

***64th Northeast Algal Symposium,
Salem State University,
April 24-26, 2026***



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64th Northeast Algal Symposium

April 24–26, 2026

Salem State University, Salem, MA

Presidential Welcome

Dear Phycophiles,

Welcome to the 64th annual Northeast Algal Symposium (NEAS) and welcome (back) to the Witch City! We have an exciting scientific program including 12 student talks, 28 student posters, and a panel on *Evolving Ecosystems*. Kudos to the 2026 convenors (Lindsay Green-Gavrielidis, Thea Popolizio, Kristina Terpis, Eric Salomaki) for organizing what I'm confident will be an excellent meeting. I would also like to thank outgoing president Brian Wysor for his many years of service to the society.



I'm excited to see you all at the meeting and I hope you have a wonderful time! I look forward to our weekend full of #PhycologyWithoutApology! I have no doubt that we will soak in an abundance of phycological excellence during the scientific program, but let's also make sure this year's auction is a record-breaker!

Phycologically and presidentially yours,

Hannah Reich, NEAS President

Pre-Symposium Events & Welcome from your Co-Conveners

We are pleased to welcome you to the 64th Annual Northeast Algal Symposium, in Salem, MA. 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, an *Evolving Ecosystems* keynote panel highlighting diverse algal habitats, and vendors ready to share their equipment and products with you! We can't wait to see you at several pre-symposium activities on Friday, April 24th that will prime a weekend of rich phycological whimsy:

1. **From 4:00 – 6:00 PM**, pick up your registration materials in the lobby of the conference hotel (Hampton Inn Salem, 11 Dodge Street, Salem, MA). After you settle in, enjoy Salem and catch up with old and new friends alike. If you can't make it to the conference hotel during this window, never fear! Registration will be available at Salem State University's Ellison Campus Center on Saturday morning.

2. **From 6:00 PM on**, continue to enjoy your time in Salem, MA with colleagues and friends! We invite you to join us informally at the [Sea Level Oyster Bar](#) (94 Wharf Street, Salem, MA 01970; about a ten-minute walk from the hotel) to catch up over lovely views of Salem Harbor. Please note that this is a gathering spot only; **food and drinks will be at your own expense**.

Thank you to our generous sponsors!

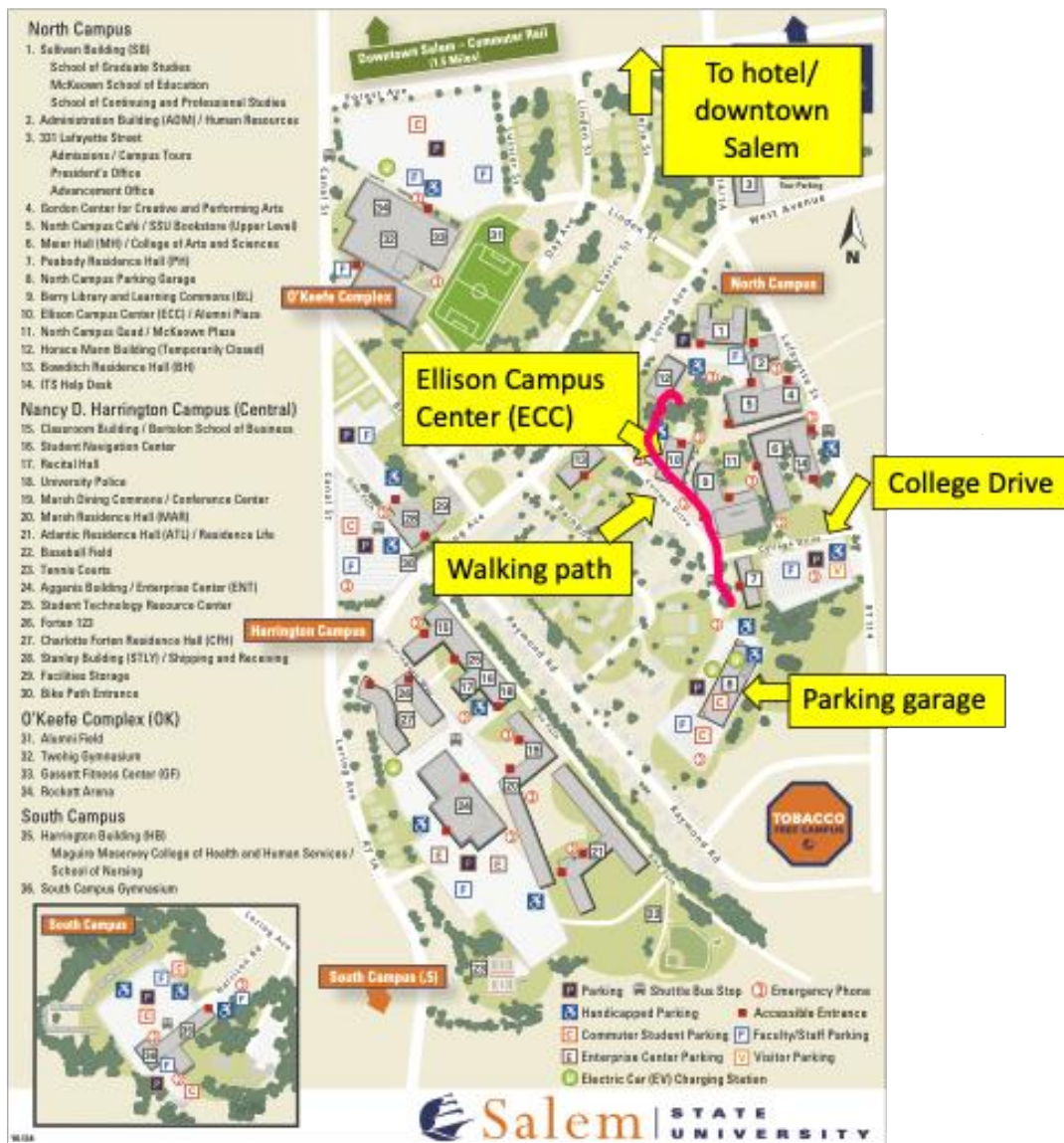
This year's meeting was made possible with the generous support of several organizations, including New England Biolabs, Inc., Nikon Instruments, Inc., and *Phycology Journal* published by BMC.



Salem State University Map

For your GPS, the address of campus is 352 Lafayette Street, Salem, MA 01970. The entrance to campus which will take you to the parking garage is on College Drive. After passing the Sophia Gordon Center (no. 4 on map) and Meier Hall (6) on your right, you will turn right onto College Drive from Lafayette Street. You will notice that this is right at the end of a construction area (Meier Hall addition, coming Fall 2027!). You will need to park in the parking garage (8 on the map). **Parking is free and does not require a parking pass.** To get there, drive down College Drive to the stop sign and take a left. From the parking garage, you can walk up College Drive, to Ellison Campus Center (10). The entrance is at the end of the “walking path” below.

Veteran’s Hall is on the second floor (the staircase is in front of you when you enter; there is an elevator to the right if you need it). You can download a campus map in [English](#) or [Spanish](#) here.



Salem State University Land Acknowledgement

The land occupied by Salem State University is part of Naumkeag, a traditional and ancestral homeland of the Pawtucket band of the Massachusett. We acknowledge the genocide and forced removal of the people of Naumkeag and their kin, and we recognize the ongoing colonization and dispossession of Indigenous homelands. We respect and honor the Massachusett tribe and the many Indigenous Peoples who continue to care for this land. We recognize our responsibility for the land we occupy and commit to continuously learning and sharing its history and that of the Massachusett and other Indigenous Peoples who have been and remain here. We commit to developing initiatives that work toward repairing ongoing injustices committed against the Indigenous Peoples of this land, and to making our environmental impact as sustainable as possible. We commit to a renewed and ongoing engagement with the Massachusett and all Indigenous Peoples in and around Salem State University. We recognize that Western science is not the sole authority on our natural world, and we commit to valuing Indigenous systems of knowledge and alternative perspectives vital to the future of our field.

Acknowledgements and Thanks

Many thanks to our judges: Ralph Christian Jones, Senjie Lin, Hilary McManus (Wilce Graduate Oral Presentation Award) Daniel Gossard, Rachael Wade, Sarah Princiotta (the President's Undergraduate Oral Presentation Award), Brian Wysor, Brandon O'Brien, Diba Khan-Bureau, (Trainor Graduate Poster Award), Gabrielle Kuba, Gordon Ober, Ursula Roese (President's Undergraduate Poster Award) and to all who volunteered to judge award presentations.

We appreciate our session moderators: Louise Lewis, John Wehr, Sarah Whorley, Stacy Krueger-Hadfield, Amanda Savoie, and of course, our well-seasoned auctioneer, Craig Schneider. We are grateful to Nick Bezio for designing our 2026 *Evolving Ecosystems* logo seen on the cover and on NEAS merchandise (p. 7). We hope our distinguished guests enjoy the impressive lineup of phycologists and the many fantastic presentations by students young and old — it should be an exciting meeting!

We thank our vendors for their auction donations and excellent deals on phycology décor and books: ***Scott Balogh, Balogh International Books, Nikon Instruments, Inc., and Phycology Journal published by BMC.***

Thanks also to Hamilton Hall, Robin Perry, and Vinwood Catering for a delicious banquet in a stunning setting. Finally, we thank the NEAS membership and all symposium participants and guests, whose ideas, fellowship and camaraderie make this annual event one that we all look forward to each year.

Your friendly symposium conveners,

Lindsay, Thea, Eric & Kristina

Support NEAS and get great gear!

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, 2021–2024. 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/>.

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



Virtual Attendance

Available times, all Eastern Standard Time:
Saturday, 8:15 AM-Noon, 1:15–2:15 PM, 3:45-5:45 PM
Sunday, 8:25 –12:15 PM

Join Zoom Meeting

<https://saalemstate.zoom.us/j/85893407299?pwd=jYJ5FLOdij3ElQ1JOt2vhngDDUOKuo.1>

Meeting ID: 858 9340 7299
Passcode: NEAS2026\$

Contact [Lindsay Green-Gavrielidis](#) for issues!

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/hosts.

Special Symposium on Evolving Ecosystems

We are excited to host a panel of scientists who will share their experiences working in **Evolving Ecosystems**. Our esteemed guests will discuss their research across a range of habitats — from Arctic environments and freshwater systems to living shoreline restoration projects. A facilitated panel discussion will follow, opening the floor for your questions. This is your chance to engage directly with our speakers about their work.

Jarrett Byrnes, Ph.D.

Associate Professor of Biology, University of Massachusetts Boston

Dr. Jarrett Byrnes is an Associate Professor of Biology at the University of Massachusetts, Boston. His lab ([CELP](#)), uses coastal ocean systems to explore questions related to the causes and consequences of change in biodiversity. In particular, the lab focuses on coastal urban ecosystems, nature-based solutions to sea level rise, and kelp forest ecosystems. Byrnes is a member of the Stone Living Lab, which recently installed three Living Seawalls here in Boston Harbor. Jarrett's *Evolving Ecosystems* presentation is entitled, ***Living Seawalls in Massachusetts: If You Build It, Who Will Come?***



Amanda Savoie, Ph.D.

*Research Scientist and Section Head, Botany
Canadian Museum of Nature, Ottawa, Canada*

Dr. Amanda Savoie's interest in seaweeds began as an undergraduate at the University of New Brunswick, where she took a marine field course set amongst the extensive intertidal zones of the Bay of Fundy. She pursued a PhD at the same institution in the Saunders Lab, focused on species diversity, taxonomy, and systematics of the red algal family Rhodomelaceae. After completing her doctorate, Amanda joined the Canadian Museum of Nature in Ottawa, home to the National Herbarium of Canada. In 2022, she launched a project to study seaweed diversity in the cold Arctic waters around Cambridge Bay, Nunavut, in Canada's central Arctic region. She enjoys the challenges of Arctic work, including SCUBA diving in freezing waters, and is contributing to a long history of Arctic botanical and phycological work at the museum. Amanda's *Evolving Ecosystems* presentation is entitled, ***Seaweeds in the Arctic: Baseline Studies and Biodiversity Patterns in a Changing Environment.***



Morgan L. Vis, Ph.D.

Professor, Department of Environmental and Plant Biology

Associate Dean, College of Arts and Sciences, Ohio University

Dr. Morgan L. Vis knew that she had found the organisms she wanted to study after taking a summer freshwater algae at the W.K. Kellogg Biological Station taught by Professor Brian Moss. She pursued an undergraduate independent project with Dr. Bob Sheath and then continued to study freshwater red algae for her MS (University of Rhode Island) and PhD (Memorial University of Newfoundland) degrees. She started her own laboratory at Ohio University in 1996 developing two foci – ecology and systematics of freshwater red algae and the use of algae for stream biomonitoring. Throughout the years, her research group has conducted studies of algae in local streams collecting physical, chemical, and biological data. One stream with a large population of *Batrachospermum gelatinosum* has been visited regularly for over 15 years. Recently, the lab has used a combination of historical herbarium records and contemporary collections for floristics studies that have yielded insights regarding changes in stream habitats. Morgan's *Evolving Ecosystems* presentation is entitled, ***Freshwater Ecosystems: Red Algae in Times of Change.***



NEAS Executive Committee

President: Hannah Reich (2026 – 2028)

Past President: Brian Wysor (2024 – 2026)

Treasurer: Lindsay Green-Gavrielidis (2023 – 2027)

Secretary: Sarah Princiotta (2022 – 2027)

Membership Director: Kristina Terpis (2025 – 2029)

Nominations: Diba Khan-Bureau (2025 – 2027)

Science Communications: Sarah Whorley (chair – 2024-2027)

Members at Large: Ken Karol (2023 – 2026); *Vacant*

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

Publications Committee: *Vacant*

Website: Chris Neefus

2024 Conveners: Brian Wysor, Lindsay Green-Gavrielidis, Craig Schneider

2025 Conveners: Hannah Reich, Hilary McManus, Ken Karol, Karolina Fučíková, Dominique Derminio

2026 Conveners: Lindsay Green-Gavrielidis, Thea Popolizio, Eric Salomaki, Kristina Terpis

2027 Conveners: *Vacant*

Please Join NEAS Executive Committee!

We will hold an election during the meeting for vacant and outgoing positions. Nominations for **Vice President, Member-At-Large, and Nominations Chair** are currently being accepted. Please contact [Diba Khan-Bureau](#) to nominate yourself or a colleague today! You can read more about each position in the [NEAS Officers Manual](#).

Program Overview

Friday, April 24, 2026

Time	Event	Location
4:00–6:00 PM	Registration	Hampton Inn Salem
6:00 PM	Friday night social	Sea Level Oyster Bar

Saturday, April 25, 2026

Time	Event	Location
7:30–8:00 AM	Poster Set-Up & Auction Donations	Ellison Campus Center Salem State University
<i>Coffee and light snacks will be available.</i>		
7:30–10:00 AM	Registration & Auction Donations	Veteran's Hall, Ellison Campus Center
8:15 – 8:30 AM	Presentation Upload Welcoming Remarks	Veteran's Hall, Ellison Campus Center
8:30–10:00 AM	<i>Session 1</i> Student Award Talks 1	Veteran's Hall, Ellison Campus Center
10:00–10:30 AM	Break <i>Visit our Vendors!</i>	Veteran's Hall, Ellison Campus Center
10:30–12:00 PM	<i>Session 2</i> Student Award Talks 2	Veteran's Hall, Ellison Campus Center
12:00–1:15 PM	Lunch Break, <i>Executive Committee Meeting</i>	Veteran's Hall, Ellison Campus Center
1:15 – 2:15 PM	<i>Session 3</i> Student Award Talks 3	Veteran's Hall, Ellison Campus Center
2:15 – 3:45 PM	Poster Session	Ellison Campus Center
3:45 – 5:45 PM	<i>Special Symposium: Evolving Ecosystems</i> Panel	Veteran's Hall, Ellison Campus Center
5:45 – 7:00 PM	Break	
7:00 – 10:00 PM	NEAS Annual Banquet & Student Benefit Auction <i>Plated Dinner Service begins at 7:15 pm</i>	Hamilton Hall, 9 Chestnut Street, Salem, MA

Sunday, April 26, 2026

Time	Event	Location
8:00 – 10:00 AM	Registration	Veteran's Hall, Ellison Campus Center
8:15 – 8:30 AM	Presentation Upload Morning Announcements	Veteran's Hall, Ellison Campus Center
<i>Coffee and light snacks will be available.</i>		
8:30 – 10:00 AM	<i>Session 4</i> Contributed Talks 1	Veteran's Hall, Ellison Campus Center
10:00 – 10:15 AM	Break	Veteran's Hall, Ellison Campus Center
10:15 – 11:45 AM	<i>Session 5</i> Contributed Talks 2	Veteran's Hall, Ellison Campus Center
11:45– 12:15 PM	Lightning Talks	Veteran's Hall, Ellison Campus Center
12:15 – 1:00 PM	Business Meeting <i>Pick up boxed lunch, if you ordered</i>	Veteran's Hall, Ellison Campus Center

Departure: See you all next year!

For those of you who did not order a boxed lunch, you can grab a bite at numerous restaurants in Salem on your way out. For delicious sandwiches, we recommend [A&J King](#) (the 48 Central Street location is open on Sundays) or [The Babe](#) (268 Washington Street). For excellent pizza, [Bambolina](#) (288 Derby Street), and for fresh seafood, [Turner's Seafood](#) (43 Church Street). If you are inclined to enjoy some local oysters, look for some from our North Shore oyster farmers, [Great Marsh Shellfish Company](#) (Ducky Doyles and River Babe Select)!

General Program: 64th Northeast Algal Symposium, Salem, Massachusetts

Friday, April 24, 2026

4:00 – 6:00 PM *Evening Registration, Hampton Inn Salem, 11 Dodge Street*
6:00 PM – *Friday Night Social, [Sea Level Oyster Bar](#), 94 Wharf Street*
(food and drinks will be at your own expense)

Saturday, April 25, 2026

7:30 – 8:00 AM **Poster Set-up & Auction Donations**
Ellison Campus Center (ECC)
Poster setup for Student Awards Competition Ellison Campus Center
Session I speakers load ppts, Veteran's Hall, ECC Second Floor

7:30 – 10:00 AM ***Morning Registration***
Veteran's Hall, ECC Second Floor

8:15 – 8:30 AM **Welcome and Opening Remarks**
Meeting Co-conveners
 Veteran's Hall, ECC Second Floor

SESSION I ***Student Award Talks 1 – Moderator, Louise Lewis***
Veteran's Hall, ECC Second Floor

8:30 – 8:45 AM *President's Award Candidate*
Comparing *Gracilaria vermiculophylla* epibiota across ecological scales.
Isabel C. Volden, Guido Bonthond, Alexander D. Geragotelis, Stacy A. Krueger-Hadfield. (Abstract 1, p. 22)

8:45 – 9:00 AM *President's Award Candidate*
Phylogenetic Analysis of Novel Chrysophyte Isolates.
Sophia Millhouse, Michael Rose, Jack Holt, and Sophie Charvet. (Abstract 2, p. 22)

9:00 – 9:15 AM *President's Award Candidate*
Unraveling Species Diversity in the Red Algal Genus *Hypnea* in Bermuda.
Olivia R. Davis & Thea R. Popolizio (Abstract 3, p. 22)

9:15 – 9:30 AM *President's Award Candidate*
Bioluminescent dinoflagellate *Pyrodinium bahamense* and diatom abundance across four bays in Vieques, Puerto Rico. **Emily Grzywacz**, Genevieve Dallmeyer-Drennen, Hannah Reich. (Abstract 4, p. 23)

- 9:30 – 9:45 AM** *Wilce Award Candidate*
Assessing the Functionality of Plant Protein Homologues in Brown Algae Using Molecular Docking. Mary Biggs & Jennifer Fletcher. (Abstract 5, p. 23)
- 9:45 – 10:00 AM** *Wilce Award Candidate*
Seaweed (*Ulva*, *Gracilaria*) significantly increases the growth rates of North Atlantic oysters, scallops, and clams in an aquaculture setting. Christopher J. Gobler, Craig S. Young, Laine H. Sylvers, Ujjal Banik, Dongkyu Seo, Michael H. Doall (Abstract 6, p. 24)
- 10:00 – 10:30 AM** **Coffee Break**
Veteran's Hall, ECC Second Floor
Session II speakers load presentations
- SESSION II** **Student Award Talks 2 – Moderator, Stacy Krueger-Hadfield**
Veteran's Hall, ECC Second Floor
- 10:30– 10:45 AM** *Wilce Award Candidate*
Applying Biogeochemical Niche Theory and Elementomes Approaches to Understand Cnidarian-Symbiodiniaceae Compatibility and Coevolution. Stefan Anthopoulos & Hannah Reich. (Abstract 7, p. 24)
- 10:45 – 11:00 AM** *Wilce Award Candidate*
Comparing thermal tolerance of sugar kelp (*Saccharina latissima*) gametophyte populations across the Gulf of Maine. Phoebe Churney, Sara Lacourciere, Adam St. Gelais, Samantha Smith, Shane Farrell, Damian Brady. (Abstract 8, p. 25)
- 11:00 – 11:15 AM** *Wilce Award Candidate*
Rethinking Apicomplexan Symbiosis: Horizontal Gene Transfer in *Nephromyces*. Peace Uche, Christopher Lane, Laura Eme. (Abstract 9, p. 25)
- 11:15 – 11:30 AM** *Wilce Award Candidate*
Determining ploidy and clonality in *Chlamydomonas* sp. via single cell genetics. Alexander Geragotelis, Trinity Hamilton, Robin Kodner, Lucie Mieuzet, Honu Pata, Solenn Stoeckel, Stacy Krueger-Hadfield (Abstract 10, p. 26)
- 11:30 – 11:45 AM** *Wilce Award Candidate*
Cross-scale functional trait analysis of *Ascomyces nodosum* in the Gulf of Maine. Marcella Heineke & David Kimbro (Abstract 11, p. 26)
- 11:45 – 12:00 PM** *Wilce Award Candidate*
Examination of Molgulid tunicate egg cells infected with *Nephromyces*. Marissa Mehrlrose & Christopher Lane. (Abstract 12, p.26)

12:00 – 1:15 PM	Lunch Veteran's Hall, ECC Second Floor Executive Committee Meeting/Lunch Ellison Campus Center <i>Session III speakers load presentations</i>
SESSION III	Student Award Talks 3 – Moderator, Sarah Whorley Veteran's Hall, ECC Second Floor
1:15 – 1:30 PM	<i>Wilce Award Candidate</i> Fine scale resolution of zooxanthellae cell wall composition and its potential role in regulating endo-symbiosis. <u>Clancy McIntyre</u> , Charles T Anderson, Hong Ma, Todd LaJeunesse (Abstract 13, p. 27)
1:30 – 1:45 PM	Who's the Dad? Paternity analyses in <i>Gracilaria vermiculophylla</i> reveal mating system dynamics. <u>Sarah L. Allen</u> & Stacy A. Krueger-Hadfield. (Abstract 14, p. 27)
1:45 – 2:00 PM	How does competition perturb cell crosstalk among phycosphere associated bacteria? <u>Genevieve Dallmeyer-Drennen</u> , Emma Healey, Hannah G. Reich. (Abstract 15, p. 28)
2:00 – 2:15 PM	Life cycle, interrupted: the ecological genetics of the invasion of soft bottom habitats. <u>Sophia V. Tearman</u> & Stacy A. Krueger-Hadfield. (Abstract 16, p. 28)
SESSION IV	Poster Session Ellison Campus Center
2:15 – 3:00 PM	<i>Poster Session A</i> Odd numbered posters
3:00 – 3:45 PM	<i>Poster Session B</i> Even numbered posters
SESSION V	Special Symposium: Evolving Ecosystems – Moderators Lindsay Green-Gavrielidis & Thea Papolizio Veteran's Hall, ECC Second Floor
3:45 – 4:10 PM	<i>Panel Talk 1</i> Living Seawalls in Massachusetts: If You Build It, Who Will Come? <u>Jarrett Byrnes</u>
4:10 – 4:35 PM	<i>Panel Talk 2</i> Seaweeds in the Arctic: Baseline Studies and Biodiversity Patterns in a Changing Environment. <u>Amanda Savoie</u>

- 4:35 – 5:00 PM** *Panel Talk 3*
Freshwater Ecosystems: Red Algae in Times of Change. Morgan Vis
- 5:00 – 5:45 PM** *Panel Time and Questions*
- 5:45 – 7:00 PM** *Break*
- 7:00 – 10:00 PM** ***Annual Banquet, Awards & Live Auction***
Hamilton Hall, 9 Chestnut Street, Salem, MA

Sunday, April 26, 2026

- 8:00 – 10:00 AM** ***Morning Registration & Coffee***
Veteran's Hall, ECC Second Floor
Session VI speakers load presentations, Veteran's Hall, second floor
- 8:25 – 8:30 AM** ***Morning Announcements***
- SESSION VI** ***Contributed Papers 1 – Moderator, John Wehr***
Veteran's Hall, ECC Second Floor
- 8:30 – 8:45 AM** Reprogramming Microalgal Carbon Flux via ZnO Nanoparticle–Induced Redox Modulation: A Systems-Level Framework for Optimized Biofuel Production. Luis Pablo Salmeron, Covarrubias, Kavitha Beluri, Hamidreza Sharifan (Abstract 17, p. 29)
- 8:45 – 9:00 AM** Reproductive mode variation in benthic and pelagic *Sargassum*: Monoecy and clonality shape population structure. Danielle C. Hatt, Frédérique Viard, Didier Aurelle, Marion Ballenghien, Edwin Cruz-Rivera, Ligia Collado-Vides, and Stacy A. Krueger-Hadfield. (Abstract 18, p. 29)
- 9:00 – 9:15 AM** Using 50 years of algal composition data to evaluate drivers of ecosystem shifts in Skaneateles Lake. Dominique S. Derminio, Rich Abbott, Liam Hawes, Christine Georgakakos, and Stephen Shaw. (Abstract 19, p. 30)
- 9:15 – 9:30 AM** Stoichiometric relationships provide insight to periphyton biomass increases due to road salt pollution. Sarah B. Whorley, Jeffrey J. Law, John D. Wehr, Jeffrey S. Heilveil. (Abstract 20, p. 30)
- 9:30 – 9:45 AM** Reproductive consequences of upper thermal thresholds for northwest Atlantic *Alaria esculenta* microscopic stages. Daniel J. Gossard, Charles Yarish, Scott Lindell. (Abstract 21, p. 31)
- 9:45 – 10:00 AM** Determining seasonal shifts in coastal phytoplankton abundance and community composition in a warming Gulf of Maine. Patricia Thibodeau, Terrance Meinardus, Emma Hutchings, Erin Anderson. (Abstract 22, p. 31)

- 10:00 – 10:15 AM** **Coffee Break**
 Ellison Campus Center
Session VII talk and Lightning Talks load ppts
- SESSION VII** ***Contributed Papers 2, Lightning Talks, & Business Meeting*– Moderator, Amanda Savoie**
 Veteran’s Hall, ECC Second Floor
- 10:15 – 10:30 AM** Random Forests and not-so-random kelp beds: remote sensing suggests that depth and species affect habitat resilience. **Constance N. Tyler**, Kim Lowell, Christopher E. Parrish, & Jennifer A. Dijkstra. (Abstract 23, p. 32)
- 10:30 – 10:45 AM** Latitudinal patterns of genetic diversity in Western Antarctic macroalgae. **Ana I. Tavares**, Charles D. Amsler, Magaret O. Amsler, Stacy A. Krueger-Hadfield. (Abstract 24, p. 32)
- 10:45 – 11:00 AM** Cilia Gene Expression in *Chlamydomonas reinhardtii*: Forward and Reverse Genetics Approaches. **Jason M. Brown**. (Abstract 25, p. 33)
- 11:00 – 11:15 AM** Exploring Mitochondrial Genome Diversity in Eustigmatophyte Algae. **Kristina X. Terpis**, Dovilė Barcytė, Marek Eliáš, Christopher E. Lane. (Abstract 26, p. 33)
- 11:15 – 11:30 AM** The Articulated Coralline Genus *Corallina* (Florideophyceae, Corallinales) as a Model for Evolution & Biogeography: Updates & Current Research. **Rachael Wade**. (Abstract 27, p. 34)
- 11:30 – 11:45 AM** Nutrient limitation mediates the susceptibility of a coccolithophore to a bacterial quorum sensing signal precursor. **Hannah G. Reich**, Maggie E. Straight, Marley Gonsalves, Anais Gentilhomme, Amanda Platt, Kristen E. Whalen, Brook Nunn, Julia Kubanek, Elizabeth L. Harvey. (Abstract 28, p. 34)
- 11:45 – 12:15 PM** ***Lightning Talks***
 Veteran’s Hall, ECC Second Floor
- 12:15 – 1:00 PM** ***Annual NEAS Business Meeting* – Hannah Reich, President**
 Veteran’s Hall, ECC Second Floor
Boxed-lunches available if ordered for the business meeting

For those of you who did not order a boxed lunch, you can grab a bite at numerous restaurants in Salem on your way out. For delicious sandwiches, we recommend [A&J King](#) (the 48 Central Street location open on Sundays) or [The Babe](#) (268 Washington Street). For excellent pizza, [Bambolina](#) (288 Derby Street), and for fresh seafood, [Turner’s Seafood](#) (43 Church Street). If you are inclined to enjoy some local oysters, look for some from our North Shore oyster farmers, [Great Marsh Shellfish Company](#) (Ducky Doyles and River Babe Select)!

Poster Presentations

President's Award Posters (see p. 40, for additional President's poster abstract, **P27**)

P1 – Assessing concentration and purification methods of *Palmaria palmata* tetraspores through flow cytometry. **Stella Defibaugh**, Nicole Poulton, Laura Lubelczyk, Thew Suskiewicz. (Abstr. 1 p. 35)

P2 – Biomagnification of cyanotoxins in an experimental food web. **Aramis Rosario González**, Elizabeth Carroll, & Sarah Princiotta. (Abstr. 2 p. 35)

P3 – Using Diatoms to Infer Paleoenvironmental Conditions in a Connecticut Vernal Pool. **Lily Bentley**, Diba Khan-Bureau, Will Ouimet. (Abstr. 3 p. 36)

P4 – Differential Expression of Receptors involved in Prey Detection Under nutrient limitation in the Mixoplankton *Cymbomonas tetramitiformis*. **Thomas Morahan** & Sophie Charvet. (Abstr. 4 p. 36)

P5 – Molecular Interactions between Maine Mixoplankton and their Bacterial Prey. **Matthew J. Crawford** & Sophie Charvet. (Abstr. 5 p. 37)

P6 – “Snapshot” Analysis of Abiotic Drivers of Harmful Algal Blooms on Two Dimictic Lakes. **Youssef Amin** & Sarah Princiotta. (Abstr. 6 p. 37)

P7 – Investigating Potential Environmental Influence on Molgulidae tunicates and their Apicomplexan Endosymbionts *Nephromyces*. **Anna Jasinski**, Peace Uche, Kristina Terpis, Christopher Lane. (Abstr. 7 p. 38)

P8 – The Effects of Salinity and pH Change on Algal Biodiversity Within Streams. **Grace Covey** & Sarah Whorley. (Abstr. 8 p. 38)

P9 – Seasonal Water Chemistry Influences on Algal Assemblages. **Bridget Thornton**, Derrick Swartz, & Sarah Whorley. (Abstr. 9 p. 39)

P10 – Herbivory Preferences of *Littorina littorea* on Invasive Versus Native Macroalgae. **Chloe Leano**, **Hannah Siegmund**, and Lindsay Green-Gavrielidis. (Abstr. 10 p. 40)

P11 – Impacts of High and Low Light Intensities on Chlorophyll pigments found in *Ulva sp.* **Cameron Boyko** & Brandon S. O'Brien. (Abstr. 11 p. 40)

P12 – Comparative Analysis of Protocols for Generating Aposymbiotic Anemones (*Exaiptasia*). **Nicole Spar**, Stefan Anthopoulos, Hannah Reich. (Abstr. 12 p. 40)

P13 – Using *Chlamydomonas reinhardtii* to Study Cilia Gene Regulation. **Emily Wassouf**, **Hayley Mello**, and Jason M. Brown. (Abstr. 13 p. 41)

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P33 – Macroalgal diversity of Virginia’s Eastern Shore: Preliminary findings and the southernmost population of *Grateloupia turuturu*? Brandon S. O’Brien, Cameron Boyko, Maddison Moser. (Abstr. 33 p. 51)

ABSTRACTS

Oral Presentation Abstracts

1 – Comparing *Gracilaria vermiculophylla* epibiota across ecological scales. Isabel C. Volden^{1, 2}, Guido Bonthond³, Alexander D. Geragotelis², Stacy A. Krueger-Hadfield². ¹William & Mary, Williamsburg, VA, USA ; ²Virginia Institute of Marine Science Eastern Shore Laboratory, Wachapreague, VA, USA ; ³Institute for Chemistry and Biology of the Marine Environment (ICBM), Carl von Ossietzky Universität Oldenburg, Oldenburg, Germany. Across eukaryotes, there is a tremendous diversity of life cycles. Yet, we lack a mechanistic understanding of the factors influencing the evolutionary maintenance of this diversity. The haploid-diploid red macroalga *Gracilaria vermiculophylla* has colonized soft bottom habitats where algal spores cannot easily grow. Despite morphological similarity, the haploid phase (the gametophyte) of the life cycle is lost. Recent work in the lab has identified phenotypic differentiation among male gametophytes, female gametophytes, and diploid sporophytes, including differences in their associated microbial communities. We sampled *Gracilaria vermiculophylla* thalli from sites along the Delmarva Peninsula. Using amplicon sequencing, we characterized their epibiota to analyze how microbial communities vary across different life cycle phases and ecological conditions, such as salinity gradients. Identifying the baseline microbial compositions under these differing conditions will therefore allow for future experimental manipulation to fully investigate the role of microbes in this alga's invasion and altered life cycle.

2 – Phylogenetic Analysis of Novel Chrysophyte Isolates. Sophia Millhouse, Michael Rose, Jack Holt, and Sophie Charvet. (President's Award candidate)

Mixoplankton are suspected of playing a very important role in aquatic food webs and biogeochemical cycles but remain understudied due to the difficulties inherent to *in situ* surveys. We therefore sought to obtain new cultures of freshwater mixoplankton in an effort to increase our ability for empirical investigations. Two flagellates were isolated from a retention pond in central Pennsylvania, and determined to be chrysophytes through morphological identification. Phylogenetic examination, using a long-read rRNA fragment (~4000 bp) covering the 18S, ITS and 28S rRNA regions, further revealed that these isolates appear to branch with *Chlorochromonas danica*. Moreover, one of these chrysophyte isolates was observed as it consumed a bacterium and both isolates were perceived to have bacteria in their food vacuoles, suggesting a capacity for mixotrophy. These new cultures will be valuable as model organisms for the study of freshwater mixoplankton ecology, behavior, and phylogenetics.

3 – Unraveling Species Diversity in the Red Algal Genus *Hypnea* in Bermuda. Olivia R. Davis & Thea R. Popolizio. Biology, Salem State University, Salem, MA, 01970, U.S.A. (President's Award candidate)

The genus *Hypnea* (Rhodophyta) is widely distributed across tropical and subtropical waters, yet accurate taxonomy remains challenging in many regions due to extensive morphological plasticity and the prevalence of cryptic species that can only be distinguished with DNA sequencing. In Bermuda, historical records are limited and genetically unconfirmed, suggesting that true species diversity remains underreported. Using a DNA barcoding approach, we are

developing molecular datasets (COI-5P; *rbcL*) for *Hypnea* collected in Bermuda, St. Croix (USVI), and the Florida Keys. We pair these with morphological comparisons across molecular clades to establish a robust framework for species delimitation. By analyzing relationships among Bermuda specimens, and comparing them with relevant taxa from other regions, we will refine species boundaries and improve understanding of the diversity and evolutionary history of *Hypnea* in Bermuda and the broader tropical northwestern Atlantic.

4 – Bioluminescent dinoflagellate *pyrodinium bahamense* and diatom abundance across four bays in Vieques, Puerto Rico. Emily Grzywacz, Genevieve Dallmeyer-Drennen, Hannah Reich. (President’s Award candidate)

Pyrodinium bahamense is a dinoflagellate responsible for bioluminescent bays, a major ecotourism attraction in Vieques, Puerto Rico. In the wake of Hurricane Maria, Vieques's bioluminescence was extinguished by wind and fresh water that destroyed mangroves, seagrasses, and *P. bahamense* populations in the water column. *P. bahamense* has two distinct life history stages. Motile *P. bahamense* cells, armored with thecal plates, are found throughout the water column and are responsible for the well-known bioluminescence. A cyst stage can be found in the sediment, a non-motile cell that germinates under favorable conditions. Understanding the distribution of *P. bahamense* in both stages is important as the frequency and severity of hurricanes increases, especially because cyst ‘seed banks’ have been implicated in the resilience of future blooms. This study investigates the density of *P. bahamense* across four bays in Vieques: Mosquito Bay, Media Luna, Sun Bay, and Puerto Ferro. Samples were collected from the water column and the sediment, which were further classified as sandy, seagrass-associated, or mangrove-associated substrates. Abundance data was calculated using flow cytometry. We also noted the presence of diatoms, other significant bloom-forming phytoplankton, as they likely compete for resources with *P. bahamense*. Further work is being done to establish image analysis protocols to characterize *P. bahamense* by life stage, including differentiating between motile and vegetative cells in the water column based on morphology. Our results show that *P. bahamense* is found in the water column and sediments across our sampling sites, and additionally the abundance of cysts is correlated with the presence of mangroves and seagrasses. Given the ecological and economic significance of the island's bioluminescent bays, our results may provide valuable insights for local organizations seeking to understand and conserve the future distribution of this vital dinoflagellate species, especially considering increased hurricane frequencies associated with climate crisis projections.

5 – Assessing the Functionality of Plant Protein Homologues in Brown Algae Using Molecular Docking. Mary Biggs^{1,2} & Jennifer Fletcher^{1,2}. ¹Plant and Microbial Biology, University of California, Berkeley, CA 94720, U.S.A.; ²USDA-ARS, Plant Gene Expression Center, Albany, CA 94710, U.S.A. (Wilce Award candidate)

The class Phaeophyceae, colloquially known as brown algae (BA), comprises hundreds of pharmaceutically, culinarily, and energetically valuable species. The rapid release of aquaculture technologies and sequenced genomes has generated high interest in elucidating the biochemistry and molecular biology of these organisms; however, while tens of thousands of protein crystal structures are available for plants and animals, there are only thirteen

available for brown algae. As a result, there is a pressing need for innovative methods to study novel BA proteins without crystal structures. Here, we have designed a pipeline for the identification of putative ligand-binding BA proteins based on homology to canonical protein receptors followed by prediction of ligand binding using molecular docking and molecular dynamics. This method leverages technologies well-established in drug design applications to assess the ligand-binding activity of BA proteins predicted to be orthologous to metabolically active plant proteins. This workflow provides a valuable precursor to in vitro and in vivo examinations and allows for the elucidation of potential molecular mechanisms of protein activity.

6 – Seaweed (*Ulva*, *Gracilaria*) significantly increases the growth rates of North Atlantic oysters, scallops, and clams in an aquaculture setting. Christopher J. Gobler¹, Craig S. Young¹, Laine H. Sylvers¹, Ujjal Banik¹, Dongkyu Seo¹, Michael H. Doall¹. ¹School of Marine and Atmospheric Science, Stony Brook University, Southampton, NY, 11968, U.S.A. (Wilce Award candidate**)**

Bivalve populations are threatened by environmental stressors, including acidification and hypoxia. The seaweed can raise the pH and dissolved oxygen (DO) levels in seawater, thereby mitigating these stressors. This study examined three commercially important North Atlantic bivalves (Eastern oysters, *Crassostrea virginica*; hard clams, *Mercenaria mercenaria*; bay scallops, *Argopecten irradians*) that were grown in the presence and absence of *Ulva* and *Gracilaria*. Environmental conditions, including pH, DO, and chlorophyll a, were continuously monitored, and DIC levels and the complete carbonate chemistry of seawater were quantified. The presence of seaweeds significantly increased shell- and tissue-based growth rates of oysters by 20–70%, of clams by 60–70%, and of scallops by 130–140% ($p < 0.05$), with both seaweeds being similarly effective. Both seaweed species caused significant increases in pH, DO, and the saturation state of calcium carbonate (Ω) during the day ($p < 0.05$), whereas differences at night were muted, with nighttime aragonite Ω levels at or below saturation in all treatments. The presence of seaweed caused a significant increase in chlorophyll a concentration, which indicates that seaweed increased the total amount and diversity of food available to bivalves. This study suggests that co-culturing seaweed with bivalves can significantly accelerate bivalve growth.

7 – Applying Biogeochemical Niche Theory and Elementomes Approaches to Understand Cnidarian-Symbiodiniaceae Compatibility and Coevolution. Stefan Anthopoulos & Hannah Reich. Department of Environmental Biology, SUNY College of Environmental Science and Forestry, Syracuse, NY 13210, U.S.A. (Wilce Award candidate**)**

The compatibility between cnidarians and their endosymbiotic algae Symbiodiniaceae is fundamental to the persistence of coral reefs. Coevolved mechanisms of metabolic cooperation likely underlie coral-algae compatibility, yet our understanding of the nutritional requirements of hosts and symbionts in coevolutionary pairings, especially the balance and exchange of macronutrients and trace metals simultaneously, is limited. This work uses elementome profiling to characterize the biogeochemical niches of Symbiodiniaceae and the model anemone *Exaiptasia pallida*. Specifically, it investigates the capacity for macronutrient and trace-metal exchange between hosts and symbionts and how species and strains occupy and

interact with their respective biogeochemical niches across coevolved and non-coevolved pairings. I will preview my dissertation research that will integrate host-symbiont combinations with physiological metrics and elementome analyses to quantify how metabolic cooperation supports holobiont resilience and assess how species- and strain-specific biogeochemical niche spaces shift under temperature and nutrient stress. This work will reveal how cohabitation reshapes resource uptake strategies and the extent to which metabolic cooperation promotes holobiont resilience in *Exaiptasia* from the standpoint of different evolutionary distances from a coevolved symbiont. These findings will inform coral reef management strategies and provide a framework applicable to other host-algae symbioses.

8 – Comparing thermal tolerance of sugar kelp (*Saccharina latissima*) gametophyte populations across the Gulf of Maine. Phoebe Churney¹, Sara Lacourciere², Adam St. Gelais², Samantha Smith¹, Shane Farrell¹, Damian Brady^{1,2} ¹School of Marine Sciences, University of Maine, Darling Marine Center, Walpole, Maine. ²Aquaculture Research Institute, University of Maine, Darling Marine Center, Walpole, Maine. **(Wilce Award candidate)**

Rapidly warming waters in the Gulf of Maine (GOM) are threatening ecologically and commercially valuable rocky reef ecosystems. *Saccharina latissima* (sugar kelp), a dominant brown alga in these habitats and one of the most widely farmed kelp species in North America, is vulnerable to elevated temperatures and marine heatwaves. This project aims to investigate whether thermal tolerance differs across sugar kelp populations in Maine by conducting temperature challenge experiments. Sorus tissue was collected from field sites that span a range of thermal regimes to establish gametophyte biobanks, safeguarding genetic diversity for farmers and researchers. Gametophytes will be exposed to various heat stress tests to determine heat-tolerance and other sub-lethal physiological responses. Experimental treatments include temperatures corresponding to historical seasonal averages and to the elevated intensities of marine heatwaves. The results of these experiments will provide insight into the persistence of wild kelp populations and provide critical knowledge for restoration and aquaculture strategies, while offering broader insight into how marine foundation species may adapt – or fail to adapt – to ocean warming.

9 – Rethinking Apicomplexan Symbiosis: Horizontal Gene Transfer in *Nephromyces*. Peace Uche¹, Christopher Lane¹, Laura Eme¹, ¹Department of Biological Sciences, University of Rhode Island, Kingston RI, USA. **(Wilce Award candidate)**

The phylum Apicomplexa consists of >5000 unicellular eukaryotes that were thought to be exclusively parasitic. However, the discovery of a commensal lineage, *Nephromyces*, challenges the traditional view of this group and provides an opportunity to study evolutionary transitions in symbiotic lifestyles. *Nephromyces* is a free-living (extracellular) commensal symbiont inhabiting the renal sac of molgulid tunicates and maintains a complex symbiosis with multiple bacterial endosymbionts. This unusual system provides a unique opportunity to investigate how symbiosis shapes metabolic evolution in eukaryotes. In this study, we investigated whether horizontal gene transfer (HGT) has contributed to the metabolic repertoire of *Nephromyces*. Transcriptomic data of *Nephromyces* obtained from the renal sac of *Molgula manhattensis* were analyzed to identify candidate HGT genes using sequence similarity searches and

taxonomic filtering, and their evolutionary origins were evaluated through phylogenetic reconstruction with diverse bacterial and eukaryotic homologs. Ongoing analyses have identified some *Nephromyces* genes that cluster with bacterial lineages rather than with other apicomplexans, consistent with potential horizontal gene transfer events. Many of these genes are associated with metabolic pathways that may contribute to nutrient cycling within the symbiotic consortium. Overall, our results suggest that HGT may play an important role in shaping the metabolic capacity of *Nephromyces* and highlight how symbiosis can reshape the evolutionary history of apicomplexans.

10 – Determining ploidy and clonality in *Chlainomonas* sp. via single cell genetics. Alexander Geragotelis¹, Trinity Hamilton², Robin Kodner³, Lucie Mieuze⁴, Honu Pata³, Solenn Stoeckel⁵, Stacy Krueger-Hadfield^{1,6}. ¹Virginia Institute of Marine Science Eastern Shore Laboratory, Wachapreague, VA, USA ²Department of Plant and Microbial Biology and The Biotechnology Institute, University of Minnesota, Saint Paul, MN, USA ³Department of Environmental Science, Western Washington University, Bellingham, WA, USA ⁴IGEPP, INRAE, Institut Agro, Université de Rennes, Le Rheu, France ⁵DECOD, L’Institut Agro, IFREMER, INRAE, Rennes, France ⁶Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA. **(Wilce Award candidate)**

The reproductive mode dictates the distribution of genetic material, and thus how populations respond to environmental change. Studying reproductive mode variation requires understanding an organism’s life cycle, yet this knowledge is lacking for many eukaryotes, including snow and glacier algae. We require genetic approaches to answer outstanding questions, including determining the ploidy of the *Chlainomonas* sp. cells forming blooms, and the reproductive mode both within blooms and throughout the year. We have developed microsatellite loci to genotype single cells – a novel approach for microbial population genetics. We have sampled blooms across Bagley Lake in Washington, finding the large, red cells have two alleles at some loci, suggesting diploidy. We also did not find repeated genotypes. Importantly, single cell population genetics holds promise to fill in some of the existing knowledge gaps of biology for the unculturable majority of eukaryotes.

11 – Cross-scale functional trait analysis of *Ascomyces nodosum* in the Gulf of Maine. Marcella Heineke¹ and David Kimbro¹. ¹Department of Marine and Environmental Sciences, Northeastern University, Boston, MA, 01908, USA. **(Wilce Award candidate)**

A central goal of ecology is to develop theories that explain biodiversity, ecosystem functioning, and nutrient cycling across scales and systems. A large step forward in this direction was the development of functional trait theory in vascular plants, which has allowed a mechanistic understanding of community assembly across terrestrial systems. Recently, these same traits have been translated into macroalgae, but the majority of the published work has been on differences across macroalgal communities. In this talk, I examine functional trait differences within *Ascomyces nodosum* beds across two scales in the Gulf of Maine, USA. The Gulf of Maine represents a large-scale thermal gradient in both air and water temperatures from north to south and within a given region the local intertidal stress gradient exacerbates these regional trends. I surveyed *A. nodosum* populations at three sites each in the north and south at three

tidal heights per site, for a total of 360 individuals sampled. Northern individuals occupied a significantly larger portion of the multivariate trait space than southern individuals. Southern individuals are denser, thicker, shorter, and have more branches, suggesting desiccation stress to be a driving force in their morphology. In conclusion, this work is a novel contribution to the budding field of functional traits in macroalgae due to the intraspecific nature and highlights the importance of studying multiple functional traits.

12 – Examination of Molgulid tunicate egg cells infected with *Nephromyces*.

Marissa Mehloose and Christopher Lane. Biological Sciences, University of Rhode Island, Kingston, RI. **(Wilce Award candidate)**

Nephromyces is a symbiotic protist in the phylum Apicomplexa, which lives within the renal sac (a closed, ductless organ) of Molgulid tunicates. Up to 20 different species of *Nephromyces* have been observed co-infecting individual renal sacs. How *Nephromyces* invades the closed renal sac is unclear, but a lack of infection during the tunicate's juvenile stage suggests that the *Nephromyces* must be taken up from the water column each spring when the tunicates emerge. However, following up on preliminary data from the Waller Lab, recent Giemsa stained egg cells revealed structures that appear to be *Nephromyces* cells residing within, or associated with, the egg cells of Molgulid tunicate. These results provide evidence that *Nephromyces* may be vertically inherited, possibly in addition to environmental acquisition. To determine what species of *Nephromyces* are present within the ovaries and renal sacs of tunicate hosts, this study amplified CO1 from the ovaries and renal sacs of *Molgula manhattensis* and *Molgula occidentalis*, using *Nephromyces* specific primers. Species composition was compared between ovary samples and renal sac samples to determine if all species present in a host's renal sac are being vertically inherited through egg cells, or if there are additional modes of infection that result in the diversely cohabitated renal sacs previously observed.

13 – Fine scale resolution of zooxanthellae cell wall-composition-and its potential role in regulating endosymbiosis

Clancy McIntyre¹, Charles T Anderson¹, Hong Ma¹, & Todd LaJeunesse¹. Biology, Penn State University, State College, PA, 16801. **(Wilce Award candidate)**

The intra-cellular mutualisms between animals and dinoflagellate endosymbionts (Family: Symbiodiniaceae) are widespread and are the foundation of coral reef ecosystems. Symbiodiniaceae are diverse and support a broad diversity of invertebrates which need them to survive. The molecular communication between both partners involving signaling, recognition, and nutrient transfer is complex and not well understood. The interface for this exchange occurs at the symbiont's cell wall, which functions as both a barrier and filter that modulates the flux of molecules necessary to maintain this mutualism. Dinoflagellate cell walls are made primarily of cellulose, proteins and glycoproteins and bound in vesicles (called amphiesma) found beneath the plasma membrane, and are thus internal. Symbionts capable of living within and outside a host undergo a visible reduction in cell wall thickness for intracellular life, but it is unknown whether a change in cell wall composition is responsible for this adaptation. Glycome profiling, an approach often used to study plants, was used to characterize pectin and

hemicellulose related moieties in *Symbiodinium microadriaticum* and *Breviolum minutum* living in vitro and in hospite. This data, in combination with bioinformatic analyses of Symbiosiniaceae cell wall modification genes, has shown previously uncharacterized carbohydrates in dinoflagellate cell walls like xylans and mixed-linkage glucans make up a significant component of Symbiodiniaceae thecae and may vary in abundance between symbiotic states.

14 – Who’s the Dad? Paternity analyses in *Gracilaria vermiculophylla* reveal mating system dynamics. Sarah L. Allen¹ and Stacy A. Krueger-Hadfield¹. ¹ Virginia Institute of Marine Science Eastern Shore Laboratory, Wachapreague, VA, 23480, USA.

Reproductive mode variation shapes genetic structure within and among populations. Many eukaryotes, including macroalgae, undergo both sexual and clonal reproduction, however quantifying sexual versus clonal rates is challenging. Furthermore, life cycle variation creates further complexities in which standard population genetic techniques cannot be easily implemented. In the red alga *Gracilaria vermiculophylla*, in hard bottom habitats, we find gametophytes and tetrasporophytes accompanied by signatures of sexual reproduction. The populations at the sites that have been studied to date vary in the relative rates of selfing to outcrossing. Our current understanding of the mating system (i.e., selfing to outcrossing) in *G. vermiculophylla* relies on indirect methods, such as genotype frequencies. Paternity analyses, however, provide direct quantification of gene flow between males siring cystocarps on a given female. Since gametes are produced by mitosis, we can easily reconstruct paternal genotypes from the diploid carposporophyte by genotyping non-reproductive female tissue. We will use microsatellites to genotype cystocarps excised from females in hard bottom populations along the Delmarva Peninsula in the Mid-Atlantic. Furthermore, we will determine the number of cystocarpic sires as well as relatedness between mating pairs. This will ultimately provide insights into gene flow and sexual reproduction in red algae, contributing to our current understanding of mating systems in haploid-diploid organisms.

15 – How does competition perturb cell crosstalk among phycosphere associated bacteria?

Genevieve Dallmeyer-Drennen¹, Emma Healey¹, Hannah G. Reich¹ ¹SUNY ESF, Syracuse New York 13210, United States of America

Coral holobionts are hotspots of biodiversity encompassing a diverse community of symbiotic dinoflagellates (Symbiodiniaceae), bacteria, fungi, archaea, and viruses. The Symbiodiniaceae phycosphere, a microenvironment surrounding the cell enriched in photosynthates, also harbors bacteria. Bacteria contribute to holobiont nutrient acquisition, disease resistance, and heat tolerance. Despite the broad benefits conferred by microbes to the holobiont, there is a paucity of understanding of the ecological roles of individual bacterial taxa, including their relationships with Symbiodiniaceae. A better understanding of phycosphere structure and function can be established through characterization of competitive interactions between phycosphere bacteria. Pairwise proximity assays using bacteria isolated from Symbiodiniaceae cultures were conducted to quantify colony growth using image analysis and capture morphological changes associated with exposure to diffusible and bacterial volatile compounds (BVCs). Comparisons across normal and partitioned agar plates, which isolate BVC-mediated

interactions, demonstrate that BVCs inhibit colony growth and motility. Emergent pink coloration observed in specific pairings will be extracted and characterized as lycopene or prodigiosin, compounds with known antimicrobial activity. Integrating phenotypic screening with comparative genomics will link competition-induced phenotypes and the genetic pathways that underpin microbial survival strategies. Understanding microbial functions that confer beneficial advantages to Symbiodiniaceae, such as disease resistance or other stress resilient phenotypes, will enhance our fundamental knowledge of this symbiosis and ultimately will enhance our ability to advance microbiome-based approaches to coral reef conservation.

16 – Life cycle, interrupted: the ecological genetics of the invasion of soft bottom habitats.

Sophia V. Tearman¹ & Stacy A. Krueger-Hadfield¹.¹Eastern Shore Laboratory, Batten School & Virginia Institute of Marine Science, William & Mary, Wachapreague, VA, 23480, U.S.A.

All eukaryotes have sex but the timing of when meiosis and fertilization occur varies widely, leading to variation in life cycle types. The main types are haploid, diploid, and haploid-diploid life cycles, upon which a myriad of variation occurs. Yet, we do not have a good understanding of the mechanisms that maintain this variation. Here, we use the haploid-diploid, red alga *Gracilaria vermiculophylla* to investigate life cycle and reproductive mode dynamics. This alga has a well-documented invasion in which tetrasporophytes and asexual reproduction prevail in soft bottom habits, such as mudflats, though relative rates of clonality differed among sites. By contrast, in hard bottom habitats, such as rocky shores, both tetrasporophytes and gametophytes are found, sexual reproduction occurs, and there was variation in the relative rates of selfing versus outcrossing. The reproductive mode variation observed in soft and hard bottom sites will be explored using single nucleotide polymorphisms to increase resolution from previous microsatellite genotyping. In concert, tetrasporophytic dominance will be explored using high throughput phenotyping comparing the phases and sexes, including temperature-salinity stress and herbivory. Population genetic patterns and ecological differentiation among phases/sexes should aid in resolving questions about the invasion success of this alga as well as advancing our understanding of the evolution of sex.

17 – A Systems-Level Framework for Optimized Biofuel Production. Luis Pablo Salmeron Covarrubias, Kavitha Beluri, **Hamidreza Sharifan**. Department of Chemistry and Biochemistry, University of Texas at El Paso.

Engineering controlled stress responses in microalgae represents a promising strategy for enhancing lipid biosynthesis without compromising biomass sustainability. In this study, we systematically investigated the nano-bio interface between zinc oxide (ZnO) nanoparticles and *Chlorella vulgaris* to elucidate how redox modulation governs metabolic reprogramming and biofuel feedstock quality. ZnO nanoparticles (20–100 mg L⁻¹) were characterized via SEM, TEM, DLS, and XPS, confirming nanoscale aggregation behavior and surface interactions with oxygenated functional groups on algal cell walls. Moderate nanoparticle exposure (20–50 mg L⁻¹) induced a hormetic oxidative response, reflected by controlled upregulation of catalase activity and partial modulation of photosynthetic pigments, resulting in a substantial shift in carbon allocation toward lipid biosynthesis. Peak lipid accumulation reached 48% at 50 mg L⁻¹, while biomass productivity remained statistically comparable to the control. However,

excessive nanoparticle concentrations (100 mg L⁻¹) triggered severe oxidative imbalance, pigment degradation, and reduced lipid yield, demonstrating a critical redox threshold beyond which metabolic efficiency collapses. To quantitatively resolve these trade-offs, we developed a Biofuel Suitability Score (BSS), integrating lipid content, biomass productivity, pigment stability, and oxidative stress into a normalized systems-level metric. The BSS peaked within the 30–50 mg L⁻¹ range, identifying an optimal redox window for sustainable biofuel production. This work establishes a mechanistic framework linking nanoparticle-induced oxidative signaling to metabolic flux redistribution in microalgae. By integrating physicochemical characterization with biochemical and systems-level modeling, we provide a scalable strategy for precision nano-enabled bioenergy optimization.

18 – Reproductive mode variation in benthic and pelagic *Sargassum*: Monoecy and clonality shape population structure. Danielle C. Hatt¹, Frédérique Viard², Didier Aurelle^{3,4}, Marion Ballenghien⁵, Edwin Cruz-Rivera⁶, Ligia Collado-Vides⁷, and Stacy A. Krueger-Hadfield¹. ¹Virginia Institute of Marine Science Eastern Shore Laboratory, Wachapreague, VA, USA. ²ISEM, Univ Montpellier, CNRS, IRD, Montpellier, France. ³Aix Marseille Univ, Université de Toulon, CNRS, IRD, MIO, Marseille, France; Institut Systématique Évolution Biodiversité (ISYEB). ⁴Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, CP 26, 75005, Paris, France. ⁵Sorbonne Université, CNRS, Adaptation and Diversity in Marine Environments, Roscoff, France. ⁶Morgan State University, Baltimore, MD, USA. ⁷Florida International University, Miami, FL, USA.

Blooms of floating pelagic *Sargassum* (Phaeophyceae) have expanded rapidly across the Atlantic since 2011, causing significant ecological and socioeconomic impacts, with annual removal costs estimated at US\$210M for the Caribbean region. Despite advances in identifying environmental drivers of these blooms, the prevailing reproductive mode of pelagic *Sargassum* remains enigmatic. Pelagic *Sargassum* species are likely clonal, as sexual reproductive receptacles have never been observed. However, no studies have explicitly tested this using population genetic approaches. We are in the process of analyzing 1,072 thalli of pelagic and benthic species of *Sargassum* collected between 2017 and 2022 from Florida, Virginia, and the U.S. Virgin Islands. Using nine polymorphic microsatellite loci, we quantified allelic and genotypic diversity to test the following hypotheses: (1) Pelagic and benthic species are genetically distinct and (2) pelagic and benthic species exhibit evidence of clonality and self-fertilization, respectively. Overall, our findings clarify the reproductive mode and population genetic structure of pelagic and benthic *Sargassum* in the Caribbean and provide the necessary population genetic framework for understanding fundamental biological processes contributing to bloom dynamics of pelagic *Sargassum* in the Atlantic.

19 – Using 50 years of algal composition data to evaluate drivers of ecosystem shifts in Skaneateles Lakes. Dominique S. Derminio¹, Rich Abbott², Liam Hawes¹, Christine Georgakakos¹, and Stephen Shaw¹. 1- Environmental Resources Engineering, SUNY ESF, Syracuse, NY 13210, 2- City of Syracuse Department of Water, Syracuse, NY 13210.

Skaneateles Lake has been an unfiltered water supply for Syracuse, NY, since 1894. To monitor drinking water quality, the City of Syracuse has conducted algal population surveys in the deep,

dimictic, oligotrophic lake since 1973 at a depth of 6 m at eight locations across the lake. While lakes often have long-term records of chlorophyll concentration, longitudinal information on algal taxa is rare, offering a unique opportunity to observe which specific genera change over time. The 50-year data showed a distinct increase in cyanobacteria concentrations across all stations in 1992, with another shift in cyanobacterial genera in 2008. These shifts in algal composition provide valuable insight into the ecological health and nutrient dynamics of Skaneateles Lake. Several explanations for the extreme shift in algal genera population that began in 1992 were examined: lake temperature, growing-season duration, water inflows, emergence of invasive species, wind, and sampling and classification methodologies. While no single explanation fully accounts for the algal population shift, the evidence suggests that the post-1992 shifts are not solely the result of methodological changes but instead reflect real changes within the lake ecosystem. These shifts highlight the complex interactions among climate variability, invasions by invasive species, and in-lake processes that drive algal growth.

20 – Stoichiometric relationships provide insight to periphyton biomass increases due to road salt pollution. **Sarah B. Whorley**¹, Jeffrey J. Law¹, John D. Wehr², Jeffrey S. Heilveil³

¹Dept. of Natural Sciences & Mathematics, Daemen University, Amherst, NY 14226; ²Louis Calder Center, Fordham University, Armonk, NY 10504; ³Biology Department, SUNY Oneonta, Oneonta, NY, 13820

After decades of seasonal winter road salt use, salinity levels in freshwater streams are rising, even during non-winter months when no road salt is used. While several recent studies have documented this increase of salinity in stream water, very little work has been done to examine the effects of this salt on stream biota. We have conducted a year-long investigation of annual road salt effects on stream water chemistry and biota throughout New York State. Selected streams across Western New York, Central New York, and the Hudson River Valley were surveyed from May 2024 to April 2025. We deployed HOB0 conductivity loggers to capture high-resolution salinity measurements. Additionally, we visited each stream monthly to collect in situ water chemistry and periphyton biomass for chlorophyll and stoichiometric analysis. Preliminary results show that periphyton algal biomass (as measured by chlorophyll concentrations) increased along with increasing salinity, contrary to expectations. Here, we examine the trends in periphyton chlorophyll and stream salinity measurements in conjunction with ambient nutrient concentrations (PO_4^{3-} , NO_3^- , NH_4^+) as well as periphyton phosphorous content. These findings will bolster future analyses of how these salinity conditions affected biodiversity and fatty acid compounds.

21 – Reproductive consequences of upper thermal thresholds for northwest Atlantic *Alaria esculenta* microscopic stages. **Daniel J. Gossard**¹, Charles Yarish¹, Scott Lindell¹

¹Woods Hole Oceanographic Institution, 177 Oyster Pond Road, Woods Hole, Massachusetts 02543

Alaria esculenta (Laminariales, Phaeophyceae) kelp beds in the Gulf of Maine are experiencing some of the most rapidly warming seawater temperatures in the world. This may have negative effects on bed persistence along this warm biogeographical edge, as gametogenesis has been

being identified as an ontogenetic point of susceptibility to high temperatures. We conducted a laboratory study using *A. esculenta* collected from Schoodic Point, Maine, and exposed recently settled meiospores to different temperatures (12C to 15C in 1C increments) and different light intensities (12, 22, and 42 μ E PPFD) with the aim to elucidate the effect of light on gametophyte temperature susceptibility on a finer scale. The probabilities of eggs and sporophytes produced by gametophytes (out of twenty per petri dish; n = 3 dishes) after 26 days were compared using generalized linear models (binomial family, logit link) testing for differences in a full factorial design. We found significant differences in interactions between temperature and irradiance for each response variable with noticeable decreases in gametogenesis and sporophyte production starting at 14C. Interestingly, we identified small proportions (ranging from 8% $\pm$ 3% to 20% $\pm$ 3%) of gametophytes producing sporophytes in the 15C level across irradiance levels. These, and other, results are discussed in the context of spatiotemporal temperature patterns across the Gulf of Maine.

22 – Determining seasonal shifts in coastal phytoplankton abundance and community composition in a warming Gulf of Maine. Patricia Thibodeau¹, Terrance Meinardus¹, Emma Hutchings¹, Erin Anderson¹ ¹University of New England, School of Marine and Environmental Programs, 11 Hills Beach Road, Biddeford, 04005, U.S.A.

Phytoplankton represent the base of most aquatic food webs and are critical for assessing ecosystem health and resilience in dynamic coastal regions. Within the Gulf of Maine (GoM), long-term declines in phytoplankton biomass were related to increasing seawater temperatures as well as shifts in GoM ocean circulation and biogeochemistry. The impact and connectivity of these changes to coastal regions is still unknown and important for predicting how bottom-up shifts in productivity will affect the rest of the GoM ecosystem. This project employed weekly sampling in Saco Bay, GoM to quantify phytoplankton community composition and abundance throughout an almost two-year time series. Phytoplankton biomass was analyzed with respect to seasonal variations in sea surface temperature, salinity, and nutrient concentrations. Results show an initial peak in phytoplankton biomass in spring with the highest recorded biomass in summer. Phytoplankton community composition was dominated by diatoms in spring, which then shifted to dinoflagellates in late summer/early fall. Cell concentration decreased until October when there was a large bloom of diatoms in late fall. These results generally reflect those observed more broadly within the GoM, but highlight the need for continued coastal monitoring efforts to elucidate a complete understanding of phytoplankton abundance and community composition in dynamic and changing regions like the GoM.

23 – Random Forests and not-so-random kelp beds: remote sensing suggests that depth and species affect habitat resilience. Constance N. Tyler¹, Kim Lowell¹, Christopher E. Parrish², & Jennifer A. Dijkstra¹. ¹Center for Coastal and Ocean Mapping/Joint Hydrographic Center, University of New Hampshire, Durham, NH, 03824, U.S.A.; ²College of Engineering, Oregon State University, Corvallis, OR, 97331, U.S.A.

Despite interspecific variation in functional traits and spatial variation in species occurrence, bed-forming kelps are often treated as a set of equivalent foundation species in terms of their ability to shape ecosystem interactions. Declines in kelp habitats are reported across much of

their historic range due to a variety of anthropogenic stressors, and these habitats are frequently replaced by filamentous red macroalgae. Many of these reports rely on diver surveys, which rarely monitor kelp habitats across their full depth range. Habitat modelling approaches show promise in improving our understanding of kelp habitat distribution and resilience. We used Random Forest models trained on acoustic bathymetry and satellite-derived sea surface temperature data to predict kelp habitats at the Isles of Shoals. These predictions, made at a spatial resolution of 30 m, indicate strong depth zonation patterns between different habitat types as well as between different kelp species. Kelp habitats were more abundant than filamentous red macroalgae habitats below 16 m depth, which coincides with a shift from shallow *Saccharina latissima* to deeper *Agarum clathratum*. We explore several potential biotic and abiotic factors related to depth may produce these patterns, including light availability, temperature, and sea urchin access and grazing behavior. Other bathymetric factors such as slope and vector ruggedness, as well as variability in sea surface temperature, also distinctly differed between some benthic habitat types. These findings suggest that kelp beds deeper in the subtidal may be less susceptible to stressors in the Gulf of Maine. Our research highlights the importance of monitoring kelp habitats across their full depth range, and cautions against treating kelp species as interchangeable.

24 – Latitudinal patterns of genetic diversity in Western Antarctic macroalgae. **Ana I. Tavares**^{1,2}, Charles D. Amsler¹, Margaret O. Amsler¹, Stacy A. Krueger-Hadfield². ¹Department of Biology, University of Alabama at Birmingham, Birmingham, Alabama, USA; ²Virginia Institute of Marine Science Eastern Shore Laboratory, Wachapreague, Virginia, USA.

The Last Glacial Maximum is thought to have induced significant range contractions and the potential loss of genetic diversity. Many species retreated from high to low latitude habitats and then rapidly re-colonized habitats during the subsequent interglacial periods. These evolutionary processes have been well-documented for many Northern Hemisphere species, while the effects of recent glaciations in the Southern Hemisphere, particularly in Antarctica, are comparatively less understood. Thus, the Antarctic Peninsula represents a key region to evaluate the effect of glaciations on the genetic diversity of macroalgae. We compared patterns of genetic diversity based on mitochondrial markers in brown (*Desmarestia menziesii*, *Himantothallus grandifolius*), and red macroalgae (*Plocamium* spp., *Iridaea cordata*, *Sarcopeltis antarctica*) sampled along the western Antarctic Peninsula. We test the hypothesis that high latitude populations show reduced genetic diversity from past extinctions and recolonization events. Overall, all species confirmed the predicted decline in diversity with latitude, except for *D. menziesii*. Across species, haplotypic diversity was generally low, except in *I. cordata*. All taxa showed low nucleotide diversity, lack of distinct genetic structure and starlike haplotype networks, patterns consistent with recent postglacial population expansion. Our results suggest that these macroalgal species went under demographic expansions linked to habitat changes associated with the last glacial–interglacial transition.

25 – Cilia Gene Expression in *Chlamydomonas reinhardtii*: Forward and Reverse Genetics Approaches. **Jason M. Brown**. Biology Department, Salem State University, Salem, MA 01970, U.S.A.

Cilia (a.k.a flagella) are complex organelles projecting from the surfaces of diverse eukaryotic cells, including most mammalian cell types and cells in many lineages of unicellular and multicellular algae. Although cilia were first described 350 years ago, the relatively recent discovery that cilia defects cause multiple syndromic human diseases lead to an explosion of interest in these elaborate biological machines over the last 25 years. One of the most critical model organisms for fundamental discoveries in cilia biology has been the unicellular green alga, *Chlamydomonas reinhardtii*. Cilia loss and subsequent regeneration can be triggered in *Chlamydomonas* with a brief pH shock. During cilia regeneration following pH shock and normal cilia growth during the cell cycle, hundreds of genes are upregulated. Despite progress on identifying calcium as an important signaling component in cilia gene induction and the identification of one transcription factor, XAP5, required to induce a subset of the cilia genes, multiple other regulatory proteins must be involved in this process. We are approaching this problem using both forward and reverse genetics tools. An insertional mutagenesis screen isolated mutants unable to normally induce a luciferase reporter of cilia gene induction. We are also using CRISPR-based mutagenesis to disrupt genes encoding candidate transcription factors. I will discuss our progress in generating and characterizing these mutants.

26 – Exploring Mitochondrial Genome Diversity in Eustigmatophyte Algae. Kristina X. Terpis¹, Dovilė Barcytė², Marek Eliáš², Christopher E. Lane¹ ¹Department of Biological Sciences, University of Rhode Island, Kingston RI, USA.; ²Department of Biology and Ecology, Faculty of Science, University of Ostrava, Czech Republic.

The class Eustigmatophyceae (Ochrophyta, Stramenopiles) comprises species that are commonly found in freshwater, marine, and terrestrial habitats. Some members of this class have been intensely studied for production of biofuels like *Nannochloropsis* and *Microchloropsis*. Although these well studied species have extensive genomic and transcriptomic data publicly available, little is known about other member of this diverse class. Here we generated the mitochondrial genome for the eustigmatophyte *Vacuoliviride crystalliferum* and compared it to other eustigmatophytes and other ochrophytes. We found that *V. crystalliferum*, like all other eustigmatophytes, encodes *atp1* on its mitochondrial genome. This feature is unique to eustigmatophytes, as all other ochrophyte classes encode the *atp1* gene in the nuclear DNA. Additionally, preliminary data from the *Candidatus* Phycorickettsia endosymbiont of *V. crystalliferum* will be discussed.

27 – The Articulated Coralline Genus *Corallina* (Florideophyceae, Corallinales) as a Model for Evolution & Biogeography: Updates & Current Research. Rachael Wade, Department of Biological Sciences, California State Polytechnic University, Humboldt.

The articulated, coralline algal genus *Corallina* is common in coastal marine ecosystems throughout polar to tropical regions, providing crucial floral and faunal settlement substrate. As with other coralline genera, there has been a collaborative effort to more accurately document the taxonomy of *Corallina*, primarily through type specimen sequencing. To that end, type specimen sequencing has been achieved for all available type specimens from the northeast Pacific, which is home to three-quarters of the known species in the genus. Thus, this region is an excellent candidate for coralline research beyond taxonomy. We are currently using

Corallina as a model to better understand coralline algal biogeography, evolution, and reproduction via a combination of traditional surveying and population demography methods with phylogenomic approaches. Organellar phylogenomic reconstructions suggested that *Corallina* evolved in the cold, northern Pacific. Putative sympatric speciation has occurred multiple times, which may be a result of reproductive isolation between gametophyte and tetrasporophyte stages. While most *Corallina* spp. have discrete distribution ranges, *C. berteroi* has a near-global distribution. Further work is needed to understand the drivers that have facilitated this distribution, as well as the barriers that have prevented other species from becoming similarly cosmopolitan. This work would not be possible without previous taxonomical treatments and is a prime example of how historical specimens can be leveraged for diverse research applications.

28 – Nutrient limitation mediates the susceptibility of a coccolithophore to a bacterial quorum sensing signal precursor. **Hannah G. Reich**¹, Maggie E. Straight², Marley Gonsalves³, Anais Gentilhomme⁴, Amanda Platt⁵, Kristen E. Whalen⁵, Brook Nunn⁴, Julia Kubanek², Elizabeth L. Harvey³ ¹Department of Environmental Biology, State University of New York, College of Environmental Science and Forestry, Syracuse, NY, 13210, USA ²School of Biosciences, Georgia Tech, Atlanta, GA, 30332, USA ³Department of Biological Sciences, University of New Hampshire, Durham NH, 03824, USA ⁴Department of Genome Sciences, University of Washington, Seattle, WA 98195 ⁵Department of Biology, Haverford College, Haverford PA, 19041, USA

Symbioses between microalgae and bacteria contribute a considerable fraction of global CO₂ sequestration, and the ocean carbon pump. The interactions between the two are ubiquitous in the photic ocean, with environmental and biological forces regulating the outcomes of these interactions. For example, widespread interactions between the cosmopolitan coccolithophore (*Gephyrocapsa huxleyi*) and bacteria (*Pseudoalteromonas piscicida*) are disrupted following bacterial production of algicidal compounds, thereby facilitating the demise of algal blooms. The bacterially produced quorum sensing signal precursor, HHQ (2-heptyl-4-quinolone), induces microalgal cell stasis and confers viral resistance with negligible impacts on photophysiology, but, at toxic levels, triggers cell lysis and ultimately cell death. To evaluate how biogeochemistry alters coccolithophore resistance to HHQ production, axenic *G. huxleyi* (CCMP 2090) were exposed to media deplete of nitrogen, phosphorus, iron, zinc, or cobalt, and exposed to the pure HHQ chemical compound. *G. huxleyi* resistance to HHQ improved for a short duration in Phosphorus deplete conditions (~1 day) and for longer spells in nitrogen deplete conditions (4+ days). *P. piscicida* were reared in deplete and ambient nutrient (nitrogen, phosphorus, iron) conditions to track HHQ production dynamics using targeted LC-MS. Under low iron conditions, *P. piscicida* produced and exported more HHQ per cell than under ambient conditions. Co-cultures of *G. huxleyi* and *P. piscicida* (A757) were also reared in ambient nutrient conditions to track the effects of algal presence on HHQ production and uptake dynamics using targeted LC-MS. *P. piscicida* exported a significantly greater fraction of HHQ in the presence of *G. huxleyi*, however, the majority of bacterially produced HHQ was not assimilated by *G. huxleyi* and remained extracellular. Taken together, these results emphasize how nitrogen and iron conditions are critical mediators of cellular crosstalk in cross-kingdom interactions. Broadly, these results provide information on the biogeochemical drivers of symbiosis success and the duration of algal blooms.

Poster Abstracts

P1 – Assessing concentration and purification methods of *Palmaria palmata* tetraspores through flow cytometry. Stella Defibaugh^{1,2}, Nicole Poulton¹, Laura Lubelczyk¹, Thew Suskiewicz³ ¹Bigelow Laboratory for Ocean Sciences, East Boothbay, ME ²University of New Haven, West Haven CT ³Atlantic Sea Farms, Biddeford, ME (**President's Award candidate**)

Palmaria palmata is a red seaweed with growing importance in the Gulf of Maine's aquaculture industries for its uses in cosmetics, medicine, and food. Its haploid tetraspores, released by the mature diploid sporophyte, are difficult to cultivate because they are large (~30 µm), non-motile, sink quickly, produce few spores, and are easily contaminated. Our research focused on two filtration methods, reverse and three variations of vacuum, that would best concentrate and purify tetraspores while developing methods to test whether the cells were vital and could continue developing to maturity. Flow cytometry was used to determine how spore vitality and concentration would change following filtration. We found that *P. palmata* tetraspores could be stained with fluorescein diacetate (FDA) to assess vitality and were most effectively concentrated and purified using vacuum filtration. Due to a lack of tetraspores released during sporulation, these methods were tested using similarly sized beads and the dinoflagellate *Alexandrium* sp. While the beads aggregated and clogged the cytometer, *Alexandrium* provided a valuable analog, confirming the effectiveness of two vacuum filtration techniques. Future work will involve applying these methods to higher initial concentrations of tetraspores and examining whether the concentrated spores maintain viability and normal development so these methods can be used on an industrial scale.

P2 – Biomagnification of cyanotoxins in an experimental food web. Aramis Rosario González¹, Elizabeth Carroll,² & Sarah Princiotta¹. ¹Pennsylvania State University Berks, Reading, PA, 19606, USA. ²Holy Family University, Philadelphia, PA, 19114. (**President's Award candidate**)

Cyanobacteria are an integral component of the aquatic ecosystem but can be toxic and form harmful algal blooms that negatively impact aquatic life and present public health risk. The dynamics of cyanotoxins in the aquatic environment are not well understood and evidence exists for bioaccumulation during feeding. However, grazer tolerance to cyanotoxicity is variable. We created an artificial food web in which *Daphnia magna*, a microcrustacean grazer, was grown with varying concentrations of toxic or non-toxic cyanobacteria (*Microcystis*), and surviving *D. magna* from each treatment were fed to the nymph stage of *Libellulidae* (dragonfly). Cell counts of *Microcystis* were conducted before and after incubation with *D. magna* and tissue analysis for total microcystins was performed. Complete mortality was observed in *D. magna* exposed to the highest concentration of toxic cyanobacteria. There was a negative effect of *Daphnia* on the abundance of both toxic and non-toxic *Microcystis*, but only at the lowest concentration of cyanobacteria studied. Microcystin bioaccumulation was observed at only the lowest concentration of toxic cyanobacteria, and appreciable levels were found in *Libellulidae*. Our results show that trophic transfer was highest at lower cyanobacterial concentrations where *D. magna* survived exposure. Therefore, the potential for trophic transfer is most likely during sublethal bloom conditions, while higher bloom intensities may destabilize food webs by consumer mortality.

P3 – Using Diatoms to Infer Paleoenvironmental Conditions in a Connecticut Vernal Pool

Authors: Lily Bentley, Diba Khan-Bureau, Will Ouimet. University of Connecticut, CT State Community College Three Rivers Campus. **(President's Award candidate)**

Vernal pools are ecologically significant features that are abundant in previously glaciated landscapes and strongly influenced by geomorphological processes. Due to their ephemeral nature, the long-term environmental history of vernal pools is often poorly understood and difficult to reconstruct. In this study, sediment cores were taken from a vernal pool in Simsbury (CT) adjacent to the Talcott Mountain/ Metacomet Ridge to examine patterns of diatom assemblages preserved within sediments. Diatoms are a diverse group of microscopic algae that inhabit a wide range of environments and are a valuable tool for inferring paleoenvironmental conditions because they are sensitive to physical, chemical, and hydrological change. Diatoms in sediment cores are identified through analysis of distinctive patterns on their silica cell walls. Samples from the core were prepped and diatoms were identified at the genus and species level since individual taxa are adapted to specific habitats and environmental gradients. Preliminary results indicate that diatom assemblages change throughout the 260 cm long core, indicating changes in environmental conditions, including shifts in hydrology and fluctuations in nutrient availability and water chemistry. These changes likely reflect broader geomorphological and landscape-level processes influencing the vernal pool over time. When paired with geomorphological analyses, diatom-based reconstructions provide an effective approach for interpreting landscape history and understanding long-term ecological and geomorphological dynamics in ephemeral aquatic systems.

P4 – Differential Expression of Receptors involved in Prey Detection Under nutrient limitation in the Mixoplankton *Cymbomonas tetramitiformis*. Thomas Morahan & Sophie Charvet, Department of Biology, Susquehanna University, 17870, PA, U.S.A. **(President's Award candidate)**

Mixoplankton are a mysterious piece of the global marine food web, due to their cryptic ability to use both photosynthesis and predation. Small mixoplankton such as the prasinophyte *Cymbomonas tetramitiformis* (PLY-262), potentially interfere with the microbial loop by feeding on bacteria. Recent studies indicate that the prasinophyte's increased bacterivorous activity under nutrient restrictions coincides with increased expression of key phagotrophy genes. We hypothesize that some of these genes encode for receptors, such as ARL (adiponectin receptor-like), that may be used to detect prey. To study this we developed qPCR assays for the ARL gene and verified housekeeping genes. We then investigated the changes in ARL expression under differential nutritional conditions. The ability to use the expression of this gene as an indicator of feeding can ultimately allow *in situ* investigations on mixoplankton activity in the ocean.

P5 – Molecular Interactions between Maine Mixoplankton and their Bacterial Prey. Matthew J. Crawford, Sophie Charvet Department of Biology, Susquehanna University, Selinsgrove, PA, 17870 **(President's Award candidate)**

Marine mixoplankton possess the ability to transition between phototrophic and phagotrophic nutritional strategies, enabling survival under oligotrophic conditions. Despite their ecological

importance, much still remains unknown about mixoplankton, including the mechanism by which they recognize and bind prey. A previous study on *Pterosperma cristatum* revealed the upregulation of receptor genes during bacterivory, suggesting a role in recognition of bacteria before ingestion. To determine if these receptors would recognize bacterial prey, we tested their molecular interaction with bacterial microbe-associated molecular patterns (MAMPs). The gene sequences of adiponectin receptor-like (ARL), folate receptor (FOLR), and Patched (PTCH), were translated into their corresponding protein sequences. Bioinformatic analyses were performed to identify domains and characterize their possible functions. A three-dimensional structure of each protein was predicted using AlphaFold2. Molecular docking simulations were performed using AutoDock vina to evaluate potential binding interactions between the predicted receptors and bacterial MAMP ligands, such as lipopolysaccharide (LPS), peptidoglycan, and lipoteichoic acid (LTA). Early results show strong binding affinity of ARL with LPS, a component of Gram-negative cell envelope. Hence, *P. cristatum* likely uses ARL to detect and attach to Gram-negative prey in the marine environment. These findings provide preliminary insights of molecular interaction during the early stages of prey recognition and ingestion in *P. cristatum*.

P6 – “Snapshot” Analysis of Abiotic Drivers of Harmful Algal Blooms on Two Dimictic Lakes

Youssef Amin¹ and Sarah Princiotta². Department of Biology, Pennsylvania State University Schuylkill, Schuylkill Haven, PA, 17972 and Berks, Reading, PA, 19606, USA. **(President’s Award candidate)**

Lakes are a widely used resource globally. Despite the implications of poor water quality, many states do not provide avenues for private lakes to conduct water quality monitoring. The present study seeks to analyze a year-long monitoring effort on two connected dimictic lakes within a private community of 1,300 homes to align preestablished ideas of exogenic eutrophication and temperature impact on the algal communities present. We conducted a “snapshot” analysis via monthly sampling of both lakes at three representative depths. Algal abundance was measured by proxy of chlorophyll-a. We opted to measure microcystins to understand trends in cyanotoxicity due to the prevalence of *Microcystis* within the region. We found that over the course of a year, the two dimictic lakes presented expected data that coincided with preestablished ideas of the impact that increasing temperature has on the formation of cyanobacterial algal blooms. Peaks in chlorophyll-a were observed during the month of May 2025 for the inlet lake, which experienced an algal bloom in late June and early July. Furthermore, the metalimnion of the inlet lake exhibited the lowest levels of dissolved oxygen recorded during the year at the time of the algal bloom. The present study also succeeded in establishing a baseline data set for future water monitoring done by the studied lakes community.

P7 – Investigating Potential Environmental Influence on Molgulidae tunicates and their Apicomplexan Endosymbionts *Nephromyces*. Anna Jasinski¹, Peace Uche¹, Kristina Terpis¹, Christopher Lane¹ ¹Department of Biological Sciences, University of Rhode Island, Kingston RI, USA. **(President’s Award candidate)**

Molgulidae tunicates are a family of sessile marine invertebrates commonly found growing on substrates and on boats or docks. These tunicates are often found in association with an apicomplexan endosymbiont *Nephromyces*, which is known to reside in their bladder-like organ known as the renal sac. The purpose of this project is to investigate the development *Nephromyces* spp. over the course of their colonization, maturation and ultimate dispersal from within *Molgula manhattensis*. We will collect multiple different tunicate tissue samples over the course of their life span, beginning in April and concluding in October. Performing RNA-seq on these various tissue types will allow us to trace the route of infection and how *Nephromyces* spp. change their RNA expression over their life cycle. In addition, cell counts will be carried out on these tissues to track the infection levels of *M. manhattensis* throughout the season. We will also collect information on environmental factors, including temperature, salinity, chlorophyll a, and pH. Through this research we hope to determine whether there is a seasonal component to the life cycle of *Nephromyces* spp. and characterize the infection to dispersal life-cycle.

P8 – The Effects of Salinity and pH Change on Algal Biodiversity Within Streams. Grace Covey & Sarah Whorley. Department of Natural Sciences & Mathematics, Daemen University, Amherst, NY, 14226, U.S.A. (President's Award candidate)

Increases in stream salinity can alter other chemical parameters and affect algal biodiversity. Throughout the span of a year, the pH and salinity values of ten streams in Western New York were measured. Out of the ten streams, two streams were identified as minimally impacted streams, and two streams were identified as agriculturally impacted. The road salt and agricultural runoff in these areas is hypothesized to be disrupting the normal pH and salinity of the two selected agricultural streams, thus affecting the diatom, green algae and cyanobacteria abundance and overall algal biodiversity compared to those minimally affected. Each stream had three fall visits to samples (September, October, November). Monthly water chemistry measurements including salinity and pH were recorded. Rock cobbles were used to collect periphyton, and these samples were then analyzed for a overall periphytic algal biodiversity as well as diatom, green algae and cyanobacteria abundance. The two agriculture streams had an average Shannon's biodiversity index average of 1.74 while the two control streams had an average Shannon's biodiversity index average of 2.13. Overall, there is a general trend of the minimally impacted streams having a higher biodiversity index compared to the agriculture streams.

P9 – Seasonal Water Chemistry Influences on Algal Assemblages. Bridget Thornton, Derrick Swartz, & Sarah Whorley. Department of Natural Sciences & Mathematics, Daemen University, Amherst, NY, 14226, U.S.A. (President's Award candidate)

Algal assemblages in streams are critical for maintaining and monitoring stream health, as these organisms act as primary producers and indicator species for environmental changes. Seasonal transitions result in dynamic changes in water chemistry including nutrient concentrations and trace metals. This may influence the growth, composition and structure of algal assemblages. This study evaluates changes in water chemistry in a single stream over a period of time involving snow melt, and the subsequent effects on freshwater algal taxonomic composition. Water samples were collected from an upstream and downstream location along a small

section of Canavan Creek (NY, US) in February 2026 (while snow was present on the ground) and March 2026 (after snow pack melt). Additionally, terrestrial snow samples were also taken from the banks, and runoff points surrounding the creek. Algal samples were taken at the upstream and downstream locations in March 2026. The proportions of major algal taxonomic groups will be determined using microscopy. All water and snow samples were measured for ammonia, nitrite/nitrate, and phosphate. These samples were further analyzed for metals including chromium, lead, manganese, and potassium. We will be comparing proportions of algal taxa to chemical conditions at the time of collection and prior water/snow collections to begin to understand the relevant time-frame in which algal assemblages can respond to environmental changes.

P10 – Herbivory Preferences of *Littorina littorea* on Invasive Versus Native Macroalgae. Chloe Leano, Hannah Siegmund, and Lindsay Green-Gavrielidis. Biology Department, Salem State University, Salem, MA 01970, U.S.A. (President's Award candidate)

Invasive species have negative impacts on the ecology and economy of the area they invade. Studying herbivore preference is crucial to understanding how some species can successfully invade and spread. To understand how these species successfully spread, we investigated the feeding preference of the herbivorous snail, *Littorina littorea*, specifically comparing the native seaweed *Chondrus crispus*, to the invasive seaweed *Grateloupia turuturu*. We conducted two trials of paired-choice preference assays and an additional experiment using freeze-dried resuspended “fake food” and monitored consumption to determine if there was a seaweed preference. Our results were mixed in our paired-preference assays: in the first trial *Littorina littorea* favored the native seaweed, while the second trial showed that *Littorina littorea* favored the invasive seaweed. Results of the “fake food” trial are currently being analyzed and will be shared. *Grateloupia turuturu* was first recorded in Rhode Island in 1997 and has expanded north. Our results suggest that a baseline preference for the native seaweed among local herbivores may have contributed to the spread of *Grateloupia turuturu*

P11 – Impacts of High and Low Light Intensities on Chlorophyll pigments found in *Ulva* sp. Cameron Boyko & Brandon S. O'Brien. Biology, Kutztown University, Kutztown, PA, 19530, U.S.A. (President's Award candidate)

Light intensity is a key environmental factor influencing pigment concentration and photosynthesis in the marine macroalgae species *Ulva*. *Ulva* sp. is a common coastal species that contributes significantly to primary productivity in coastal ecosystems and is used as a model organism for studying algal responses to environmental change. Because available light intensity can vary widely due to factors such as turbidity, natural coverings, and seasonal variation, understanding how *Ulva* sp. responds to different light intensities can provide insight into its adaptability and ecological success. This study investigated the effects of high ($\sim 45\text{--}50\ \mu\text{mol m}^{-2}\ \text{s}^{-1}$) and low ($\sim 5\text{--}10\ \mu\text{mol m}^{-2}\ \text{s}^{-1}$) light intensity exposure on chlorophyll pigment concentration in *Ulva* sp. collected from Belmar Beach, New Jersey. Chlorophyll pigments were extracted every 2 weeks and analyzed using spectrophotometry to measure absorbance at chlorophyll-specific wavelengths. Pigment concentrations will then be calculated. Preliminary results showed an initial decrease in chlorophyll absorbance across all treatments following

removal from the natural environment. However, over time, samples exposed to high light intensity maintained higher absorbance values compared to those in low light conditions. This suggests the low-light treatment fell below the optimal light threshold required for sustained chlorophyll production. These findings indicate that light intensity plays a critical role in chlorophyll production of the *Ulva* sp. Understanding how this species responds to light variability may help explain its success in dynamic coastal environments and improve predictions of macroalgal productivity under changing environmental conditions.

P12 – Comparative Analysis of Protocols for Generating Aposymbiotic Anemones (*Exaiptasia*).

Nicole Spar¹, Stefan Anthopoulos¹, Hannah Reich¹ ¹SUNY College of Environmental Science and Forestry, Syracuse, NY **(President's Award candidate)**

Cnidarian-algal symbioses between reef-building corals and dinoflagellate algae (Symbiodiniaceae) are crucial to growth of the biodiversity and productivity hotspots that form coral reef ecosystems. The association between host and symbiont, and the processes that maintain this mutualism, are highly specific as a result of their coevolutionary history. As climate change driven stressors increasingly threaten these vital ecosystems, understanding this symbiosis at a species- or strain-specific level has become imperative. *Exaiptasia pallida*, a small subtropical sea anemone, maintains a comparable endosymbiotic association with Symbiodiniaceae. *Aiptasia* is readily cultured and experimentally manipulated under controlled laboratory conditions, particularly by the removal of the symbionts, making it an effective model system for coral symbiosis research. This study aims to characterize three protocols for creating aposymbiotic (endosymbiont-free) *Exaiptasia* through the tracking rates of algal symbiont loss and changes in the bacterial community. The protocols that we compared include dark exposure, cold-shock (4 °C), and menthol treatments (n = 18 per treatment), along with an experimental tank control treatment (25 °C incubation). The change in algal and bacterial symbionts from the tissue homogenate of the *Exaiptasia* (n=3 per week per treatment) were monitored by cell densities. Improved knowledge of the different aposymbiotic methods will help to improve future studies by understanding the effective protocols for removing the symbionts, consequently expanding coral symbiosis experimental studies with various host-symbiont pairings.

P13 – Using *Chlamydomonas reinhardtii* to Study Cilia Gene Regulation. Emily Wassouf, Hayley Mello, and Jason M. Brown. Biology Department, Salem State University, Salem, MA 01970, U.S.A. (President's Award candidate)

Cilia are hairlike organelles extending from various eukaryotic cells that provide important functions, such as the ability to swim and sense the environment. Defects in cilia cause many human diseases, or ciliopathies. While much is known about the structure and function of cilia, the regulation of cilia building genes is not well understood. One currently proposed model of cilia gene regulation is the Repressor Sequestration Model (Perlaza 2023). This model suggests the presence of a constitutively expressed repressor that inhibits upregulation of cilia building genes in cells with steady state cilia. Upon deciliation, the repressor is sequestered into rapidly growing cilia, allowing the upregulation of cilia building genes and subsequent cilia growth.

Using the unicellular, biciliated green alga, *Chlamydomonas reinhardtii*, we generated a workflow capable of producing a mutant with a disrupted repressor gene to further test this model. As an approach to further investigation of cilia growth regulation, we applied a bioluminescent reporter gene and qPCR to measure the expression of *LC8*, a gene known to be upregulated during cilia regeneration, in wild-type cells. Expression of the endogenous and inserted sequences was compared to evaluate the efficacy of these methods in this application. Our results suggest these techniques could be implemented to examine gene regulation in mutant strains in the future.

P14 – Variation of salinity preferences among Symbiodiniaceae

Kara Meaney¹, Hannah Reich¹. ¹SUNY ESF, Syracuse, NY, 13210, U.S.A. (**President's Award candidate**)

Marine dinoflagellates within the family Symbiodiniaceae form symbiotic relationships with corals, bivalves, and jellyfish hosts where they translocate photosynthetic products to their host and receive host waste products in return. Although Symbiodiniaceae microalgae are known for their symbiotic associations, they can persist in a free-living state, and are culturable in laboratory settings. Using cell cultures, free-living algae's responses to abiotic stressors can be observed in the absence of the host, supporting the deconstruction of the symbiosis for targeted experimentation. In this experiment, the selected stressor was salinity, where liquid media was modified to be 24, 32, 35, and 42 parts per thousand (ppt) to understand the effects of hypo- and hyper- saline conditions on growth of Symbiodiniaceae species *Symbiodinium tridacnidorum*, *Breviolum minutum*, *Effrenium voratum*, and *Cladocopium infusutulum*. To track cell density, samples were counted using flow cytometry with species specific gating protocols based on cell size and granularity. *S. tridacnidorum* preferred higher salinities and displayed reduced growth in low salinities, whereas *B. minutum* shows the opposite salinity preferences. Based on varying growth rates, salinity tolerance varies among the four species. *B. minutum*, a symbiont of jellyfish and corals, may benefit the associated host by providing wider salinity tolerance. By conducting cell culture experiments, we can attain a greater understanding of how salinity impacts Symbiodiniaceae and how their invertebrate hosts are vulnerable to climate change consequences such as temperature, ocean acidification, and osmotic shock.

P15 – Rockin' Trio: Three Experiments on Epilithic Algal Response to N & P Additions. Amanda Gracia & Raymond Kepner. Biology Department, Marist University, Poughkeepsie, NY 12601, U.S.A. (President's Award candidate)

Three different microcosm experiments explored how epilithic algae respond to elevated concentrations of nitrate (+N), phosphate (+P), and/or a combination of nitrate and phosphate (+NP) in Hudson River water, as would occur with continued cultural eutrophication. Methods of these studies varied but in all cases algal & cyanobacterial growth on replicate granite tiles submerged in control and nutrient-amended water were assayed via pigment analysis using a bbe moldaenke Fluoroprobe II.. In all experiments total chlorophyll levels were in the order Control < +P < +N < +NP. Thus N appears to be more important in regulating biomass

accumulation than P. Large differences were observed in epilithic taxa. In two experiments conducted with water collected in March, pennate diatoms dominated communities with virtually no cyanobacteria present. However in a study conducted with water collected in early November, cyanobacteria increased significantly in +N & +NP treatments, with BG chlorophyll levels reaching a mean of nearly 2 $\mu\text{g cm}^{-2}$. Differences in community composition responses between the 3 experiments were certainly a function of differences in microcosm set up and the season of sample collection, but most importantly by the nutrient additions. This project highlights the value of managing nutrient inputs to maintain ecosystem stability and avoid the enrichment of epilithon in cyanobacteria which may act as seed material for cyanohABs, an increasing problem in the Hudson.

P16 – Analyzing shifts in plankton biomass across spatiotemporal gradients in the Gulf of Maine. Julia Hobbs¹, Shea Leary¹, Jessie Mahowald¹, Patricia Thibodeau¹

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Plankton are key components of marine food webs and serve as indicators of ecological health. Phytoplankton fix inorganic carbon that can then be consumed by zooplankton to support higher trophic levels, as well as impact nutrient cycling and the movement of carbon throughout the ecosystem. Three years (2014-2016) of sampling data collected across the Gulf of Maine, both north to south and coast to shelf, were analyzed to determine spatial and temporal patterns in zooplankton biomass. In situ observations were then combined with satellite data to examine how environmental factors, including chlorophyll a, a proxy for phytoplankton biomass, sea surface temperature, and salinity, influence zooplankton biomass. Preliminary results identified higher zooplankton biomass in the Southern Gulf of Maine compared to the northern Gulf of Maine region. Significant differences were observed for chlorophyll-a concentration and zooplankton biomass between 2014 and 2015. These results provide insight into broader ecosystem changes occurring in the Gulf of Maine and improve our ability to anticipate how marine food webs may respond to ongoing environmental variation and climate-driven shifts.

P17 – Temperature and Salinity Tolerances of *Gracilaria* sp. Farrah Bryan & Brandon S. O'Brien. Biological Sciences, Kutztown University, Kutztown, PA, 19530, U.S.A (**President's Award candidate**)

The marine macroalgae genus *Gracilaria* is a highly diverse and widely distributed Rhodophyta. This red alga is one of the most cultivated macroalgae for the production of agar, however it is also known to support marine ecosystems for being a biofilter species that can remove organic or inorganic matter, heavy metals, etc. from the water column. This genus is found in many coastal marine ecosystems worldwide including the east coast of the United States. However, climate change impacts in this region are resulting in increasing temperatures and salinity fluctuations. In this study, we tested the effects of changes in temperature and salinity on the growth of *Gracilaria* sp. in a controlled laboratory setting. Five experimental treatments were designed: low temperature (15 °C), high temperature (32 °C), low salinity (20 ppt), high salinity

(40 ppt), and a control group (room temp, 30 ppt). To allow algae time to acclimate, all treatments began at the control conditions (room temp, 30 ppt), then were gradually changed until reaching the final high or low temperature or salinity conditions. Samples were kept at these experimental conditions for six and half weeks. Measurements of both external morphological traits (thallus length, mass, and coloration) and internal pigmented cell traits (cell shape and size) were taken bi-weekly. Preliminary results indicate that *Gracilaria* has mixed responses to changes in temperature or salinity. *Gracilaria* thallus length decreased, while the mass increased in response to the control conditions, low temperatures, low salinity, and high salinity conditions. However, *Gracilaria* thallus length and mass increased in response to high temperatures after the first temperature increase but decreased when the temperature was increased further. These findings could potentially provide further insight into *Gracilaria* sp. temperature and salinity tolerance. As coastal ecosystems continue to change, it is important to understand how common macroalgae such as *Gracilaria* will be affected.

P18 – Impact of nutrient addition on algal growth and toxin production in Skaneateles Lake. Emily Garlock & Gregory L Boyer (Trainor Award candidate)

Skaneateles Lake is an important drinking water source for the City of Syracuse. Over the past decade, it has experienced an increasing number of harmful algal blooms. As the lake is historically reported to be phosphorus limited, the source and type of nutrients driving these blooms is unknown. Here we used bottle experiments incubated *in situ* to measure the impact of nutrient additions on the growth of the algae over the course of the season. Natural water samples were spiked with 10x the ambient levels of nitrogen (N) and phosphorus (P) and incubated in lake under natural conditions of light and temperature. Bottles were harvested on days 0, 3, and 7, and chlorophyll, photosynthetic yield, and toxin concentrations measured. Nutrient additions indicated that Skaneateles Lake was largely P-limited in June and July, then transitioned to co-limited by N and P in August and September. October reverted to be primarily P-limited. Green algae dominated the algal flora in these bottle experiments; the cyanobacteria contribution was minor and observed only in August and September. Microcystin toxin levels were low but measurable in these bottles starting in August through October. Significant changes were observed in the microcystin congener profile over the season. These experiments are the first step in establishing the type and critical nutrient thresholds for Skaneateles Lake.

P19 – New records of marine macroalgae from 2025 rapid assessment survey of southern Nova Scotia, Canada. Margaret M. Cassidy¹, Claire Goodwin^{2,3,4} & Gary W. Saunders¹. ¹Centre for Environmental and Molecular Algal Research, University of New Brunswick, Fredericton, Canada; ²Huntsman Marine Science Centre, St Andrews, NB, Canada; ³Department of Biological Sciences, University of New Brunswick, Saint John, NB, Canada; ⁴New Brunswick Museum, Saint John, NB, Canada. (Trainor Award candidate)

Rapid assessment surveys aim to detect non-indigenous or cryptogenic species and document their distribution, particularly in areas where human-mediated vectors of dispersal such as recreational and/or commercial boat traffic may accelerate species' spread. These surveys have been employed in the Northeastern United States periodically since 2000, however comparable

monitoring efforts in Atlantic Canada were largely lacking, particularly of marine macroalgae. In August 2025, we conducted hour-long surveys of 15 marinas in southern Nova Scotia, recording macroalgal species present on floating docks, tires, buoys or other subtidal habitats. Species were identified using morphological and molecular tools, with DNA barcodes (*tufA* for green algae, *rbcL*-3P for red algae and *rbcL* for brown algae) generated for 62 of 159 records. Our results revealed numerous range extensions including four new records for Nova Scotia and/or Canada (including one invasive species) and smaller scale coastal spread of two previously introduced species, as well as the continued presence of five well established non-indigenous species. DNA barcoding also uncovered three genetic groups in need of taxonomic treatment likely previously undetected owing to morphological cryptic. These records for both new and previously documented non-indigenous species, as well as the novel cryptic species complexes, call for the implementation of ongoing monitoring with molecular and morphological tools. Any potential mitigation strategies to reduce the impact on native species require early and accurate monitoring of the flora to discover and monitor the spread of these newcomers.

P20 – Utilizing Metabolomics and Transcriptomics to Establish a Host-Independent Culture System for a Commensal Apicomplexan. Christina Lim¹, Christopher Lane¹ Department of Biological Sciences, University of Rhode Island, Kingston, RI, USA 02881. **(Trainor Award candidate)**

Commensal microbial communities often rely on the unique environmental niches of their host to establish stable populations and take advantage of accessible nutrients. *Nephromyces* is a protist genus of dozens of species, primarily found in Molgulidae tunicate renal sac, a fluid-filled, bladder-like structure rich in oxalic and uric acids. Though *Nephromyces* spp. can utilize these acids for purines and carbon sources, preliminary data suggests that *Nephromyces* can thrive in renal sac fluid outside of the tunicate host. To determine whether host-independent culture is possible, we propose a plan to characterize the metabolite composition of the renal sac fluid and monitor for transcriptional changes of *Nephromyces* over time. Renal sacs from *Molgula occidentalis* will be dissected out and the fluid will be filtered through a 35uM and 0.22uM filter to allow for simultaneous observation of metabolite change with and without the presence of *Nephromyces*. Time series sampling of renal sac fluid will be collected for NMR and HPLC analysis. In tandem, *Nephromyces* cells present in the renal sac fluid at each time point will be harvested for transcriptomic profiling to measure any changes in gene expression that may be related to prolonged separation from host tunicate environment. Using metabolomics and transcriptomics, this study aims to connect protist gene expression with renal sac nutrient availability to see whether *Nephromyces* is amenable to long-term host-independent culturing. Additionally, this serves a way to determine what are the necessary metabolites needed to maintain *Nephromyces* viability and perhaps to induce specific life history stages for future culturing assays.

P21 – Determining the viability of MALDI-TOF imaging to map the presence and spread of allelopathic compounds in *Ulva lactuca* grown in various cultures. Cecelia Williamson¹ & Gordon Ober¹. ¹School of Science & Technology, Endicott College, Beverly, MA, USA 01915 **(Trainor Award candidate)**

Mass spectrometry imaging (MSI) can be a powerful tool to understand the spatial distribution of compounds and molecules within tissues. From inhibiting the growth of competing seaweeds to reducing survival of molluscs, production of allelopathic compounds in seaweeds have been well-studied. *Ulva lactuca*, commonly found in intertidal and shallow subtidal environments, is a bloom-forming species that creates a suite of allelopathic compounds that have been shown to reduce populations of competing species. Here we cultured *Ulva lactuca* in monocultures with high and low density as well as co-cultures, growing *Ulva lactuca* alongside *Chondrus crispus* in high and low densities. This research explores the potential of using MALDI-TOF MS imaging (matrix assisted laser desorption ionization - time of flight mass spec) as a method to investigate the presence and location of allelopathic compounds within *Ulva* thalli across cultures. Previous methods have used mass spectrometry to identify and quantify allelopathic compounds within plant extracts. With the addition of whole thalli imaging, spatial peak distributions were used to map *Ulva*'s production of compounds of interest. Based on these findings, we attempt to elucidate the mechanism by which *Ulva* transmits allelopathic compounds to the surrounding environment and how monoculture co-culture influences the presence and spread of these compounds.

P22 – Light beyond Chloroplasts: Functional Exploration of Proton Pump Rhodopsin in Marine Phytoplankton. Yifan Gu¹ & Senjie Lin¹ ¹Department of Marine Sciences, University of Connecticut, Groton, CT, 06340, U.S.A. **(Trainor Award candidate)**

Proton-pump rhodopsins (PPRs) represent an alternative light-driven energy pathway that may supplement chlorophyll-based photosynthesis in marine microorganisms. PPR generates a proton motive force through retinal-dependent photochemistry, potentially sustaining ATP production when photosynthetic electron transport is limited by environmental stress including nutrient deficiency or suboptimal light. Recent genomic and transcriptomic evidence suggests that PPR widely occurs in marine algae. However, the physiological roles and underlying regulatory mechanisms of PPRs in eukaryotic phytoplankton remain poorly understood. Here, we hypothesize that a diatom PPR functions in coping with nutrient stress. Proton-pumping activity will be quantified using patch-clamp electrophysiology and light-driven pH assays. We have transformed *Phaeodactylum tricornutum* a PPR gene. We are also using the CRISPR/Cas9 genome-editing tool to knockout this gene for physiological comparison with the PPR-overexpressing strain and the wild-type strain. ATP production, photosynthetic efficiency, growth, and carbon fixation, N or P-metabolism transcriptomic responses will be analyzed. The outcome of this project will shed light on whether PPRs play similar roles in diatoms and dinoflagellates.

P23 – Identifying Histones in Typical Dinoflagellates. Trent Norred¹ & Senjie Lin¹ ¹Department of Marine Sciences, University of Connecticut, Groton, CT, 06340, U.S.A. **(Trainor Award candidate)**

Dinoflagellates exhibit highly atypical chromosomal organization, including permanently condensed chromosomes, a different nucleus structure called a dinokaryon, and the apparent absence of canonical nucleosome structure. Despite this, genomic and transcriptomic data has shown the presence and expression of histone genes. To date, histone proteins have only been

tentatively isolated in dinoflagellates, raising questions about their abundance, detectability, and functional role and creating a longstanding discrepancy between the genomic/transcriptomic evidence and actual protein observations. In this study we aim to determine whether histone proteins can be reproducibly isolated and identified across dinoflagellate taxa using targeted protein extraction methods and downstream analytical techniques such as acid extraction, salt-fractionation, and western blots. Specifically, we are planning to determine whether all core histone subunits are detectable, evaluate their relative abundance, and investigate whether their presence is consistent across a variety of growth stages and conditions. This project will help resolve whether histones are minimally expressed but functionally the same or still low abundance but repurposed in dinoflagellates.

P24 – Conserved and Divergent Heat Shock Responses in Diatoms and Dinoflagellates Revealed Using Fluorescent Reporter Systems in *Phaeodactylum tricornutum*. Alexander Francoeur, Yifan Gu, Jackson Sanders, and Senjie Lin. (Trainor Award candidate)

Sensory and stress-response systems in SAR phytoplankton remain poorly characterized, particularly in genetically intractable groups such as dinoflagellates. The heat shock response is one of the most conserved cellular stress pathways, yet its conservation and divergence across major phytoplankton lineages are not well understood. Here, we test (1) the conservation of heat shock regulatory systems between diatoms and dinoflagellates and (2) their differential responses to thermal stress. To do so, we developed GFP-based reporter constructs in the model diatom *Phaeodactylum tricornutum*, driven by promoters containing heat shock elements (HSEs) identified by homology in both *P. tricornutum* and the coral symbiont *Durussinium trenchii*. All constructs exhibited increased expression under heat stress (35 °C), supporting conservation of HSE-mediated transcriptional regulation across these lineages. Heat response was similar in timing, but much stronger with the native HSE. A HSP20–GFP fusion reporter further enhanced signal intensity, enabling more sensitive detection of heat-induced responses. These results demonstrate that core components of the heat shock response are conserved between diatoms and dinoflagellates. This work establishes *P. tricornutum* as a tractable surrogate system for comparative functional studies of dinoflagellate genes and provides a foundation for dissecting thermal stress responses in ecologically important but experimentally challenging phytoplankton, including coral symbionts.

P25 – Genetic and Environmental Regulation of Glycerol Production in Symbiodiniaceae: Trade-offs Between Growth and Symbiotic Function. Jackson Sanders¹, Yifan Gu^{#1}, Trenton Norred^{#1}, Senjie Lin^{1 1} Department of Marine Sciences, University of Connecticut, Groton, CT, 06340, United States # Authors contributed equally (Trainor Award candidate)

Endosymbionts of the family Symbiodiniaceae are central to coral health, largely due to their production of glycerol, a key metabolite transferred to the host. Despite its importance in sustaining coral–algal symbiosis, the regulation of glycerol production, both environmental and genetic, remains poorly understood. Here, we systematically characterize glycerol production across multiple Symbiodiniaceae strains representing major clades under phototrophic and heterotrophic conditions, and identify environmental and strain-specific factors that modulate its production. We show that glycerol output varies substantially among strains, indicating a

strong genetic component underlying glycerol production. Environmental drivers, including nutrient availability, salinity, and light, further modulate this trait. Notably, cells experiencing stress produced orders of magnitude more glycerol than non-stressed controls, revealing a positive relationship between stress and glycerol production. In particular, nutrient limitation significantly enhanced glycerol production relative to nutrient-replete conditions. Together, these results demonstrate that glycerol production is governed by an interaction between intrinsic (genetic/strain-level) capacity and extrinsic environmental conditions. This provides a potential mechanistic link between nutrient enrichment and reduced coral performance, as elevated nutrient levels may suppress glycerol production. More broadly, our findings highlight a trade-off between growth and stress response that shapes symbiotic function. This study establishes a comparative framework for dissecting the genetic and environmental regulation of glycerol production in Symbiodiniaceae.

P26 – Temperature stability and distribution of compounds in the brown alga *Fucus vesiculosus* with antimicrobial properties against gram-positive bacteria. Ethan Case, Katharina H.C. Roese, Mackenzie Beauvais, Emma E. Tobin, Ursula S.R. Röse, School of Biological Sciences, University of New England, 11 Hills Beach Road, Biddeford, Maine, 04005, U.S.A.

Fucus vesiculosus, a brown macroalgal species on the rocky intertidal coast of Maine was explored as a source of bioactive compounds. This research focuses on the potential use of these compounds against three gram-positive microbes, deemed priority pathogens in regards to the need for antibiotic development by the World Health Organization. These three microbes include methicillin-resistant *Staphylococcus aureus* (MRSA) strain USA300, methicillin-sensitive *Staphylococcus aureus* strain Newman (MSSA), and *Staphylococcus epidermidis*. Methanol extracts were prepared from algae and antimicrobial properties were then evaluated in a disk assay. Extracts showed antimicrobial activity against all three pathogens. This antimicrobial activity was more pronounced from extracts of the thallus compared to reproductive parts of algae. In addition, antimicrobial activity could be extracted by submersing algae in solvent for a short time indicating that they are associated with the surface of algae. Antimicrobial compounds were further tested for their storage temperature stability by comparing -80C, -20C, +4C, and room temperature.

P27 – Advancing Macroalgal Biodiversity Research in North-Western Iberia Using DNA Barcoding. Gabriela Borer^{1,2,3}, Stacy Krueger-Hadfield⁴, Filipa MS Martins^{1,2}, Fernando P Lima^{1,2} & Cátia Monteiro^{1,2}. ¹CIBIO, Research Centre in Biodiversity and Genetic Resources - InBIO Associate Laboratory, Campus of Vairão, University of Porto, Vairão, Portugal. ²BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus of Vairão, Vairão, Portugal. ³ICBAS, School of Medicine and Biomedical Sciences, University of Porto, Porto, Portugal. ⁴ Virginia Institute of Marine Science Eastern Shore Laboratory, Wachapreague, VA, USA.

Traditional macroalgal biodiversity studies rely on morphological species identification, but morphology can be misleading or inadequate. Molecular techniques, including DNA barcoding and DNA metabarcoding, are valuable additions to these studies, yet their effectiveness is constrained by incomplete and geographically biased reference databases. Expanding barcode representation for regions such as the North-Western Iberian Peninsula (NWIP) is therefore

essential. The NWIP is biogeographically important because it is where the range boundaries of several warm- and cold-water species are located. This high diversity of macroalgae is also characterized by high morphological variation, challenging correct identification based on traditional guides using morphological characters. Improving DNA barcoding databases for the region would improve the detection of changes in the distribution of cryptic or more challenging species to identify morphologically. This study aims to develop barcodes for macroalgal species in the NWIP to improve database coverage and support the application of molecular methods in biodiversity assessments. Finally, this increase in biodiversity knowledge could support measures to conserve and restore coastal systems impacted by climate change.

P28 – Effects of ammonium concentration and salinity on the growth of two *Pseudochloris wilhelmii* strains under controlled laboratory conditions. Luka Žilić, Maria Blažina, Sunčana Geček. Ruđer Bošković Institute, Rovinj, Croatia

Nutrient availability and salinity are one of the major environmental factors that have effect on the physiology and productivity of marine microalgae. Understanding the tolerance and responses of various strains within a single species provides important knowledge into their ecological adaptability and biotechnological potential. Microalgae from the genus *Pseudochloris* are characterized by rapid growth and tolerance to a wide range of nutrient concentrations and salinity, which makes them well suited to high-density biomass production and wastewater bioremediation. In this study, two strains of *Pseudochloris wilhelmii* (SAG 55.87 and SAG 1.80) were cultivated under various ranges of salinity and ammonium concentrations to assess their growth under controlled laboratory conditions. *P. wilhelmii* strains were cultivated in 96-well microplates using a modified BG11 medium adjusting it to the Redfield ratio, ensuring balanced nutrient availability. Experiments were set up with salinity ranging from 2 to 24 PSU and ammonium concentrations from 0.3 to 19.2 mM. Experiments were conducted in controlled environment and were maintained at 24 °C under a 12:12 h light:dark photoperiod and a photon flux density of 75 $\mu\text{mol m}^{-2} \text{s}^{-1}$. Spectrophotometry was used to assess growth by measuring optical density at 690 nm as a proxy for cellular biomass and metabolic activity. Additional comparisons were made between cultures grown in artificial seawater and those maintained in aged natural seawater to determine potential influences of trace constituents on growth yield. The obtained results show distinct strain-specific responses to both salinity and ammonium concentrations, with *P. wilhelmii* 55.87 showing greater tolerance across the tested range and enhanced growth under intermediate salinity and moderate nitrogen content. These findings improve our understanding of strain-specific nutrient and salinity adaptations in *P. wilhelmii* and provide guidance for optimizing cultivation conditions in controlled environments or biotechnological applications.

P29 – Reproduction we cannot see: microbial population genetics. Stacy Krueger-Hadfield¹, Alexander Geragotelis¹, Trinity Hamilton², Robin Kodner^{3,4}, Solenn Stoeckel⁵

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Unicellular and partially clonal eukaryotes are found across evolutionarily diverse lineages, including many algae. Yet, our understanding of their evolution is limited due to inherent challenges of using tools and predictions that were developed in multicellular and often obligately sexual taxa. These tools are often not tractable in microbial eukaryotes where extracting DNA from unique individuals is difficult. Further, population-level work on microbial eukaryotes has been done primarily on culturable taxa, thereby imposing artificial selection and leading to unrepresentative views of natural diversity. The characterization of microbial reproductive modes (i.e., sex vs. clonality) cannot be predicted by the observation of organisms themselves, especially for the unculturable majority. Therefore, characterization of microbial reproductive modes in natural populations is only possible through population genetic approaches. This poster will highlight recent single cell techniques and appropriate population genetic analyses.

P30 – Routine DNA Barcoding of Maine Seaweeds Uncovers Previously Unreported Taxa and Range Expansions. Jordan Chalfant¹ & Amanda Savoie². ¹Maine Natural History Observatory, Gouldsboro, ME, 04609, U.S.A.; ²Canadian Museum of Nature, Ottawa, Ontario, K1P 6P4, Canada.

Between 2021 and 2025, we conducted routine sampling and DNA barcoding to develop a reference library for Maine's marine macroalgal flora. We surveyed more than 100 sites spanning Maine's coastline, from the Piscataqua River at the southern border to Cobscook Bay in the north. Intertidal sampling was conducted year-round during spring tides, with additional subtidal sampling via SCUBA at select sites. Collecting locations encompassed a broad range of habitats, including tidal freshwater zones of eight river estuaries, numerous floating docks, open coastal locations, and six offshore islands. These efforts produced multiple new DNA-confirmed state records including *Gracilaria vermiculophylla* (Ohmi) Papenfuss, *Antithamnion* cf. *sparsum* Tokida, *Antithamnionella spirographidis* (Schiffner) E.M.Wollaston, *Gaillona rosea* (Roth) Athanasiadis, *Seirospora* cf. *interrupta* (Smith) F.Schmitz, *Acanthosiphonia echinata* (Harvey) Savoie & G.W.Saunders, *Leptosiphonia brodiei* (Dillwyn) Savoie & G.W.Saunders, and *Melanothamnus eastwoodiae* (Setchell & N.L.Gardner) Díaz-Tapia & Maggs. We also documented range expansions for *Grateloupia turuturu* Yamada, *Dasya* cf. *pedicellata* (C.Agardh) C.Agardh, and *Dasya elegans* (G.Martens) C.Agardh. Barcoding further revealed an undetermined Callithamniaceae species closely matching a GenBank sequence tentatively designated *Aglaothamnion pseudobyssoides* (P.Crouan & H.Crouan) Halos. These findings demonstrate that DNA barcoding significantly enhances regional biodiversity inventories and improves detection of cryptic diversity and shifting species distributions in the Gulf of Maine.

P31 – Comparing AI and Manual Image Analysis Methods to Streamline Intertidal Macroalgae Monitoring. Abigail St. Jean^{1,2}, Courtney Schmidt¹, Reuben MacFarlan². ¹Narragansett Bay Estuary Program Providence, RI, 02908, U.S.A.; ²Rhode Island Department Environmental Management Division of Marine Fisheries Jamestown, RI, 02835, U.S.A.

Three contrasting methodologies for evaluating intertidal macroalgae are compared using standardized images from sites in Rhode Island with the goal of finding an efficient system for extracting quantifiable data for use by resource managers. Large amounts of drift and fixed macroalgae dominate the coastal waters of Narragansett Bay and long-term monitoring is vital to understanding their ecological roles, responses to environmental changes, impacts on aquaculture, fisheries, and other coastal activities. Using quadrat image data is an effective way to provide information on taxonomic composition and percent coverage. Manual analysis of quadrat images is time intensive which can limit dataset size, frequency and increase costs spent on labor. Out of a variety of image analysis platforms that can be utilized for this type of research we chose two that leveraged artificial intelligence, and one that did not: Darwin V7 BIIGLE and Image J. By using the same set of images across three platforms we evaluated the relative differences between the three methods from the standpoint of efficiency, usability, cost, and how closely data outputs matched. Ultimately, this work will contribute to systematic long term monitoring efforts led by the Seaweed Ecology and Assessment Collaborative – Rhode Island (SEAC-RI).

P32 – Seaweed Sorter: Northwest Atlantic Edition: a digital application for seaweed species identification. **Gabrielle M. Kuba**¹, Lindsay Green-Gavrielidis², Brian Wysor³ and Patrick T. Martone⁴. ¹Rhode Island Department of Health, Center for Environmental Sciences, Providence, RI, 02903 USA; ²Salem State University, Department of Biology, Salem, MA, 01970 USA; ³Roger Williams University, Department of Biology, Marine Biology & Environmental Science, Bristol, RI 02809 USA; ⁴University of British Columbia, Department of Botany & Biodiversity Research Center, Vancouver, BC, V6T 1Z4, Canada.

Have you ever explored beach drift or rocky intertidal algae in the Northwest Atlantic and wished you had a dichotomous key on your phone to identify a seaweed? Lucky for you, we will soon be launching the Seaweed Sorter: Northwest Atlantic Edition! This updated version of Martone's original "Seaweed Sorter" includes 100+ of the most common species found throughout the northwest Atlantic Ocean. The app uses a series of questions designed to be easily answered by non-specialists, based on (mostly) macroscopic morphological attributes. An image of each morphological trait is presented to help decipher answers. Questions are formatted to have answers of "yes", "no", or "maybe" and through a process of elimination, a short list of possible species results. For each species, descriptions and images are provided that help to confirm the identification. The app will be handy for students new to phycology and non-specialist audiences and can point specialists unfamiliar with the local flora to additional, technical resources. The app is currently in beta-testing and will be available on iOS and Android.

P33 – Macroalgal diversity of Virginia's Eastern Shore: Preliminary findings and the southernmost population of *Grateloupia turuturu*? **Brandon S. O'Brien**^{1,2}, Cameron Boyko¹, Maddison Moser¹

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Macroalgae diversity on the Eastern Shore of Virginia has been historically overlooked, and regional reference books and species lists are sorely outdated. As such, this study began a preliminary survey of macroalgal diversity in this region, with a particular interest in documenting any introduced species. Field surveys were conducted in July 2025 at 19 sites along the Eastern Shore. Sites primarily consisted of publicly-accessible docks, marinas, and boat launches. All macroalgae samples collected from the field were identified to species if possible, and herbarium voucher specimens were made. Taxa groups that could not be confidently identified to species (such as *Ulva* sp.) were instead assigned to morphotypes pending further analysis. In total, 36 unique macroalgae taxa were identified: 15 Chlorophyta, 20 Rhodophyta, and 1 Phaeophyceae. Taxon richness varied from 1 to 12 unique taxa per site, with an average of 5.79 taxa. Four introduced species were identified during the survey: *Codium fragile* subsp. *fragile*, *Gracilaria vermiculophylla*, *Lomentaria clavellosa*, and *Grateloupia turuturu*. *G. turuturu* was found at only one site, in Chincoteague, VA. Targeted collections of *G. turuturu* from this site identified both vegetative thalli and female gametophytes. This is not a new location record for this species, but it is notable that *G. turuturu* was not found in any other locations during this survey, even at sites with similar environmental conditions and boat traffic. We believe that Chincoteague currently represents the southernmost known population of *G. turuturu* on this coast. Given the invasive impacts of *G. turuturu* that have been documented in other regions, we plan to investigate this population further, and monitor for southward spread. This preliminary survey highlights the need for additional research on macroalgal distribution in this understudied region.