake to determine where excessive nutrient levels originate.

P25 – Cyanopodoviruses Infecting Clade I *Synechococcus* spp. Possess Unique Gene Sequences. **Michaela L. Johnson**, Michael G. Briggs & Marcia F. Marston. Biology and Marine Biology, Roger Williams University, Bristol, Rhode Island, 02906, USA. **(President's Award candidate)**

Synechococcus cyanobacteria are important primary producers in coastal marine environments and are phylogenetically diverse. Previous studies have identified over 20 clades of marine *Synechococcus* that differ in their geographic distribution and temporal patterns of abundance. In Southern New England, *Synechococcus* spp. in Clade 1 are dominant during the winter months and can be genetically placed into different subgroups. In this study, viruses were isolated from winter Narragansett Bay seawater using *Synechococcus* strains MV1320 and MV0917, which were isolated at the Martha's Vineyard Coastal Observatory and belong to different subgroups of Clade 1. We predict that *Synechococcus* in different subgroups will be susceptible to different viruses. To test this, dilutions of seawater were incubated with the *Synechococcus* strains. Interestingly, we were unable to isolate any viruses that infect *Synechococcus* MV0917. In contrast, over 30 viruses infecting *Synechococcus* MV1320 were isolated. Whole genome sequencing of a subset of these viruses found that they were all closely related podoviruses with identical structural genes, but they possessed highly variable tail-fiber genes. Metagenomic data will be used to examine if a relationship exists between the temporal patterns of abundance in Clade 1 *Synechococcus* spp. and the podoviruses characterized in this study.

P26 – An Evaluation of Planar Waveguide Biosensor for Detection of Cyanotoxins in Freshwater Systems. **Sydney Hall** & Gregory L. Boyer. Department of Chemistry, SUNY College of Environmental Science & Forestry, Syracuse, NY 13210, USA.

Cyanobacterial harmful algal blooms (cHABs) have negative impacts on ecological, economic, and human health due to biomass and cyanotoxin production. Current methods use indirect measures to determine if a HAB is present but they do not provide direct information on cyanotoxins, the main threat to human health. Standard analytical cyanotoxin detection methods can take a long time and require laboratory equipment. There is a need for a rapid, portable, multiplexed method for cyanotoxin detection. The LightDeck biosensor is a planar waveguide fluorescence-based immunoassay, that could potentially fill that gap. This biosensor can simultaneously detect microcystins, cylindrospermopsins, and saxitoxins. This research focused on evaluating the biosensor for accuracy of cyanotoxin measurement compared to standards and standard analytical methods.Quality assurance tests were run on the biosensor to determine its accuracy, precision, and linearity with certified standards. Field water samples from a wide variety of lakes, hypereutrophic, eutrophic, and mesoligotrophic, were analyzed for cyanotoxins by the biosensor in 2022 and 2023 to assess the application of the biosensor with natural samples. Overall, the LightDeck biosensor was determined to be a potential rapid screening method for analytical cyanotoxin detection methods that can be used to remove samples and prioritize others primarily for recreational water quality.