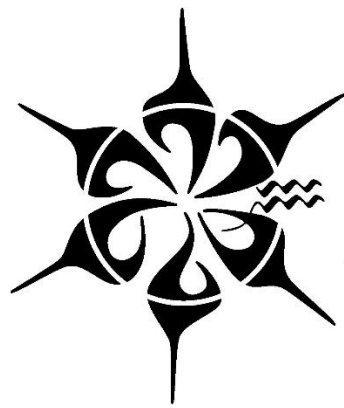


Phycology in a changing climate: biodiversity, blooms, and beyond



**Phycological
Society** of
America

77th Annual Meeting, Providence, Rhode Island, USA
June 26-29, 2023

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MESSAGE FROM THE PRESIDENT

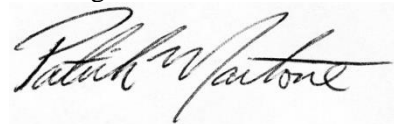
Dear Phycophiles,

Greetings and welcome to the 77th annual meeting of the Phycological Society of America in Providence, Rhode Island! Whether you are a local New Englander or have traveled a great distance... whether you are here to see old friends or to make new connections... it is safe to say that all of us are here to share our enthusiasm for algae and to learn about new research and discoveries in the field of phycology!

The annual PSA meeting is a wonderful place to get inspired! Big thanks to our Program Director Schonna Manning and Deputy Program Director Wade Huang for pulling together a great program. Every day we have a great line up of invited speakers, talking about a wide range of topics from micro- to macroalgae, interspersed with exciting contributed oral and poster sessions. Don't miss the Bold Symposium, highlighting the outstanding research of our graduate students, and the Lang Lecture, delivered this year by Lang Fellow Dr. Trevor Bringle. Our IDEA committee (Inclusivity, Diversity, Equity, and Access) will be hosting a lunch discussion and symposium, led in part by our very own Dr. Ligia Collado-Vides, and I would encourage everyone to attend as we strive to make PSA more inclusive and accessible to all. Students, be sure to join the social event on Tuesday evening, organized by PSA Student Rep Soren Schipper, which will be phycological and fun (phun?). And for those of you who need to top-up your supply of phycological swag, on Wednesday evening there will be a lively auction hosted by our lively auctioneer Dr. Chuck Amsler. On Thursday evening, join your friends and colleagues at the PSA Business Meeting to hear society updates and to help steer the society into a vibrant future.

One more thing. It may sound silly but, for me, some of the most important aspects of our annual meeting are the lunch and coffee breaks. Take this opportunity to strengthen our phycological community; introduce yourself to a young researcher and tell them how much you enjoyed their talk; ask your phycological hero for their perspective on an idea. Phycologists are a friendly group, and I hope everyone is able to take advantage of this time together.

Once again welcome to Rhode Island and best wishes for a wonderful meeting!



Patrick T. Martone
President, Phycological Society of America
Professor, University of British Columbia



MESSAGE FROM THE ORGANIZERS

Greeting Phyco-phanatics,

We are delighted you are here in Providence, Rhode Island for PSA 2023! To make your algal experience as replete as possible, we have a schedule packed with numerous Special Symposia we hope will inspire you here and beyond PSA 2023. We are thankful to everyone who has contributed to the meeting, including invited speakers, oral contributors, poster presenters, as well as field trip and workshop facilitators.

We would also like to acknowledge our sponsors for their generous financial support:



And, as part of this year's meeting, we have representation from the scientific community. The following vendors will have tables in the L'Apogee Reception area, so please stop by to visit and discuss your science:

Balogh International
Fluid Imaging Technologies
Leica Microsystems
Loving Blind Productions
McLane Research Laboratories

Coffee, tea, and water will be available Monday – Thursday from 8 AM – 5 PM on the 17th floor, and light snacks will be provided during the coffee-discussion breaks. If getting lunch on your own, we hope you will take advantage of being in the hub of downtown Providence with numerous options within walking distance. There is a coffee shop in the lobby of the Graduate (Poindexters), and if you are looking for something more substantial, Reiner's is located on the first floor. They are a sports-themed pub with something for everyone. They also have printed maps located near the front entrance to help you navigate downtown Providence, or you may use Google to guide your adventures.

We are very excited to have everyone back for our first in-person PSA meeting since 2019 and look forward to a phantastic week of phycological phun!

Sincerely,
The Program Committee

Schonna Manning, PSA Program Director
Wade Huang, Deputy Program Director
Katherine Perri, Vendor and Sponsorship Chair
Chris Lane, Local Organizer

*** Discounted admission for PSA 2023 meeting attendees at the New Bedford Whaling Museum ***



A singularly marine & fabulous produce: The Cultures of Seaweed

This major exhibition of over 125 works probes humankind's fascination with seaweed from 1780 to today, tracking changing aesthetics and modes of representation, all while underscoring a continuous and unwavering interest in this singularly marine & fabulous produce, as described by Thoreau.

Nineteenth-century American, French, and English audiences were drawn to the myriad unique and mysterious qualities of this vegetation of the sea. Seaweed was a subject of middle-class parlor entertainments, personal gift giving practices, serious scientific study, industrial application, "making-do" working-class culture, culinary experimentation, and aesthetic examination in painting, photography, sculpture, decorative arts, and textiles. In various locations, seaweed appealed to working class laborers and farmers, and to middle and upper class collectors and scientists. It also appeared as a subject and a material in fine art, personal scrapbooks, and various shoreline industries, and is today a celebrated subject and material in contemporary art.

This major exhibition at the NBWM includes loans from over thirty lenders along the Eastern seaboard and the publication of a 222-page hardcover scholarly catalogue, with contributions by 12 leading interdisciplinary scholars. Public programs, including scholarly roundtables, tidepool exploration workshops with local Lands Trust partners, and children's programming, extend the exhibition themes.

The programming and catalogue make connections between the cultural histories of seaweed and urgent environmental issues of today related to climate change, global food insecurity, and restorative aquaculture. How was seaweed a material of interest in the past, and providing critical answers to our future?

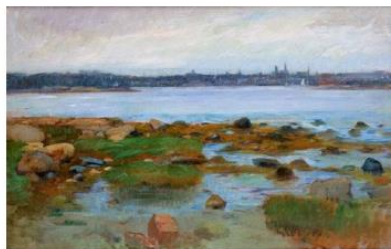
Discount Admission: Between June 24-30, PSA meeting attendees who show their conference badge at the Front Desk receive a 25% off admission.



Founded as The Old Dartmouth Historical Society in 1903, the New Bedford Whaling Museum ignites learning through explorations of art, history, science and culture rooted in the stories of people, the region and an international seaport.

The Museum is the City's leading cultural institution, typically attracting 100,000 visitors, not only from this city and surrounding SouthCoast communities, but from across the Northeast, all 50 states and 30+ countries around the world. Nearly 15,000 of these visitors are K-12 students, and 50% of visitors utilize one of the Museum's 20+ programs to secure free or reduced-cost admission.

The Museum serves its community first and foremost, and inspires all visitors to reflect on the complex issues that shaped the past, remain critical today, and inform a sustainable future.

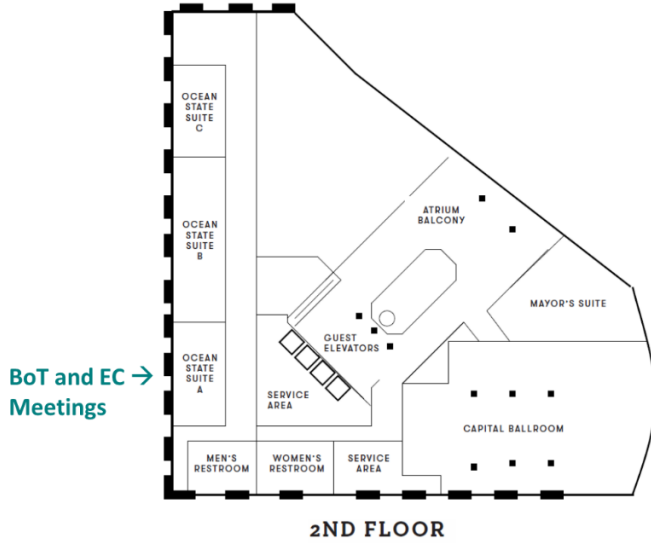


PROGRAM AT-A-GLANCE

PROGRAM	Saturday 6/24/2023	Sunday 6/25/2023	Monday 6/26/2023	Tuesday 6/27/2023	Wednesday 6/28/2023	Thursday 6/29/2023		
7:30 AM 8:00 AM			Early Career Breakfast Summit Reception 18th Floor					
			Opening Remarks Biltmore Ballroom, 17th Floor					
9:00 AM	Ocean Suite A Board of Trustees Meeting 2P-5P Roger Williams University BioBlitz - Seaweed collection, identification, and pressing 6:30A-6P	Ocean Suite A Executive Committee Meeting 9A-5P Narragansett 1P-3P Inclusivity in Teaching Workshop 3:30P-5:30P Figure-making Workshop	Presidential Symposium: Fabien Burki	Special Symposium: Don Anderson	Special Symposium: Kate Hubbard	Special Symposium: Raphael Kudela		
10:00 AM			Coffee-Discussion Break L'Apogee Reception					
			Coleman		Ansler		Alberto	
			Powell		Brawley		Krueger-Hadfield	
11:00 AM			Siver		Breitkreutz		Paight	
			Supratya		Iselin		Shanker-Connelly	
12:00 PM			Lunch break		IDEA Lunch and Discussion		Lunch break	
			Business Meeting Lunch		Student Symposium: Ester Serrão		IDEA Symposium: Ligia Collado-Vides	
1:00 PM			Special Symposium: Cayne Layton		Lang Lecture: Trevor Bringloe		Moore Symposium: Margaret Brisbin	
2:00 PM			Coffee-Discussion Break L'Apogee Reception				Fray	
	Mazzei		Brodie		Calhoun			
	Korabik		McCoy		Cahoon			
	Lees		Oswalt		Krinos			
3:00 PM	Musor		Parfrey		Madrid-Con			
	Kao		Kamel		Butler			
	Necchi		Levine		Dittrich			
4:00 PM	Penn		Richardson		Huang			
	Piango		Schneider		Wade			
	Rolf		Schipper		Delwiche			
	Thornton		Whalen		Genot			
	Robertson		Crowell		Kurtz			
	Tribute: Dr. Steidinger		Kodner		Reich			
	Schenk		Fumo		Yarish			
5:00 PM	Break					Break		
6:00 PM	Break		Poster Session I		Poster Session II			
	Opening Mixer		Auction					
7:00 PM						PSA Awards Banquet		
8:00 PM							Student Social	
9:00 PM								

IMPORTANT: Presenting authors are listed in the schedule above; full authorship for presentations is provided in the abstract sections.

THE GRADUATE HOTEL – FLOOR GUIDE

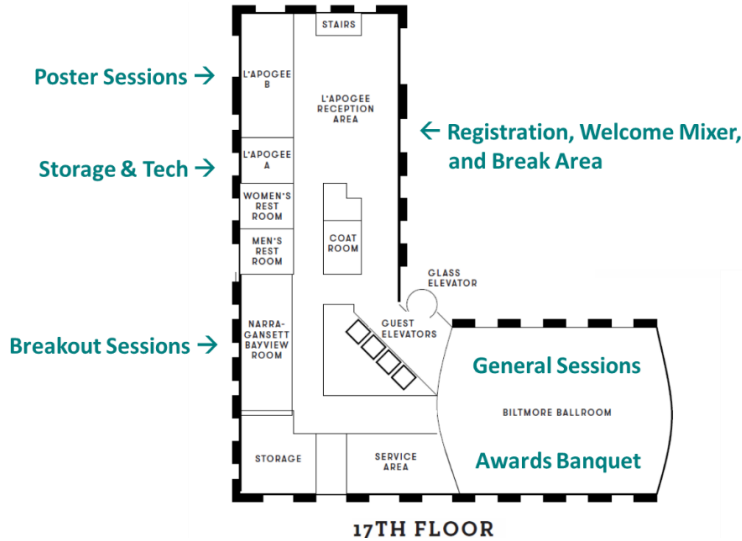


2nd floor

BoT and EC Meetings – **Ocean Suite A**

Editorial Board Lunch – **Ocean Suite A**

2ND FLOOR



17th floor

Registration – **near elevators**

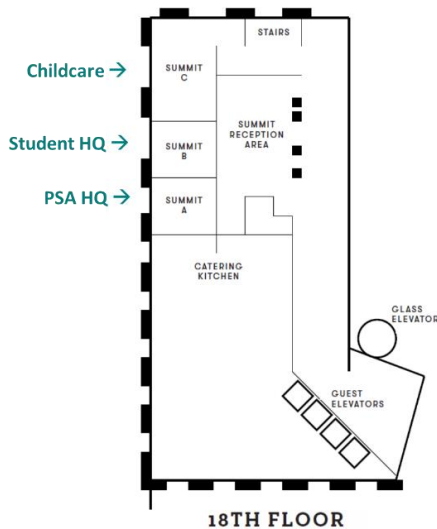
PSA Tech HQ – **L'Apogee A**

General Sessions – **Biltmore Ballroom**

Breakout Sessions – **Narragansett**

Poster Sessions – **L'Apogee B**

17TH FLOOR



18th floor

PSA HQ – **Summit A**

PSA Student HQ – **Summit B**

PSA Childcare – **Summit C**

18TH FLOOR

PSA MEETING REGISTRATION

The registration table is located on the 17th floor directly across from the elevators. There will be volunteers available to check in registrants starting Sunday, June 25th, from 8 AM – 6 PM. During the week, Monday – Thursday, someone will be available to check in registrants 8 – 9 AM and during the breaks.

We've gone 100% green – to reduce our carbon footprint, the program is digital. Please check the PSA website for the Final Program and emails for updates. Daily announcements will be provided during the opening remarks to highlight each day's activities.

INSTRUCTIONS FOR PSA 2023 CONTRIBUTORS

Oral Presentations

Please upload your PowerPoint presentations no later than 8:45 AM on the day of your talk in the PSA Tech HQ located in L'Apogee A, 17th floor. Add your file to the folder with the appropriate room (Biltmore vs Narragansett) and name your file accordingly: TIME(24-HR)_DAY(ABBREV)_LASTNAME, e.g., 1500_TUE_HUANG.

DO NOT YOUR LOAD YOUR PRESENTATION AT THE PODIUM – this takes time away from your presentation and is a distraction to others.

Poster Presentations

Please have posters up and displayed in L'Apogee B (17th floor) at your numbered location before 5 PM on Monday, June 26th, 2023. Take down your posters no later than noon on Thursday, June 29th, 2023, so the poster boards can be disassembled and returned to the rental company.



PSA MEETING CODE OF CONDUCT

PSA meetings are open to PSA members as well as others interested in psychology. PSA is committed to providing a safe, productive and welcoming environment for all meeting participants. All participants including, but not limited to, attendees, speakers, volunteers, exhibitors, and service providers are expected to abide by this PSA Meeting Code of Conduct. This Code of Conduct applies to all PSA meeting-related events including those sponsored by organizations other than PSA but held in conjunction with PSA events, in both public and private facilities. This Code applies to in-person and virtual events.

Expected Behavior

- All participants, attendees, and vendors are treated with respect and consideration, valuing a diversity of views and opinions.
- Be considerate, respectful, and collaborative.
- Communicate openly with respect for others, critiquing ideas rather than individuals.
- Avoid personal attacks directed toward other attendees, participants, and suppliers/vendors.
- Be mindful of your surroundings and of your fellow participants. Alert PSA leadership if you notice a dangerous situation or someone in distress.
- Respect the rules and policies of the meeting venue, hotels, PSA contracted facility, or any other venue.

Unacceptable Behavior

- Harassment, intimidation or discrimination in any form will not be tolerated.
- Physical or verbal abuse of any attendee, speaker, volunteer, exhibitor, service provider or other meeting guest will not be tolerated.
- Examples of unacceptable behavior include, but are not limited to, verbal comments related to gender, gender identity and expression, sexual orientation, disability, physical appearance, body size, race, religion, national origin, as well as inappropriate use of nudity and/or sexual images in public spaces or in presentations, and threatening or stalking any attendee, speaker, volunteer, exhibitor, service provider or other meeting guest.
- Recording or taking photography of another individual's presentation without the explicit permission of the presenter is not allowed.
- Disruption of talks at oral or poster sessions, in the exhibit hall or at other events organized by PSA at the meeting venue, hotels, or other PSA contracted facilities is not allowed.

Consequences

- Anyone requested to stop unacceptable behavior is expected to comply immediately.
- PSA leadership (or their designee) or security may take any action deemed necessary and appropriate, including immediate removal from the meeting without warning or refund.
- PSA reserves the right to prohibit attendance at any future meeting.

Reporting Unacceptable Behavior

- If you are the subject of unacceptable behavior or have witnessed any such behavior, please immediately notify a member of the PSA leadership.
- Notification should be done by contacting PSA leadership on-site or e-mailing your concern to one or more of the following representatives for 2021: Eric Linton, PSA President (executive@psaalgae.org), Schonna Manning, Program Director (schonna.manning@fiu.edu).
- Anyone experiencing or witnessing behavior that constitutes an immediate or serious threat to public safety at a PSA meeting is advised to either tell a security guard or locate a venue phone and ask for security.

PSA 2023 PRE-MEETING WEEKEND

SATURDAY, JUNE 24th, 2023

- 6:30 AM BioBlitz: Seaweed Collection, Identification, and Pressing at Roger Williams University (By Registration)
- 1:00 PM Board of Trustees Meeting (Ocean Suite A)

SUNDAY, JUNE 25th, 2023

- 9:00 AM Executive Committee Meeting (Ocean Suite A)
- 1:00 PM Workshop: Inclusive Teaching in Phycology (By Registration, Narragansett)
- 3:30 PM Workshop: Figure Preparation: A primer in FUJI and Journal of Phycology Requirements (By Registration, Narragansett)
- 6:00 PM** ***WELCOME RECEPTION (L'Apogee Reception Area)***
-

PSA 2023 MEETING DAILY PROGRAM

MONDAY, JUNE 26th, 2023

- 7:30 AM *Early Career Breakfast (By Reservation; 18th Floor Summit Reception Area)*
- 8:45 AM Opening Remarks (Biltmore Ballroom)
- 9:00 AM **Presidential Symposium, Fabien Burki**
Moderator: Patrick Martone (Biltmore Ballroom)



Fabien Burki is an Associate Professor in the program of Systematic Biology at Uppsala University (Sweden). He moved to Sweden in 2016 to start his lab, after undergraduate and graduate studies at the University of Geneva and a postdoc at the University of British Columbia in Vancouver. He is also a platform scientific director at the microbial single-cell genomic facility at SciLifeLab, and an Associate Editor in the journal *Molecular Phylogenetics and Evolution*. Fabien's work in phylogenomics has contributed to obtaining a modern understanding of the tree of eukaryotes, which he uses to frame essential diversification processes during eukaryote evolution such as endosymbiosis. Currently, his lab's main interest is the study of plastid origin, for which he is supported by an ERC Consolidator grant. Website: <https://www.burki-lab.net/>

ENDOSYMBIOSIS: HOW MUCH IS ENOUGH?

- 10:00 AM *Coffee and Discussion Break (L'Apogee Reception)*

10:30 AM **Climate Change, Moderator: Deb Robertson (Biltmore Ballroom)**

10:30 AM Coleman et al., FUTURE PROOFING KELP FORESTS

10:45 AM Powell et al., THERMOTOLERANT SYMBIODINACEAE ASSOCIATED WITH CORAL HOLOBIONTS MAY PROMOTE PERSISTENCE IN EXTREME ENVIRONMENTS AND AFFECT BACTERIAL COMMUNITY STRUCTURE

11:00 AM Siver et al., HISTORY OF THE GIRAFFE PIPE LOCALITY INFERRED FROM MICROFOSSIL REMAINS: A THRIVING SUBARCTIC LAKE ECOSYSTEM DURING THE WARM EOCENE

11:15 AM Supratya et al., VARIATION IN THERMAL TOLERANCE BETWEEN POPULATIONS AND LIFE STAGES OF THE BULL KELP *NEREOCYSTIS LUETKEANA*

11:30 AM *Lunch Break (On Your Own)*

1:00 PM **Student Symposium, Ester Serrão**
Moderator: Soren Schipper (Biltmore Ballroom)



Ester Serrão is a Professor at the University of Algarve (Portugal), Pew Marine Fellow. Ester studies biogeography, evolutionary ecology and conservation, with a special focus on marine forests of macroalgae, temperate corals, seagrasses. With collaborators from all oceans, she studies evolutionary processes driving hotspots of rich and unique genetic variability of marine forests globally. She has a large experience in academic training and her global research on marine conservation and restoration is also applied to local challenges involving and training citizens and stakeholders in practical actions for conservation of marine forests. She published > 300 international peer-reviewed research papers, that have been widely cited (Scopus H-index 55). Ester will present her talk, CLIMATE-DRIVEN EVOLUTION AT RANGE MARGINS OF

MARINE FORESTS.

2:00 PM *Coffee and Discussion Break (L'Apogee Reception)*

2:30 PM **Bold Award Session I, Moderator: Matt Ashworth (Biltmore Ballroom)**

2:30 PM Fray et al., MULTI-MARKER METABARCODING REVEALS INCREASED DIVERSITY AND EVIDENCE OF BIOGEOGRAPHIC INFLUENCE ON MICROBIAL MATS OF LOW-OXYGEN, HIGH-SULFUR SPRINGS

2:45 PM Korabik et al., INVASIVE SPECIES AND CHANGING CLIMATE IMPACT THE REPRODUCTION OF ESTUARINE KELP POPULATIONS

3:00 PM Lees et al., KELPS MAY COMPENSATE FOR LOW NITRATE AVAILABILITY BY USING ALTERNATIVE FORMS SUCH AS UREA AND AMMONIUM

3:15 PM Musor et al., A STICKY SITUATION: CHEMICAL AND CELLULAR INVESTIGATION OF ADHESION IN THE KELP *ALARIA MARGINATA*

3:30 PM *Coffee and Discussion Break (L'Apogee Reception)*

- 4:00 PM** **Bold Award Session II, Moderator: Matt Ashworth (Biltmore Ballroom)**
- 4:00 PM Penn et al., THE ROLE OF MACROALGAL MICROBIOMES IN THE UPTAKE OF MERCURY BY COASTAL AND ESTUARINE SEA LETTUCE (*ULVA* SPP.)
- 4:15 PM Rolfe et al., ECOPHYSIOLOGICAL ADAPTATIONS OF ABUNDANT MESOPHOTIC MACROALGAE IN THE MAIN HAWAIIAN ISLANDS: SHEDDING LIGHT ON MACROALGAL PHOTOSYNTHESIS
- 4:30 PM Thornton et al., CHARACTERIZING THE REPRODUCTIVE SYSTEM IN TWO INVASIVE AVRAINVILLEA POPULATIONS
- 4:45 PM** **A tribute to the life and career of Dr. Karen Steidinger (1938-2023)**
- 5:00 PM *Discussion Break*
- 6:00 PM** **POSTER SESSION I (Odd-Numbered Presenters)**
- 8:00 PM *Conclude Session*
-

TUESDAY, JUNE 27th, 2023

- 8:45 AM *Opening Remarks*
- 9:00 AM** **Special Symposium, Don Anderson**
Moderator: Schonna Manning (Biltmore Ballroom)



Don Anderson is a Senior Scientist in the Biology Department of the Woods Hole Oceanographic Institution. He earned three degrees from MIT – a BS in Mechanical Engineering in 1970, and a MS (1975) and PhD in Civil and Environmental Engineering in 1977. He joined the scientific staff at WHOI in 1978. Anderson is the former director of WHOI’s Coastal Ocean Institute (COI), and presently serves as Director of the Cooperative Institute for North Atlantic Research (CINAR). Anderson also serves as Director of the U.S. National Office for Harmful Algal Blooms. Anderson is the author, co-author, or editor of over 330 scientific papers and 14 books. Don will present his talk, BLOOM DYNAMICS AND PHYSIOLOGICAL ECOLOGY OF THE HARMFUL ALGAL BLOOM (HAB) SPECIES ALEXANDRIUM CATENELLA IN TEMPERATE AND ARCTIC WATERS.

- 10:00 AM *Coffee and Discussion Break (L’Apogee Reception)*
- 10:30 AM** **Ecology I, Moderator: Julie Koester (Biltmore Ballroom)**
- 10:30 AM Amsler et al., STRONG CORRELATIONS OF SEA ICE COVER WITH MACROALGAL COVER ALONG THE ANTARCTIC PENINSULA: RAMIFICATIONS FOR PRESENT AND FUTURE BENTHIC COMMUNITIES
- 10:45 AM Brawley et al., ZONE, SPECIES, AND TISSUE ALL SHAPE THE INTERTIDAL MACROALGAL MICROBIOME

- 11:00 AM Breitkreutz et al., DOES FLOW SPEED AFFECT BLADE NUMBER IN THE BULL KELP, *NEREOCYSTIS LUETKEANA*?
- 11:15 AM Iselin et al., THE MYSTERIOUS WORLD OF BULL KELP: ECOLOGICAL STORYTELLING WITH A DESIGNER'S INTENTION, AN ARTIST'S EYE, AND A WRITER'S EAR
- 11:30 PM *IDEA Lunch and Discussion (By Reservation; Biltmore Ballroom)*
- 1:00 PM IDEA Symposium, Ligia Collado-Vides**
Moderator: Robin Kodner (Biltmore Ballroom)



Ligia Collado-Vides obtained her PhD at the National Autonomous University of México. She is a marine botanist with main research emphasis on subtropical and tropical marine macroalgae, including ecological and floristic approaches. Her laboratory and team address local, regional, and global ecological questions and issues, from quantifying and comparing carbon contribution of calcareous algae in South Florida and Yucatan, to Atlantic wide macroalgal blooms. She has more than 55 peer-review publications plus chapters in books and many scientific reports. Her group is a combination of graduate and undergraduate students from different cultures, origins and living in different countries. She is a Full Teaching professor and the Associate Chair of the Department of Biology at Florida International University.

Ligia will present her talk, LARGE SCALE MACROALGAL BLOOMS ARE A SYMPTOM OF GLOBAL CHANGE POSING LARGE SCALE CHALLENGES THAT REQUIRES RESOURCE MANAGERS, THINKERS, AND SCIENTISTS WITH A GLOBAL, DIVERSE, EQUANIMOUS, AND INCLUSIVE PERSPECTIVE.

2:00 PM *Coffee and Discussion Break (L'Apogee Reception)*

2:30 PM Ecology II, Moderator: Stacy Krueger-Hadfield (Biltmore Ballroom)

2:30 PM Mazzei et al., PHYTOPLANKTON ASSEMBLAGE STRUCTURE, DRIVERS, AND THRESHOLDS IN A LARGE, SHALLOW, AND EUTROPHIC LAKE IN FLORIDA, USA

2:45 PM McCoy et al., PREDATION, COMMUNITY ASYNCHRONY, AND METACOMMUNITY STABILITY IN BENTHIC CYANOBACTERIAL MATS

3:00 PM Oswald et al., DOES ICE COVER IMPACT MACROALGAL CHEMICAL COMPOSITION IN THE WESTERN ANTARCTIC PENINSULA?

3:15 PM Parfrey et al., DO ECOLOGICAL DISTRIBUTIONS OF MICROBIAL SYMBIONTS HELP IDENTIFY PROBIOTICS?

2:30 PM Biodiversity and Cell Biology I, Moderator: Melinda Coleman (Narragansett)

2:30 PM Brodie et al., BIODIVERSITY OF SOUTH ATLANTIC AND SOUTHERN OCEAN SEaweEDS: RICH, CHARISMATIC, AND UNDESCRIBED ISLAND FLORAS

2:45 PM Cahoon et al., LESSONS LEARNED FROM LINEAGE DIRECTED METABARCODING PRIMERS - EUSTIGMATOPHYTES AND CRYPTOMONAS

3:00 PM Krinos et al., INTRASPECIFIC DIFFERENCES IN THERMAL ACCLIMATION IMPACT THE ECOLOGICAL NICHE OF COCCOLITHOPHORES

- 3:15 PM Madrid-Concepcion et al., DIVERSITY AND RELATIONSHIPS OF GRACILARIA SPECIES FROM THE PACIFIC COAST OF PANAMA
- 3:30 PM *Coffee and Discussion Break (L'Apogee Reception)*
- 4:00 PM Ecology III, Moderator: Trevor Bringlee (Biltmore Ballroom)**
- 4:00 PM Richardson et al., A NOVEL FORM OF CHROMATIC ACCLIMATION BY CRYPTOPHYTES OF THE GENUS *HEMISELMIS*
- 4:15 PM Schipper et al., LIGHT IMPACT ON CRUSTOSE CORALLINE ALGAE FROM THE GREAT BARRIER REEF GROWING ON ARTIFICIAL SUBSTRATE IN AQUACULTURE
- 4:30 PM Whalen et al., LASTING IMPACTS OF A HISTORIC MARINE HEATWAVE ON ROCKY INTERTIDAL SEAWEED COMMUNITIES
- 4:45 PM Kodner et al., PATCHY AND PINK: DYNAMICS OF A *CHLAINOMONAS* SP. (CHALMYDOMONADALES, CHLOROPHYTA) ALGAL BLOOM ON BAGLEY LAKE, NORTH CASCADES, WA
- 4:00 PM Biodiversity and Cell Biology II, Moderator: Karolina Fučíková (Narragansett)**
- 4:00 PM Huang et al., SCREENING THE PLANKTON ASSEMBLADGE IN YORK RIVER USING THE IMAGING FLOWCYTOBOT
- 4:15 PM Delwiche et al., CELL DIVISION AND GROWTH IN COLEOCHAETE (STREPTOPHYTA) EXAMINED BY CONFOCAL MICROSCOPY
- 4:30 PM Genot et al., ETHYLENE SIGNALING IN *CYANOPHORA PARADOXA*: REVEALING HORMONE USAGE IN A GLAUCOPHYTE ALGA
- 4:45 PM Reich et al., FRENEMIES WITH PHYSIOLOGICAL CONSEQUENCES: ENVIRONMENTAL PERTURBATIONS SWAY CELLULAR CROSSTALK WITHIN MICROALGAL-BACTERIAL INTERACTIONS
- 5:00 PM *Discussion Break*
- 6:00 PM POSTER SESSION II (Even-Numbered Presenters)**
- 8:00 PM *Conclude Session*
- 8:00 PM STUDENT SOCIAL (By Reservation; 18th floor Summit Reception Area)**
Host: Soren Schipper, PSA Student Representative
-

WEDNESDAY, JUNE 28th, 2023

- 8:45 AM *Opening Remarks*
- 9:00 AM Special Symposium, Kate Hubbard (Biltmore Ballroom)**
Moderator: Wade Huang



Kate Hubbard leads the harmful algal bloom (HAB) monitoring and research program for the Florida Fish and Wildlife Conservation Commission’s Fish and Wildlife Research Institute (FWC-FWRI). She also directs the FWC Center for Red Tide Research and for the past decade has been a Guest Investigator at Woods Hole Oceanographic Institution. She works with a broad network of partners to sustain and advance comprehensive and interdisciplinary HAB observations. She is involved with projects in polar to subtropical systems, focused on using these observations to better predict blooms and mitigate their impacts. She received her B.A. in Biology from New College of Florida and M.S. and Ph.D. degrees in Biological Oceanography from the

University of Washington. Kate will present her talk, **EXPLORING LATITUDINAL CONSTRAINTS (OR LACK THEREOF?) ON HARMFUL ALGAL BLOOMS.**

10:00 AM *Coffee and Discussion Break (L’Apogee Reception)*

10:30 AM Evolution, Moderator: Sophie McCoy (Biltmore Ballroom)

10:30 AM Alberto et al., **THE RESILIENCE OF HIGH GENETIC DIVERSITY IN CALIFORNIA'S CANOPY-FORMING KELPS**

10:45 AM Krueger-Hadfield et al., **IS AN ISOMORPHIC ALTERNATION REALLY ISOMORPHIC? INVESTIGATING THALLUS SIZE AND SHAPE IN AN ‘ISOMORPHIC’ MACROALGA**

11:00 AM Paight et al., **FUNCTIONAL REDUNDANCY AND METABOLIC ADAPTATION: INSIGHTS FROM GENOMIC AND TRANSCRIPTOMIC ANALYSIS**

11:15 AM Shainker-Connelly et al., **INVESTIGATING THE REPRODUCTIVE SYSTEM OF A MONOICOUS, HAPLOID-DIPLOID MACROALGA**

11:30 PM *Lunch Break (On Your Own)*
Editorial Board Lunch (Ocean Suite A)
PSA Student’s Philosopher’s Café (Biltmore)

1:00 PM Special Symposium, Cayne Layton (Biltmore Ballroom)
 Moderator: Patrick Martone



Cayne Layton is a Research Fellow and Lecturer at the University of Tasmania in Australia, where he focusses on the ecology of kelp forests and temperate reef systems, and also kelp aquaculture. Cayne combines field and lab experiments to examine ecosystem function and ecophysiology, especially in response to increasing anthropogenic stressors. Overall, he seeks to address fundamental ecological questions while ensuring his research has practical applications for habitat conservation, restoration, and management. Cayne also has a keen interest in scientific diving, Traditional Ecological Knowledge, and the engagement of science with education and policy. Cayne will present his talk, **KELP FORESTS AND RESTORATION ON AUSTRALIA’S GREAT SOUTHERN REEF.**

2:00 PM *Coffee and Discussion Break (L’Apogee Reception)*

- 2:30 PM** **Molecular Biology I, Moderator: Charles Delwiche (Biltmore Ballroom)**
- 2:30 PM Calhoun et al., EXPLORING ABIOTIC STRESS RESPONSES OF BIOFUEL-RELEVANT ALGAE THROUGH MULTI-OMICS PROFILING AND INTEGRATION
- 2:45 PM Jourdain et al., IDENTIFYING PUTATIVE CALCIFICATION GENES IN THE ARTICULATED CORALLINE ALGA *CALLIARTHRON TUBERCULOSUM*
- 3:00 PM Kamel et al., ELUCIDATION OF PICOCHLORUM CELERI'S VARIOUS STRESS TOLERANCE MOLECULAR PATHWAYS THROUGH MODELING AND MULTIOMICS INTEGRATION
- 3:15 PM Kao et al., LIFE-CYCLE DIFFERENTIATION IN A COSMOPOLITAN MICROALGA: A MULTI-OMIC APPROACH
- 2:30 PM** **Phylogenetic Taxonomy I, Moderator: Jennifer Wolny (Narragansett)**
- 2:30 PM Ashworth et al., MORPHOLOGICAL AND MOLECULAR DIVERSITY IN MARINE CONOPEATE *NITZSCHIA* (BACILLARIOPHYCEAE) SPECIES LEADS TO REVIVAL OF *HOMOEACLADIA*
- 2:45 PM Cabrera et al., MORPHOTYPES OF HAWAIIAN *AMALTHEA* (HALYMENIALES, RHODOPHYTA): DISTINCT SPECIES OR PHENOTYPIC PLASTICITY?
- 3:00 PM Butler et al., WHEN SOFTIES GET PICKY: HOW LIFE STRATEGIES OF SOFT CORALS SHAPE THE EVOLUTION OF THEIR SYMBIONTS
- 3:15 PM Necchi et al., A RECONSIDERATION OF THE GENUS *VISIA* (BATRACHOSPERMALES, RHODOPHYTA) WITH THE PROPOSAL OF NEW GENUS AND SPECIES
- 3:30 PM *Coffee and Discussion Break (L'Apogee Reception)*
- 4:00 PM** **Molecular Biology II, Moderator: Amy Carlile (Biltmore Ballroom)**
- 4:00 PM Piango et al., GENE EXPRESSION ANALYSIS OF SEXUAL MATURITY TRANSITION IN *MACROCYSTIS PYRIFERA* GAMETOPHYTES
- 4:15 PM Ramarui et al., PROTEOMIC AND PHOSPHOPROTEOMIC INVESTIGATION OF A *HAEMATOCOCCUS PLUVIALIS* MUTANT EXHIBITING INCREASED HETEROTROPHIC GROWTH
- 4:30 PM Robertson et al., CHARACTERIZATION OF NITRIC OXIDE SYNTHASES WITH DIVERSE EVOLUTIONARY ORIGINS IN DIATOMS AND OTHER SELECT ALGAL GROUPS
- 4:45 PM Schenk et al., THE BACTERIAL COMMUNITY OF *SACCHARINA LATISSIMA* IS STABLE ACROSS TIME, SPACE, AND STRESS GRADIENTS
- 4:00 PM** **Phylogenetic Taxonomy II and Biogeography, Moderator: Dale Casamatta (Narragansett)**
- 4:00 PM Schneider et al., ON EUROPEAN SPECIES NAMES BEING APPLIED TO WESTERN ATLANTIC MARINE MACROALGAE BY WORKERS IN THE 19TH CENTURY
- 4:15 PM Wade et al., RESOLVING CRYPTIC *CORALLINA* SPECIES (CORALLINALES, RHODOPHYTA) ACROSS THE EASTERN PACIFIC, WITH COMMENTS ON BIOGEOGRAPHY

- 4:30 PM Crowell et al., PHYLOGEOGRAPHY OF THE FRESHWATER RED ALGA *BATRACHOSPERMUM GELATINOSUM* (RHODOPHYTA) IN THE EASTERN UNITED STATES
- 4:45 PM Fumo et al., MODELING DISPERSAL OF *CHONDRIA TUMULOSA* (RHODOMELACEAE, RHODOPHYTA) IN THE PAPAĀNAUMOKUĀKEA MARINE NATIONAL MONUMENT: RAFTING TO NEW FRONTIERS
- 5:00 PM *Discussion Break*
- 6:00 PM **PSA AUCTION, Auctioneer: Chuck Amsler (Biltmore Ballroom)**
- 8:00 PM *Conclude Sessions*
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THURSDAY, JUNE 29th, 2023

- 8:45 AM *Opening Remarks*
- 9:00 AM **Special Symposium, Raphael Kudela (Biltmore Ballroom)**
Moderator: Kirsten Müller



Raphael (Raphe) Kudela is a Distinguished Professor of Ocean Sciences at University of California Santa Cruz. Dr. Kudela has conducted research on aquatic ecology (emphasis on marine systems, but also including land/sea interface and freshwater systems) for more than two decades. His research focuses on the factors and processes linking phytoplankton productivity to higher trophic levels, including the ecology, mitigation, and prediction of harmful algal bloom events, changes in global productivity and fisheries, and linkages to human use of aquatic systems. Kudela previously served as Chair of the Global Ecology and Oceanography of Harmful Algal Blooms program (IOC/SCOR) and as Vice Chair of GlobalHAB, and is an ex-officio member (former co-Chair) of the US National HAB Committee. Within the Ocean Observing framework he serves on the Executive Committee for the Central and Northern California Ocean Observing System (CeNCOOS).

Raphael will present his talk, EMERGING HARMFUL ALGAL BLOOM ISSUES IN THE CALIFORNIA CURRENT: SHIFTING PATTERNS AND NEW ISSUES DRIVEN BY CLIMATE?

- 10:00 AM *Coffee and Discussion Break (L'Apogee Reception)*
- 10:30 AM Harmful Algal Blooms I, Moderator: Wade Huang (Biltmore Ballroom)**
- 10:30 AM Badshah et al., INHIBITING CO₂ FIXATION: A PROMISING STRATEGY FOR COMBATING HARMFUL ALGAL BLOOMS
- 10:45 AM Hatt et al., THE EFFECT OF SARGASSO INUNDATIONS ON NEARSHORE SEAGRASS COMMUNITIES
- 11:00 AM Kausch et al., BLOOM-FORMING, NON-HETEROCYSTOUS *LIMNORAPHIS BIRGEI* GROWS WITHOUT DISSOLVED NITROGEN

11:15 AM Muhlbach et al., IMPLEMENTING THE IMAGING FLOWCYTOBOT (IFCB) WITHIN FLORIDA'S HARMFUL ALGAL BLOOM OBSERVATION NETWORK TO EVALUATE ESTUARINE DYNAMICS DURING *KARENIA BREVIS* BLOOMS

11:30 PM *PSA BUSINESS MEETING LUNCH (Biltmore Ballroom)*

1:00 PM Lang Lecture: Trevor Bringloe (Biltmore Ballroom)
Moderator: Sophie McCoy



Trevor Bringloe is currently a research scientist with the Department of Fisheries and Oceans Canada, and a former McKenzie fellow with the University of Melbourne. His research focuses on the application of whole genome sequencing for phylogenomic, population genomic and metagenomic analysis. His recent work, funded in part by the Phycological Society of America's Norma J. Lang Fellowship, explores global diversity in the kelp genus *Alaria* and the insights gained when moving from DNA barcoding to sequencing whole genomes. Trevor will present the Lang Lecture, USHERING IN AN ERA OF HIGH-RESOLUTION GENETICS IN EVOLUTIONARY PHYCOLOGY.

1:30 PM Moore Foundation Symposium, Margaret Brisbin (Biltmore Ballroom)
Moderator: Chris Lane



Maggi Brisbin completed her Ph.D. at the Okinawa Institute of Science and Technology in Japan and is currently a Simons Foundation Marine Microbial Ecology Postdoctoral Fellow at the Woods Hole Oceanographic Institute working with Harriet Alexander and Mak Saito. Maggi is joining the University of South Florida's College of Marine Science as an Assistant Professor this fall. The MICO lab at USF will study Microbial Interactions in a Changing Ocean with a focus on how interactions between marine microbes contribute to biogeochemical cycles and ecosystem function, how these interactions might respond to climate change, and how changes in the dynamics of these relationships will feedback on climate change impacts. Maggi is particularly enamored with radiolarians and the haptophyte *Phaeocystis* for their many interesting symbiotic relationships. Maggi will present her talk, THE MANY-FACETED SYMBIOSES OF COSMOPOLITAN PHAEOCYSTIS ALGAE.

2:00 PM *Coffee and Discussion Break (L'Apogee Reception)*

2:30 PM Harmful Algal Blooms II & Applied Phycology I, Moderator: Schonna Manning (Biltmore)

2:30 PM Nissimov et al., THE CURIOUS CASE OF CYANOBACTERIA: A TALE OF LIGHT AND DARKNESS

2:45 PM Sung-Clarke et al., BIOPHYSICAL TRAPPING AS A DRIVER OF *DINOPHYSIS ACUMINATA* BLOOM DEVELOPMENT AND PERSISTENCE IN NAUSET MARSH

3:00 PM Watervoort et al., RECENT HARMFUL ALGAL BLOOMS OF *PRYMNESIUM PARVUM* IN TEXAS CONSIST OF MULTIPLE CRYPTIC SPECIES

3:15 PM Levine et al., ALGAE FOUNDATION'S WORKFORCE DEVELOPMENT AND EDUCATION INITIATIVES: ALGAE TECHNOLOGY EDUCATIONAL CONSORTIUM (ATEC) AND THE ALGAEPRIZE 2022-2023

3:30 PM *Coffee and Discussion Break (L'Apogee Reception)*

4:00 PM Applied Phycology II, Moderator: Juliet Brodie (Biltmore Ballroom)

4:00 PM Dittrich et al., INDOOR CULTIVATION PROTOCOLS FOR THE RHODOPHYTES, *DEVALERAEA MOLLIS* AND *PALMARIA HECATENSIS* FROM ALASKA

4:15 PM Gonzalez et al., ASSESSING HEAT TOLERANCE IN SUGAR KELP

4:30 PM Kurtz et al., BIOFOULING ADHESION BY FIELD-SAMPLED AND LABORATORY-CULTURED *ULVA* SPP.

4:45 PM Yarish et al., RECENT ADVANCES IN SEAWEED AQUACULTURE IN THE USA: FROM THE FARM TO BLUE FOOD

5:00 PM *Discussion Break*

7:00 PM PSA AWARDS BANQUET (Biltmore Ballroom)

10:00 PM *Adjourn Meeting*

POSTER PRESENTATION NUMBERS

IMPORTANT: Presenting authors are listed; full authorship for presentations is provided in the abstract section.

1. Allsopp et al., PSEUDOCRYPTIC LINEAGES OF *GLOIOCLADIA* (FAUCHEACEAE, RHODOPHYTA) AND VERTICAL DISTRIBUTION OF THE GENUS IN HAWAIIAN MESOPHOTIC CORAL ECOSYSTEMS
2. Amsler et al., MACROALGAL ASSEMBLAGES AND VERTICAL DISTRIBUTION ALONG A SEA ICE GRADIENT IN THE CENTRAL WESTERN ANTARCTIC PENINSULA
3. Byington et al., ASSESSING DESICCATION STRESS EFFECTS ON MORTALITY RATES AND COMMUNITY COMPOSITION OF DIATOMS RESIDING IN STREAMS PRONE TO DROUGHT
4. Cahoon et al., CRYPTOMONAS PYRENOIDIFERA ORGANELLAR GENOMES AND ESTIMATION OF ITS ITS2 SEQUENCE DIVERSITY USING LINEAGE DIRECTED BARCODE PRIMERS
5. Camara et al., CHARACTERIZATION OF *CHLAINOMONAS SP.* IN SEDIMENT CORE SAMPLES FROM BAGLEY LAKE IN CORRELATION WITH SEDIMENT COMPOSITION AND GLACIAL HISTORY
6. Candelario Rodríguez et al., VIABILITY DETERMINATION OF THE HCT-116 COLORECTAL CANCER CELL LINE TREATED WITH FUCOIDAN EXTRACTED FROM SARGASSUM SPP. IN PUERTO RICO
7. Castillo et al., LIVING SNOW PROJECT: ENGAGING THE COMMUNITY IN ALGAE RESEARCH AND EDUCATION IN A CHANGING CLIMATE
8. Carlile et al., DIVERSITY AND DISTRIBUTION OF *ULVA* SPECIES IN LONG ISLAND SOUND
9. Cho et al., TWO NEW SPECIES OF *ENDOPLURA* (RALFSIALES, PHAEOPHYCEAE) FROM KOREA
10. Chraïbi et al., EPIBIOTIC DIATOM ASSEMBLAGES ON TEXAS FRESHWATER TURTLES
11. Chraïbi et al., EPIZOIC DIATOM DIVERSITY OF GULF OF MEXICO SEA TURTLES
12. *Dunn et al., *HALIMEDA DISCOIDEA* MICROBIOME DIVERSITY IN THE HAWAIIAN ARCHIPELAGO: LOCATION AND TIME MEAN EVERYTHING *Lewin Competition
13. Fučíková et al., FIRST INSIGHTS INTO GREEN ALGAE FROM NEW MEXICO SOILS
14. Greeley et al., LIGHTING THE WAY TO IDENTIFYING THE COMMUNITY COMPOSITION OF BIOLUMINESCENT DINOFLAGELLATES IN THE SALISH SEA
15. Hamsher et al., PHYLOGENOMICS AND TAXONOMIC REVISION OF RHOPALODIALES - DIATOMS WITH OBLIGATE CYANOBACTERIAL ENDOSYMBIONTS
16. Hayes et al., PHYCOCOSM: JGI ALGAL GENOMICS IN 2023
17. Kang et al., DETERMINING THE UPTAKE OF INORGANIC NITROGEN IN MARINE PHYTOPLANKTON ASSEMBLAGES THROUGH THE ¹⁵N-TRACER TECHNIQUE AND METATRANSCRIPTOME

18. *Kuba et al., UNDERSTANDING THE CELLULAR AND MOLECULAR CHANGES OF CHOREOCOLAX POLYSIPHONIAE AND VERTEBRATA LANOSA IN RESPONSE TO INFECTION *Lewin Competition
19. *Marquez et al., NUISANCE *DIDYMO* BLOOMS - EXPLORATION OF DYNAMIC MICROBIAL COMMUNITY COMPOSITION AND FUNCTION *Lewin Competition
20. McCourt et al., THE MACROALGAE HERBARIUM CONSORTIUM PORTAL, PAST AND FUTURE
21. McManus et al., FINDING *EUASTROPSIS* (SPHAEROPLEALES, CHLOROPHYCEAE)
22. Millán Rivera et al., OPTIMIZATION OF DISINFECTION METHODS FOR *CITRUS AURANTIFOLIA* AND *CITRUS SINENSIS* MICROPROPAGATION
23. Müller et al., CHARACTERIZATION OF THE MICROBIAL COMMUNITY ASSOCIATED WITH THE GREAT LAKES INVADER, *BANGIA ATROPURPUREA* (BANGIALES, RHODOPHYTA)
24. Ogushi et al., MORPHOLOGICAL ANALYSIS OF *CORALLINA* SPECIES IN THE NORTHEAST PACIFIC
25. Ortiz Rodriguez et al., INSIGHTS ABOUT A COLLECTION OF *CALOGLOSSA* FROM A FRESHWATER STREAM IN PUERTO RICO
26. Pata et al., POPULATION DYNAMICS OF SNOW ALGAE, *CHLAINOMONAS SP.*, THROUGHOUT A BLOOM CYCLE
27. Patterson Holsworth et al., CAN A PHYCO-SPHERE ASSOCIATED BACTERIUM BE USED AS A BIOLOGICAL CONTROL FOR THE *MICROCYSTIS AERUGINOSA* (CYANOBACTERIA)?
28. Peckol et al., INTRIGUING INTRODUCTIONS: DO INTRODUCED *LITTORINA LITTOREA* AND NATIVE *L. OBTUSATA* PREFER NATIVE OR INVASIVE MACROALGAE?
29. Pestana et al., THE GLOBAL DISTRIBUTION OF DIVERSITY IN GIGARTINALES (RHODOPYTA)
30. Pistorius et al., CONTRASTING NATIVE AND INVASIVE ALGAL PHYSIOLOGY TO UNDERSTAND COMPETITIVE ABILITIES BETWEEN DIFFERENT HABITATS OF CHARLESTON, SC
31. Price et al., NOVEL FLORA OF DIATOMS ASSOCIATED WITH A MESIC EDWARDS PLATEAU CLIFF COMMUNITY IN TEXAS
32. Radek et al., CYANOBACTERIAL CONTRIBUTION TO ANNUAL CYCLES OF PHYTOPLANKTON IN LAKE MURRAY, SC
33. *Radick et al., CHARACTERIZING INVERTEBRATE COMMUNITIES ASSOCIATED WITH THE CRYPTOGENIC ALGA *CHONDRIA TUMULOSA* IN THE PAPAĀNAUMOKUĀKEA MARINE NATIONAL MONUMENT, HAWAII *Lewin Competition
34. Schenk et al., LONG-TERM MONITORING OF MACROALGAL BIODIVERSITY IN STANLEY PARK, VANCOUVER, BRITISH COLUMBIA
35. Smith et al., DIFFERENCES IN PHYTOPLANKTON POPULATIONS IN AGRICULTURAL IRRIGATION PONDS BASED ON SAMPLING TIME AND DEPTH AS REVEALED BY CELL AND PHOTOSYNTHETIC PIGMENT CONCENTRATIONS

36. Supratya et al. KELPS ON DEMAND: CLOSED-SYSTEM PROTOCOLS FOR CULTURING LARGE BULL KELP SPOROPHYTES FOR RESEARCH AND RESTORATION
37. *Thornton et al., CHARACTERIZING THE REPRODUCTIVE SYSTEM OF *FUCUS VESICULOSUS* ALONG THE EASTERN SHORE OF VIRGINIA *Lewin Competition
38. White et al., CHARACTERIZATION OF MACROALGAL ABUNDANCE, DIVERSITY, AND SEASONALITY AT POTENTIAL FORAGING SITES IN SOUTH CAROLINA
39. Wolny et al., NOVEL USE OF THE COVARIS ML230 FOCUSED-ULTRASONICATOR FOR RECOVERING DNA FROM ARMORED DINOFLAGELLATES
40. Won et al., ASSESSING THE BENEFITS OF ANTIOXIDANT AND ANTIBIOTICS TREATMENTS FOR CRYOPRESERVATION OF THE MODEL ALGA *ECTOCARPUS SILICULOSUS* AND THE ENDEMIC ALGA *ACINETOSPORA ASIATICA*

ORAL ABSTRACTS (alphabetical by first author; the presenting author is underlined)

Alberto, F., University of Wisconsin-Milwaukee, United States, albertof@uwm.edu; Raimondi P., University of California at Santa Cruz, United States, raimondi@ucsc.edu; Piango, S. C., University of Wisconsin-Milwaukee, United States, scpiango@uwm.edu; Liggan, L. University of Wisconsin-Milwaukee, United States, lmiggan@uwm.edu

THE RESILIENCE OF HIGH GENETIC DIVERSITY IN CALIFORNIA'S CANOPY-FORMING KELPS

The extension and contraction of species distributions during glacial-interglacial cycles frequently produced pockets of high genetic diversity at the species trailing edges. In the northeast Pacific, glacial refugia likely explain why high genetic diversity is observed at the southern ranges of giant (*Macrocystis pyrifera*) and bull kelp (*Nereocystis luetkeana*). Ironically, with climate change, these regions face a heightened extinction risk threatening the loss of an ancient intraspecific biodiversity layer in these kelps. Recent disturbance to California's kelp forests allowed us to run a before-after analysis of the genetic diversity of both canopy-forming kelps. Despite substantial demographic declines of sporophyte kelp forests, within and between genetic diversity showed remarkable resilience. We discuss the implications of these results for our knowledge of kelp mating systems and dispersal, including dispersal in time (dormancy), and suggest areas of future research to elucidate kelp resilience.

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STRONG CORRELATIONS OF SEA ICE COVER WITH MACROALGAL COVER ALONG THE ANTARCTIC PENINSULA: RAMIFICATIONS FOR PRESENT AND FUTURE BENTHIC COMMUNITIES

Macroalgal forests dominate shallow hard bottom areas along the northern portion of the western Antarctic Peninsula (WAP). Macroalgal biomass and diversity are dramatically lower in the southern WAP but few reports

detail the distributions of macroalgae or associated macroinvertebrates in the central WAP. We used satellite imagery to identify 14 sites differing in sea ice coverage but similar in terms of turbidity along the central WAP. Divers recorded replicate videos of vertical transects between 5 m and 20–40 m. Fleshy macroalgal cover was strongly, negatively correlated with ice concentration, but there was no significant correlation between macroinvertebrate cover and sea ice. Overall community diversity was negatively correlated with sea ice concentration and positively correlated with fleshy macroalgal cover although macroinvertebrate diversity alone was negatively correlated with macroalgal cover. Changes in macroinvertebrate assemblages and overall community metrics were generally linear with sea ice and macroalgal cover. Nonparametric, multivariate analyses of the overall communities resulted in three site clusters corresponding to high, medium, and low fleshy macroalgal cover. Based on predicted likely sea ice decreases by 2100, projected increases in macroalgal cover at sites which currently have high ice cover and low macroalgal cover are substantial. Such changes would have important ramifications to future benthic food web structure, and the potential for Antarctic macroalgae to contribute to future blue carbon sequestration.

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BLOOM DYNAMICS AND PHYSIOLOGICAL ECOLOGY OF THE HARMFUL ALGAL BLOOM (HAB) SPECIES *ALEXANDRIUM CATENELLA* IN TEMPERATE AND ARCTIC WATERS

Alexandrium is one of the major harmful algal bloom (HAB) genera with respect to the diversity, magnitude and consequences of blooms. The ability of *Alexandrium* to colonize multiple habitats and to persist over large regions through time is testimony to the adaptability and resilience of this group of dinoflagellate species, some of which produce potent neurotoxins. Many *Alexandrium* species have complex life histories that include sexuality and the formation of resting cysts that play a major role in bloom dynamics. This talk will focus on *Alexandrium catenella*, a producer of saxitoxins and thus a significant threat to human and ecosystem health worldwide. Ecophysiological studies in three habitats will be highlighted: 1) blooms in shallow, isolated embayments on Cape Cod where complete bloom cycles can be observed in exquisite detail; 2) widespread blooms in temperate coastal waters of the Gulf of Maine; and 3) blooms transported into, and originating within, Pacific Arctic waters of northwestern Alaska. All of these studies include investigations of resting cyst distribution, abundance, and physiology that underlie key aspects of vegetative cell dynamics, and all benefit greatly from the application of new technologies, including autonomous in situ sensors, species-specific rRNA probes for cell identification, and enumeration, and population dynamics models, among others. The response of *A. catenella* populations to a warming climate in these three habitats will also be discussed, highlighting the complications that arise with cyst-forming species in climate assessments.

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MORPHOLOGICAL AND MOLECULAR DIVERSITY IN MARINE CONOPEATE *NITZSCHIA* (BACILLARIOPHYCEAE) SPECIES LEADS TO REVIVAL OF *HOMEOCLADIA*

The diatom family Bacillariaceae is a diverse assemblage of genera and species which bear a distinctive raphe morphology called a “canal raphe”, which is elevated above the frustule surface and supported internally by siliceous perpendicular struts. The most species rich and well-known genus in this family is likely *Nitzschia* Hassall, with species commonly found in the benthos of freshwater and marine habitats. The frustule morphology within *Nitzschia* is variable with respect to the morphology of the pores, valve cross-sectional ultrastructure and even the orientation of the canal raphe, which can be located eccentrically or centrally on the valve. Multiple genera and informal taxonomic sections have been erected based on this morphological variation, but molecular data have suggested that the family itself is not monophyletic. Phylogenies based on DNA sequence data resolved the Bacillariaceae into two clades: one with eccentric canal raphes and one with central canal raphes. One clade within the central canal raphe assemblage features a siliceous sheets emerging from the canal raphe called a “conopeum”. The described diversity of this clade has grown significantly over the past five years with exploration of the benthic diatom flora of Micronesia. While these new taxa all bear conopeate, central canal raphes and are monophyletic by

DNA sequence data, they have introduced a still-growing degree of morphological and genetic variation to the clade. To reflect this, we have proposed to resurrect the genus *Homoeocladia* C. Agardh for these taxa.

Badshah, S. L., The University of Toledo, United States, Syed.Badshah@utoledo.edu; Stirbet, A., Kang, D., Bridgeman, T., Seo, Y.

INHIBITING CO₂ FIXATION: A PROMISING STRATEGY FOR COMBATING HARMFUL ALGAL BLOOMS

Anthropogenic activities and rising temperatures have led to increased growth of toxic cyanobacteria in freshwater systems. Among these, *Microcystis aeruginosa* is the most common and prevalent, producing over 200 toxins, including the hepatotoxin microcystin-LR. This study investigates a novel approach to target toxic cyanobacteria by inhibiting carbon dioxide fixation in the Calvin cycle. The inhibition of carbon dioxide fixation through various chemicals can be a promising non-oxidative control method for toxic cyanobacteria involved in cyanobacterial harmful algal blooms (cyanoHABs). Glycolaldehyde was found to completely shut down carbon dioxide fixation in *Microcystis*. This inhibition of CO₂ fixation results in a decline in cell density and biomass (photosynthetic pigment content) during the early logarithmic growth phase of *M. aeruginosa*. The efficiency of photosynthesis was monitored in terms of the quantum yield (QY) of photosystem II (PSII), and the excitation energy trapping and electron transfer processes across the photosynthetic proteins were observed from chlorophyll a fluorescence transients. A decline in QY of PSII and variable fluorescence showed inhibition of electron transfer process within few hours of glycolaldehyde treatment of *Microcystis*. The results suggest that CO₂ fixation inhibitors could be used in water treatment to control harmful algal blooms.

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DOES FLOW SPEED AFFECT BLADE NUMBER IN THE BULL KELP, *NEREOCYSTIS LUETKEANA*?

The bull kelp *Nereocystis luetkeana* is a foundational species of temperate, nearshore environments. Its sporophytes, known for their large size and unique, multi-bladed morphology, begin life with a single blade. Additional blades are formed by dissecting existing ones lengthwise as the thallus grows. Blade morphology in this species is plastic and responsive to environmental flow speed. Mature thalli from more exposed sites tend to have more blades than those from protected sites, suggesting that blade number—not just blade morphology—may be plastic. The drag experienced by an intact bull kelp thallus is only a fraction of what its many blades experience in isolation, suggesting that splitting blades into increasingly subdivided parts has a hydrodynamic benefit. Thalli might respond to high flow by increasing their blade number, or blade number could be genetically determined, with site variations due to genetic drift or local adaptation. We investigated if blade number is plastic in response to flow by growing sporophytes from a single site for 28 days in three different flow treatments under otherwise identical culture conditions. Sporophytes developed significantly more blades in faster flow, suggesting that blade number may be a plastic trait in response to flow speed and that increasing blade number may be another drag-reducing strategy in the bull kelp.

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USHERING IN AN ERA OF HIGH-RESOLUTION GENETICS IN EVOLUTIONARY PHYCOLOGY

The age of DNA barcoding has transformed the field of phycology, revealing remarkable levels of cryptic diversity, unexpected phylogeographic structure, and novel evolutionary insights. Whole genome sequencing (WGS), that is sequencing all the genomic information present in a set of samples, represents a powerful big-data approach that can deliver high-resolution information for the above-mentioned purposes, but has not yet been widely applied in phycology. Steep learning curves and standardization of bioinformatic workflows present major barriers for the uptake of WGS. Here, we showcase a basic workflow for distilling WGS datasets for the purposes of phylogenomic,

population genomic, and metacommunity analyses. We then present key insights derived from the application of WGS in the kelp genus *Alaria*. These insights include the discovery of an Arctic species of *Alaria* previously overlooked by DNA barcoding; species hybridizations that conflate organellar phylogenetic signal; gradients of genomic diversity wherein Northeast Pacific *A. marginata* sits in the speciation “grey zone”; high latitude glacial refugia in North Atlantic *A. esculenta*; and the second ever report of a parasitic brown alga, among other epi-endobiotic associations, including highly novel algal sequences and a suite of animal taxa. By encouraging the assimilation and accessibility of whole genome sequencing in phycology, we can usher in an era of high-resolution genetics in phycology, which promises to reveal new lineages of life, evolutionary insights, and holobiome associations.

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BIODIVERSITY OF SOUTH ATLANTIC AND SOUTHERN OCEAN SEAWEEDS: RICH, CHARISMATIC, AND UNDESCRIBED ISLAND FLORAS

The Falkland Islands in the South Atlantic and South Georgia in the Southern Ocean support rich seaweed floras. The seaweeds provide food, shelter and foraging habitats for many species, while maintaining inshore productivity and contributing substantially to nutrient and carbon cycling and offshore fisheries. Between 2018 and 2021 expeditions were made to the islands resulting in collections of c. 2500 seaweed specimens. Prior to our research, the seaweeds from these regions had been poorly studied, and identification was based on morphological identification and outdated species concepts. Using a molecular-assisted taxonomic approach, results have revealed that many species remain undescribed and each island flora has its own distinctive characteristics. Potential endemics are being revealed, e.g. probably a new giant brown *Himantothallus* species on South Georgia. There are biogeographic signals between the islands and with related areas. The presence of a non-native, predominantly northern hemisphere Sea Lettuce *Ulva fenestrata*, has been confirmed on both islands. Phylogenetic analysis of key taxonomic groups indicates the immense task to document their diversity, and an effort is underway by the seaweed community to develop robust global phylogenies that will provide the basis for this research and its applications. There is also evidence of structural colour in seaweeds in the Falkland Islands and South Georgia, including “Funky Jazz Weed”, *Myriogramme manginii*, *Lessonia* sp. and *Desmarestia* sp. This presentation will summarize our findings and highlight the need for more collections and intensive work to be undertaken on the seaweeds from these regions to fully characterise their diversity.

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GENOMIC FOOTPRINT OF PLASTID ENDOSYMBIOSIS: HOW MUCH IS ENOUGH?

The massive transfer of endosymbiotic genes (EGTs) to the host nuclear genome is considered a hallmark of plastid endosymbiosis and is typically viewed as an early event in the endosymbiont integration. The product of these EGTs may continue to function in the organelle after the evolution of a protein-targeting system, or may take on functions in other cellular compartments, constituting a genomic footprint of endosymbiosis. By extension, the presence or absence of EGTs in genomes has been used to predict ancient, cryptic endosymbioses or even the loss of plastids. In this presentation, I will discuss our recent results from two very different systems—an archaeplastid without a plastid (Picozoa), and a kleptoplastidic centrohelid (*Meringosphaera*)—in light of other studies to provide a contrasting view on the timing and fate of EGTs during plastid symbiosis. I will suggest that our lack of fundamental expectations as to when the bulk of EGTs happens during plastid integration, and what happens to the transferred genes once a plastid is lost, raise important questions about the process of plastid origins.

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WHEN SOFTIES GET PICKY: HOW LIFE STRATEGIES OF SOFT CORALS SHAPE THE EVOLUTION OF THEIR SYMBIONTS

Dinoflagellates of family Symbiodiniaceae form mutualisms with a diverse range of host organisms, including soft corals (Class Octocorallia). Many soft corals, unlike hard corals, are doing well under increasing ocean temperatures in the Indo-Pacific and are seeing increases in reef coverage. Yet, there has been little attention to the identity, ecology, and evolution of their algal partners, so much so, that no soft coral symbionts of family Symbiodiniaceae have yet to be properly described as formal species. For this project, we used genetic, ecological, and morphological data to assess symbiont species identity and provide proper species descriptions. Samples of soft corals all across the Indo-Pacific Ocean were collected to examine the breadth of biodiversity of Octocorals across many different environments. We found that regardless of environment, soft corals that directly obtain their endosymbionts from the environment tended to share the same symbionts in their respective sites, whereas soft corals that passed symbionts along their maternal line tended to have their own, specialized lineages per host genus. Ultimately, as soft coral coverage increases, these species descriptions will enhance our own understanding of their dinoflagellate partners, and further, be able to explore more rigorous research questions about the evolution of the symbiosis.

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MORPHOTYPES OF HAWAIIAN *AMALTHEA* (HALYMENIALES, RHODOPHYTA): DISTINCT SPECIES OR PHENOTYPIC PLASTICITY?

Morphological and molecular analyses of expanded red blades from the Hawaiian Archipelago revealed numerous undescribed species, including a unique and divergent clade in the genus *Amalthea*— a new genus record to the Hawaiian Islands. Hawaiian *Amalthea* specimens from different locations exhibited two distinct blade forms: in the Main Hawaiian Islands (MHI) specimens were mahogany-colored, had thick blades, and were collected from 106–107 m; specimens from the Papahānaumokuākea Marine National Monument (PMNM) were fuschia-pink and had thin blades, and were collected from 90 m. To assess evolutionary relationship and potential adaptations to the mesophotic environment, next-generation sequence data were generated and used to assemble and compare both of their mitochondrial and plastidial genomes. Our analyses revealed that plastomes were similar in terms of presence of standard plastidial marker genes, gene content, and length, but some unique genes were documented for each lineage. On the other hand, mitogenomes were more variable, with divergent nucleotide sequence variation of selected mitochondrial marker genes, gene content and length. The observed morphological and genome variations are inferred to be adaptations to different ecological niches in the mesophotic environment. New genomic resources for mesophotic red blade species illuminate adaptations to the twilight depths and enhance understanding of algal biodiversity.

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LESSONS LEARNED FROM LINEAGE DIRECTED METABARCODING PRIMERS - EUSTIGMATOPHYTES AND CRYPTOMONAS

Large scale eDNA metabarcoding surveys using “universal” primer sets such as the V4 region of the 18S ssu RNA gene have allowed phycologists to compare diverse aquatic habitats and answer broad questions about the presence/absence of many microalgal lineages and their ecology. Unfortunately, surveys using only 18S primers under-identify or completely miss some microalgal lineages. Data from two studies will be presented, one using primers targeting Eustigmatophytes, the other targeting *Cryptomonas*. In both studies samples were collected from bodies of water in Southwestern Virginia and attempts made to identify as many of each group as possible using 18S primers versus lineage-directed primers. For the Eustigmatophyceae, primers were designed to target the plastid

rbcL gene and produced a 370bp amplicon from all known lineages. Use of this marker enabled the recovery of 187 distinct Eustigmatophyte sequences from our samples and could distinguish Eustigmatophyte lineages in a Maximum Likelihood phylogeny. In comparison, 7 distinct Eustigmatophyte sequences were recovered from the same samples using the 18S marker. For *Cryptomonas*, primers were designed to target the nuclear rRNA ITS2 region which produced amplicons ranging from 251 – 488 bp that could distinguish known *Cryptomonas* species equally as well as much longer nuclear ribosome markers. For this study a single small ephemeral pool was sampled over the course of a single spring-summer-fall and 13 distinct *Cryptomonas* species were recovered using the ITS2 targeted primers. In comparison, 6 *Cryptomonas* sequences were recovered using the 18S marker and a single *Cryptomonas* sp. was recovered using a culture-based approach.

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EXPLORING ABIOTIC STRESS RESPONSES OF BIOFUEL-RELEVANT ALGAE THROUGH MULTI-OMICS PROFILING AND INTEGRATION

Microalgae are of interest for applications in biofuel production due to their ability to convert carbon dioxide into lipids. During outdoor cultivation, algae are exposed to environmental changes, but the underlying mechanisms that control physiological responses and adaptation to environmental pressures are largely unknown. We have developed a pipeline to produce multi-omics datasets of algal strains that will guide identification of biochemical pathways that promote stability and productivity under variable environmental conditions, such as temperature, salinity, and pH. We've profiled five algal biofuel-relevant strains by measuring omics data, such as RNA, metabolite, and protein levels, over time. One candidate production strain, *Scenedesmus obliquus* UTEX 393, exhibits high biomass and lipid accumulation, but shows diminished growth at higher salinities. To understand the effects of salt stress on *S. obliquus* UTEX 393, we applied our pipeline to discover biochemical pathways that are responsible for adapting to salinity stress. Through integration of the datasets, we identified a Myb-like transcription factor that may be a key regulator of diurnal gene expression. Because some of its predicted gene targets are related to lipid biosynthesis, establishing these regulatory interactions is a critical step towards improvement of lipid productivity. The integration of these multi-omics data provides a foundation to explore the potential of algal strains for biofuel applications and expands our understanding of regulatory mechanisms of algae in applied systems.

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ZONE, SPECIES, AND TISSUE ALL SHAPE THE INTERTIDAL MACROALGAL MICROBIOME

Descriptive and experimental studies of the microbiomes of three closely related species of the rockweed *Fucus* (high-intertidal *F. spiralis*, mid-intertidal *F. vesiculosus*, low-intertidal *F. distichus*) in Acadia National Park (ANP,

Maine, USA) suggested that bacteria have different tolerances to the vertical stress gradient of the intertidal zone, as is well known for the host macroalgae (Quigley, C., Capistrant-Fossa, K. *et al.* 2020. *Front. Microbiol.* 11:563118). However, even though these species are closely related, there might still be a different host factor affecting differentiation of the microbiome. Here, we characterize the microbiomes associated with a single species, the red alga *Porphyra umbilicalis*, in two contiguous populations (high- intertidal, mid-intertidal) at ANP, and in *P. linearis*, which grows intermixed with the higher population of *P. umbilicalis*. We obtained DNA sequences of the V4 region of the 16S ribosomal gene from blades and holdfasts of sampled individuals. MED analysis generated bacterial amplicon sequence variants (ASVs). The microbiomes of *P. umbilicalis* separated in NMDS plots by high-zone versus mid-zone populations. Recorded temperatures during emersion differed between the two zones, but the exact environmental drivers remain unknown. Blade and holdfast microbiomes were distinctive, and most *P. linearis* and *P. umbilicalis* separated in NMDS plots. All three factors – zone, species, and tissue – shape the *Porphyra* microbiome. (Supported by NSF 1442231, 1442106)

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FUTURE PROOFING KELP FORESTS

Climate change is causing widespread habitat deterioration and destruction and presents one of the biggest threats to species and global ecological function. Underwater kelp forests underpin fisheries and vast economic values on temperate coasts but are declining due to climate change. There is an urgent need to develop novel and proactive solutions to combat, reverse and prevent this habitat loss. Using 2 species of kelp from Australia as examples, I will discuss how genomic data is providing the evidence we need to assess vulnerability of kelp forests and “future-proof” management under climate change. By identifying heritable genetic variation in thermal tolerance, we have identified target populations and individuals that could be used in assisted adaptation and restoration actions to boost resilience to future climate change.

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LARGE SCALE MACROALGAL BLOOMS ARE A SYMPTOM OF GLOBAL CHANGE POSING LARGE SCALE CHALLENGES THAT REQUIRES RESOURCE MANAGERS, THINKERS AND SCIENTIST WITH A DIVERSE, EQUAL AND INCLUSIVE PERSPECTIVE.

A holistic perspective based on principles of diversity, equity, inclusion, access, and justice is discussed to address environmental crises, such as macroalgal blooms. resulting from the accumulation of stressors over time and accelerated in the last 60 years by a resource-extractive lifestyle. Macroalgal bloom’s frequency, spatial dimension, and time interval are becoming a global problem with a critical human dimension component. The sargasso bloom is exposing social inequalities, loss of diversity, poor inclusion of mitigation actions leaving many without access to vital resources, and the unjust case of a region impacted by problems with sources from other parts of the world. Global learning and collaborative online international education are powerful tools that prepare students to work in international teams addressing problems in collaboration with faculty and students from different disciplines, countries, and cultures. Through those practices we can increase the awareness, participation, and engagement of new generations of thinkers and scientist transforming the perspective that sustains the paradigm of progress, towards a scientific-humanist perspective that accepts the empowerment of the community to find solutions to complex problems. New generations of scientists equipped with skills to face the current crisis need a transformation of consciousness in scientists and educators and educational institutions. As conscious scientific societies we can promote such changes in our daily research practices and education programs.

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PHYLOGEOGRAPHY OF THE FRESHWATER RED ALGA *BATRACHOSPERMUM GELATINOSUM* (RHODOPHYTA) IN THE EASTERN UNITED STATES

The freshwater red alga, *Batrachospermum gelatinosum*, has a well-documented distribution in streams in eastern North America from Alabama to Newfoundland. Although *B. gelatinosum* has a broad geographic range, it may have been established by a few long-distance dispersal events since no desiccation-resistant propagule is known. In addition, its macroscopic gametophyte and attached microscopic carposporophyte are potentially involved in dispersal, but are short-lived. In order to better understand the wide geographic distribution of this seemingly poor disperser, we investigated the genetic diversity in five major drainage basins of eastern North America. We sampled 359 gametophytes at 21 sites across these drainage basins and assessed genetic variation using 12 polymorphic microsatellite loci. Initial observations suggest that genetic variation is low among gametophytes in streams within the same drainage basin and considerably higher among drainage basins. This pattern would suggest that there is some gene flow within a drainage basin but more restricted among drainage basins. One explanation may be establishment by few long-distance dispersal events and subsequent gene flow within each drainage basin.

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CELL DIVISION AND GROWTH IN COLEOCHAETE (STREPTOPHYTA) EXAMINED BY CONFOCAL MICROSCOPY

Coleochaete is a genus of streptophyte (charophyte, s.l) green alga that is structurally complex and a close relative of embryophytes (land plants), although in whole genome analyses somewhat more distant than are members of the Zygnematophyceae. Although the comparative structural study of *Coleochaete* and embryophytes dates back to the 19th century, recent molecular phylogenetic advances have greatly clarified the relationship among lineages of Streptophyta and Embryophyta, and imaging techniques are now available that permit high-resolution imaging of living thalli. *Coleochaete pulvinata*, *C. orbicularis*, and *C. irregularis* thalli were stained with calcofluor white and conjugated antibodies specific to pectin moieties, and imaged with a Leica Stellaris 8 confocal microscope equipped with a white-light laser and a resonant scanner. This combination permits flexible use of fluorochromes and high-resolution imaging in living thalli while minimizing photon damage. Selective staining of pectin revealed cell-specific expression of individual cell wall components, and provided new insights into patterns of growth and development in *Coleochaete*. For example, in *C. soluta*, jim7 antibodies selectively bind to maturing zoospores, with much weaker staining of the mucilage layer covering the thallus.

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INDOOR CULTIVATION PROTOCOLS FOR THE RHODOPHYTES, *DEVALERAEA MOLLIS* AND *PALMARIA HECATENSIS* FROM ALASKA

The Alaska Mariculture Alliance has set a target for mariculture in the state of generating \$100 million in revenue over the next decade. To achieve this goal and enhance economic resilience, it is essential to diversify the species produced. Currently, the industry primarily focuses on cultivating large brown algae, even though red seaweeds have high commercial value. While cultivation protocols for analogous ecotypes of a red seaweed species in the *Devaleraea/Palmaria* genera exist, these protocols have not been proven for Alaskan specimens. Therefore, this study aims to develop reliable cultivation methods for producing two specific red seaweed species, *Devaleraea mollis* and *Palmaria hecatensis*, in indoor systems. Successfully establishing these cultivation methods would lay the groundwork for future seaweed cultivation at sea in Alaska. To achieve this objective, the study is identifying the optimal combination of temperature, photoperiod, light intensity, and nutrient media to maximize growth in indoor tumble cultures while keeping costs low. Preliminary results indicate that a 16:8 L:D photoperiod and a temperature of 8 °C promote adequate growth in both species. The following steps in creating a working cultivation protocol involve assessing different light intensities and comparing growth using commercially available nutrient

media. Overall, this study aims to enhance the Alaskan mariculture industry by diversifying the species cultivated, focusing on red seaweeds, and developing effective cultivation methods specific to the Alaskan environment.

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MULTI-MARKER METABARCODING REVEALS INCREASED DIVERSITY AND EVIDENCE OF BIOGEOGRAPHIC INFLUENCE ON MICROBIAL MATS OF LOW-OXYGEN, HIGH-SULFUR SPRINGS

High-sulfur, low-oxygen environments formed by karstic underwater sinkholes and springs create extreme habitats populated by microbial mat communities. To explore the diversity and biogeography of these mats, samples were collected from five sites in northern Michigan, southern Michigan, and Florida. We investigated previously undescribed eukaryotic diversity in these habitats, and further explored bacterial and archaeal communities. Mat samples, water parameters, and nutrients were collected from sulfur spring sites throughout the growing season of 2022. Cyanobacteria and diatoms were cultured from mat subsamples to create a culture-based DNA reference library. Remaining mat samples were used for metabarcoding of the 16S and *rbcL* regions to explore bacterial and diatom diversity, respectively. Analyses of water chemistry, alpha diversity, and beta diversity revealed a range of high-sulfur, low-oxygen habitats, each with its own distinctive microbial mat community. Conductivity, pH, dissolved oxygen, temperature, sulfate, and chloride had significant influences on community composition, but explained a low percentage of the total variance. Community differences were significantly correlated with both geographic distance and differences in water parameters between sites. We provide novel information on microbial mat community composition, and present evidence for distinctive microbial biogeography in these unique communities.

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MODELING DISPERSAL OF *CHONDRIA TUMULOSA* (RHODOMELACEAE, RHODOPHYTA) IN THE PAPAĀNAUMOKUĀKEA MARINE NATIONAL MONUMENT: RAFTING TO NEW FRONTIERS

The red alga *Chondria tumulosa* A.R.Sherwood & J.M.Huisman was first observed in 2016 at the island of Manawai (Pearl and Hermes Atoll) in the Papahānaumokuākea Marine National Monument and has since spread to cover much of the atoll. It forms large mounds of several square meters covering live coral and grows sufficiently thick to stifle growth. As the Hawaiian Archipelago has a robust history of algal invasions causing damage to nearshore reefs, it is of great importance to determine the potential for the spread of this species. In 2022, *C. tumulosa* was confirmed at Kuaihelani (Midway Atoll), ~130 km to the west-northwest of Manawai, the first observed range expansion of the species. With several potential means of spread it is unclear whether this inter-island leap was through vegetative fragmentation, anthropologically mediated fragment dispersal, or sexual reproduction. One way of understanding how the species has spread across this barrier is to model the likelihood of each means of dispersal for reaching Kuaihelani. The Connectivity Modeling System and oceanographic data sets were used alongside the approximated physical properties of *C. tumulosa* fragments and spores throughout a study period of 2019-2023 to model the release and dispersal of both spores and rafting fragments. None of the modeled tetraspores reached Kuaihelani above the species' observed depth limit of 25 m, with 99.7% of modeled particles sinking out of this range within five days of release. Rafting fragments, however, successfully settled in suitable habitat at a rate of 1% (1171 of 116890) with 1063 of these to Kuaihelani, 79 to Hōlanikū (Kure), 27 to Kapou (Lisianski), and 2 to Kamole (Laysan). Further modeling of fragment dispersal is necessary to understand the potential spread of *C. tumulosa* in the largest fully marine protected area in the world.

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ETHYLENE SIGNALING IN *CYANOPHORA PARADOXA*: REVEALING HORMONE USAGE IN A GLAUCOPHYTE ALGA

Glaucophytes, an enigmatic group of freshwater algae, occupy a pivotal position within the Archaeplastida, providing insights into the early evolutionary history of plastids and their host cells. These algae possess unique plastids, known as cyanelles, that retain certain ancestral features, enabling a better understanding of the plastid transition from cyanobacteria. We investigated the role of ethylene signaling, a potent hormone used by land plants to coordinate stress responses, in the glaucophyte alga *Cyanophora paradoxa*. We demonstrate that *C. paradoxa* converts 1-aminocyclopropane-1-carboxylic acid (ACC), the ethylene precursor in land plants, into gaseous ethylene and produces ethylene natively in response to abiotic stress. In addition, reactive oxygen species accumulation occurs following abiotic stress and ACC treatment, leading to growth inhibition in *C. paradoxa*. Using transcriptomics, we also reveal that ACC treatment induces the upregulation of senescence-associated proteases in *C. paradoxa*, consistent with the observation of growth inhibition. This is the first report of hormone usage in a glaucophyte alga, extending our understanding of hormone-mediated stress response coordination to the base of the Archaeplastida. By unraveling hormone signaling pathways in glaucophytes, we pave the way for a more comprehensive understanding of the evolution and diversification of hormone-mediated communication across the tree of life, ultimately enhancing our knowledge of the adaptive strategies employed by diverse lineages.

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ASSESSING HEAT TOLERANCE IN SUGAR KELP

Warming sea temperatures are threatening sugar kelp populations, and for the future of kelp aquaculture and restoration, we need to identify individuals with natural adaptations to cope with heat. We conducted an experiment to assess heat tolerance in sugar kelp gametophytes by exposing them to three temperatures representing current (12 C), anomaly (20 C), and future (24 C) average annual temperatures in the Gulf of Maine, U.S.A., and measuring their photosynthetic performance and fertility following heat stress. For each temperature treatment, 93 gametophytes (fragmented from clonal cultures) were maintained in 96-well microplates, with 3 replicate wells per gametophyte per treatment. Temperatures were gradually increased from 12 C over several days, maintained at the treatment temperature for two weeks, and then decreased to 12 C for a three-week recovery period, after which the fertility of each gametophyte was tested by introducing gametophytes of the opposite sex. Photosynthetic performance of each gametophyte was measured every 2-4 days as the ratio of chlorophyll a fluorescence emitted at 684 and 735 nm (F684/F735). The mean percent decrease in F684/F735 during the two weeks of temperature treatment was significantly greater in the 24 C and 20 C treatments compared to the 12 C control, but 84% of gametophytes exposed to heat were still fertile. GWAS analysis revealed several potential candidate genetic loci related to heat tolerance. Currently, we are working on assessing the relationship between gametophyte and sporophyte heat tolerance.

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THE EFFECT OF SARGASSO INUNDATIONS ON NEARSHORE SEAGRASS COMMUNITIES

Seagrass beds are one of the most productive ecosystems but have been declining globally due to increased coastal development and subsequent declines in water quality. Recently, nearshore seagrass communities across the Atlantic have been impacted by large influxes of pelagic *Sargassum* (hereby referred to as Sargasso), a brown macroalgae

that accumulates along shorelines. Decomposing Sargasso increases dissolved organic matter and contributes to 'brown-tides', which reduce water quality. To examine the effects of Sargasso events on nearshore seagrass communities, monthly surveys were conducted in the north and south regions of Crandon Park (Miami, USA). In each region, three 50m transects, each 60m apart and perpendicular to the shoreline were used. Along each transect, ten 1m² fixed quadrats, each 5m apart, were quantified for benthic percent cover method. Co-occurring Sargasso biomass was also estimated using four quadrats along a 1km transect. In north Crandon Park, seagrasses initially dominated, covering an average of 30% of the area surveyed. But by November 2022, the first survey after the brown-tide subsided, seagrass coverage had declined by 50% and the edge of the seagrass bed receded by 20m. In south Crandon Park, where Sargasso is removed daily (but then directly re-buried in the sand), seagrass initially covered an average of 40% of the area but declined to 6% after the Sargasso event. Declining seagrass beds can cause problems locally with reduced ecosystem services to coastal communities and reduced linkages as a subsidy to marine and terrestrial systems.

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SCREENING THE PLANKTON ASSEMBLADGE IN YORK RIVER USING THE IMAGING FLOWCYTOBOT

Harmful algal blooms (HABs), defined as the rapid increase in algal population, have adverse impacts on the environment. The consequences of HABs vary greatly by algal species, ranging from the reduction in food quality to as severe as animal mortality. Traditionally, the identification of bloom species has relied on microscopy; however, microscopic identification requires an extensive amount of time and labor. A combination of the Imaging FlowCytobot (IFCB) and the computational artificial neural network (ANN) model has been applied to achieve real-time plankton identification in the York River, Chesapeake Bay, VA. The IFCB combines flow cytometry and photography to capture high-resolution images of suspended particles. These images are manually sorted into algal groups to build a reliable ANN classifier for real-time identification. Continuous physical parameters (e.g., water temperature and turbidity) collected by Virginia Estuarine and Coastal Observing System will be correlated with the algal community structure to determine how these parameters affected the succession of algal communities. Overall, the dominant algal groups had a seasonal variation due to water temperature, salinity, and turbidity differences. Dinoflagellates and diatoms (e.g., *Dinophysis* and *Pseudo-nitzschia*) dominated the winter plankton community, while zooplankton (e.g., *Mesodinium*) and cyanobacteria are the most abundant groups in summer. In spring, the community was composed of the most diverse groups of planktons. The utilization of IFCB in the algal monitoring effort reduced the amount of labor required in microscopic identification, making real-time monitoring available to resource managers.

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THE MYSTERIOUS WORLD OF BULL KELP: ECOLOGICAL STORYTELLING WITH A DESIGNER'S INTENTION, AN ARTIST'S EYE, AND A WRITER'S EAR

Josie Iselin will use her artwork as the conduit for telling seaweed stories and the history of the science surrounding seaweed taxonomy and natural history. She will include accounts of her visual inspiration for *The Curious World of Seaweed* (published in 2019) and recent work as co-director of *Above/Below*, whose mission is to bring much needed recognition to the bull kelp forests of the North Pacific coastal waters. *Above/Below* is creating a comprehensive web story, titled *The Mysterious World of Bull Kelp*, describing *Nereocystis* and its community (including urchin, abalone, sea otter, sunflower sea stars, humans, *Pterygophora* and others) in eight different regions throughout its range from Central California to the Aleutian Islands. Motivated by the radically divergent state of bull kelp from decimated kelp beds in Northern California to abundant bull kelp in Southeast Alaska, and the plethora of kelp restoration activities initiated across the entire region, *Above/Below* sees a need for comprehensive scientific storytelling about bull kelp across regions and across species within the bull kelp forest

community. Josie's approach to scientific communications is deeply rooted in design disciplines, commitment to good writing, and an artistic eye, bringing a wider audience into complex ecological stories with a sense of wonder. Her work is on view at josieiselin.com and at Above/Below.

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A NOVEL FORM OF CHROMATIC ACCLIMATION BY CRYPTOPHYTES OF THE GENUS *HEMISELMIS*

Cryptophytes are eukaryotic microalgae found in aquatic environments that range from tea-colored ponds and lakes to the blue-water open ocean. The presence of cryptophytes in such diverse light environments is related to their phycobiliprotein (PBP) accessory pigments, which absorb wavelengths of light (greens, yellows, and oranges) that are not well absorbed by chlorophylls. PBPs play an important role in the acclimation of cryptophytes to short-term changes in spectral quality. Our early work showed that one species, *Hemiselmis cryptochromatica*, adjusts to changes in spectral quality by modifying the absorbance spectra of their PBPs to increase the absorption of newly available wavelengths. This novel type of phenotypic plasticity may be common across the *Hemiselmis* clade. *Hemiselmis pacifica*, which contains a PBP that absorbs maximally at 577 nm (Cr-PC 577), was grown under full spectrum, green, and red light of equal intensity (30 mmol m⁻² s⁻¹). PBPs were extracted for absorbance measurements. When shifted from full spectrum to green light, the wavelength of maximum absorption of Cr-PC 577 in *H. pacifica* shifted from its initial position of 577 nm to a wavelength of 562 nm (closer to the max spectral output of the green lamps) in just two weeks. When cultures were moved back to full spectrum irradiance, the maximum absorbance peak shifted back to its original position (577 nm) in just one week. Thus, this form of chromatic acclimation is relatively fast, reversible, and should be of great ecological advantage to cryptophytes in dynamic, eutrophic environments.

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IDENTIFYING PUTATIVE CALCIFICATION GENES IN THE ARTICULATED CORALLINE ALGA *CALLIARTHRON TUBERCULOSUM*

Coralline algae are ecologically important calcifying red algae that cement together coral reefs, provide structural support, and create habitat and food in marine ecosystems. Despite the significance of calcification to the ecology and physiology of corallines, we know little about the mechanism itself, especially at the molecular level. We sequenced, assembled, and compared tissue specific transcriptomes for calcified (intergenicular) and non-calcified (genicular) tissues in the articulated coralline alga *Calliarthron tuberculosum* to identify putative calcification genes. Results showed that 17.4% of contigs were differentially expressed between calcified and non-calcified tissues, with 11% upregulated (and 6.4% downregulated) in calcified compared to non-calcified tissues. Based on KEGG and gene ontology analysis, preliminary results identified genes that encode carbonic anhydrases, calcium transport proteins and ribosome biogenesis proteins as differentially expressed between calcified and non-calcified tissues. Additionally, transcriptomes were assembled for actively decalcifying tissue (i.e., genicular tissues in the process of forming) and results showed 1.8% of contigs were differentially expressed between decalcifying and calcified tissues. 1.4% of those contigs were upregulated in decalcifying tissues and could represent genes uniquely utilized in the decalcification process. These results not only contribute to our overall understanding of coralline calcification but will also permit investigation into future physiological responses to climate change.

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ELUCIDATION OF PICOCHLORUM CELERI'S VARIOUS STRESS TOLERANCE MOLECULAR PATHWAYS THROUGH MODELING AND MULTIOMICS INTEGRATION

To develop industrially relevant algal strains a deep understanding of algal metabolism and stress responses is needed. The industrially important marine alga *Picochlorum celeri* has high biomass productivity and rapid growth. *Picochlorum* sp. has some of the smallest genomes and cell sizes amongst chlorophytes. This genus has evolved the ability to cope with many stressors due to its harsh, salty, and temperature-variable habitat. *P. celeri* has one of the highest outdoor open pond biomass productivities, but even moderately low temperatures (approximately 20 °C) severely limit its seasonal cultivation window and annual biomass productivity.

In this work, *P. celeri* was grown at a salinity of 15 PPT and 50 PPT under simulated summer growth conditions and an autumn cold-front temperature event. Transcriptomics, metabolomics, lipidomics, proteomics, DNA affinity purification sequencing (DAP-seq), network analysis, and metabolic modeling highlighted transcription regulatory modules involved in diurnal gene expression control and in responses to salt and temperature stresses.

By modeling and integration of the above multi-omics datasets, we pinpointed stress regulatory mechanisms that help explain *P. celeri*'s observed lipid and metabolic profiles and key adaptations for osmotic stress. The data and analytical frameworks pioneered in this study will speed up strain improvement and biosynthetic capability prototyping in *P. celeri* and other algae.

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LIFE-CYCLE DIFFERENTIATION IN A COSMOPOLITAN MICROALGA: A MULTI-OMIC APPROACH

Emiliania huxleyi is a globally abundant species that plays a crucial role in the carbon cycling through both photosynthesis and the formation of inorganic CaCO₃ exoskeletons (calcification). This species has a diploid calcifying non-flagellate phase and a haploid non-calcifying flagellate phase, both of which are free-living and asexually reproduce through mitosis. In this study, we constructed the *de novo* genome assemblies of a pair of diploid and haploid strains isolated from the same single-cell-derived culture over 20 years ago and compared their transcriptomes, proteomes, and methylomes to explore the genetic basis of haploid-diploid differentiation. By comparing the genome assemblies of the two strains, we found hundreds of structural variations, including aneuploidy, translocation, relocation, and insertion/deletion of large fragments. The haploid has more insertions than deletions, while the diploid is the opposite, resulting in a larger monoploid genome size in the haploid. The calcifying diploid strain was enriched with transmembrane transporter and signaling receptor genes, while the

flagellate motile haploid strain was enriched with genes related to motility. The contrasting patterns of gene/protein expression between the two strains can be attributed to various causes, including differential methylation and transcriptional/translational regulation mechanisms.

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BLOOM-FORMING, NON-HETEROCYSTOUS *LIMNORAPHIS BIRGEI* GROWS WITHOUT DISSOLVED NITROGEN

Cyanobacteria harmful algal blooms produce surface scums that diminish light availability and degrade aquatic ecosystems. *Limnорaphis birgei* is a bloom-forming cyanobacterium lacking heterocytes for which little ecological data exist, despite documented blooms in many US states. To test the influence of dissolved nitrogen on growth, phosphorus uptake, and nutrient stoichiometry, we conducted experiments using unialgal cultures of *L. birgei* isolated from North Lake (NY), which has been impacted by annual blooms. Experiments were run in replicate flasks inoculated with nitrogen-depleted filaments in 50 mL modified BG-11 medium amended with 0 mM N, 0.1 mM NO₃⁻, 0.1 mM NH₄⁺, or 0.05 mM NH₄NO₃. In 0 mM N treatments, dry mass increased 18-fold, confirming the ability of *L. birgei* to sustain growth under near-zero nitrogen conditions. Dry mass increased in all +N treatments, but to a lesser extent than in zero-N added treatments: 15-fold in 0.1 mM NO₃⁻ and 0.05 mM NH₄NO₃, and least (11-fold) with 0.1 mM NH₄⁺ as the sole N source. Phosphorus uptake by *Limnорaphis* was significantly correlated with growth rate and depleted by 99% in all zero-N or NO₃⁻ added treatments, but only by 76% in the 0.1 mM NH₄⁺ treatment. C:N ratios in *Limnорaphis* increased in all treatment conditions over time. Together, these results suggest that growth of *L. birgei* and nitrogen availability are uncoupled, and that blooms of this species can occur even under very low dissolved nitrogen conditions.

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INVASIVE SPECIES AND CHANGING CLIMATE IMPACT THE REPRODUCTION OF ESTUARINE KELP POPULATIONS

Estuarine habitats are at particular risk of both climate driven changes and biological invasions. Along the western shoreline of Tomales Bay, CA, several locations support dense stands of both giant kelp (*Macrocystis pyrifera*) and the invasive wireweed (*Sargassum muticum*). While several studies have investigated the interactions of the adult stages of these species, there is little understanding of how microscopic stages of these two species will be influenced by climate change and invasion. Using laboratory kelp culture methods in a factorial design, we tested the interacting effects of projected levels of decreased salinity, increased temperature, and *Sargassum* presence on *Macrocystis* early life stages collected along the estuarine gradient in Tomales Bay. Our results indicate that 1) *Macrocystis* gametophytes from more marine-influenced populations were better able to survive temperature and salinity stress, 2) invasive *Sargassum* had little effect on *Macrocystis* gametophytes, but accelerated development of sporophytes, and 3) under all three stresses, high temperatures resulted in the greatest reduction of giant kelp gametophyte survival. These results imply that giant kelp reproduction and presence within estuaries was more influenced by temperature than salinity and microscopic-stage competition with invasive species

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INTRASPECIFIC DIFFERENCES IN THERMAL ACCLIMATION IMPACT THE ECOLOGICAL NICHE OF COCCOLITHOPHORES

Coccolithophores are a diverse, ecologically-important phytoplankton group ubiquitous in the global ocean and more abundant in colder, oligotrophic waters. Recent studies have suggested that coccolithophores are the least resilient phytoplankton functional type to high (>30°C) water temperatures, while others show that warm coastal areas are important coccolithophore habitats. To examine how intraspecific diversity and acclimation shape plankton populations, we grew 13 strains of *Emiliania huxleyi* isolated from regions of different temperature for ~45 generations (2 months) each at 6-8 temperatures. We characterized the thermal response curve and flow cytometry-derive cell sizes of each strain. There was a mean difference of 0.63 ± 0.3 day⁻¹ between maximum and minimum growth rates observed within-strain, while different strains had up to a 0.89 day⁻¹ difference in maximum growth rate. Even with virtually identical temperature optima and overlapping cell size, strain growth rates varied between 0.45-1 day⁻¹. While some thermal curves were effectively symmetrical, others had slowly declining growth rates above the “thermal optimum”. We place our experimental results in global context using an ecosystem model simulation of coccolithophores in which several “thermal types” are scaled by cell size, and show how coccolithophore realized niches vary. Taken together, these observed intraspecifically-diverse thermal traits may reveal coccolithophores’ capacity to persist under unusually warm temperatures and exploit seasonal nutrient limitation in a changing ocean.

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IS AN ISOMORPHIC ALTERNATION REALLY ISOMORPHIC? INVESTIGATING THALLUS SIZE AND SHAPE IN AN ‘ISOMORPHIC’ MACROALGA

All sexual eukaryotes undergo meiosis, recombination, and fertilization at some point during their life cycle, resulting in the alternation of a larger and a smaller ploidy level. Macroalgae exhibit life cycle diversity representative of that found across eukaryotes and may therefore help resolve the conflict between genetic and ecological predictions. The expectation that ecological differences exist between strongly heteromorphic life stages makes intuitive sense. It is seemingly more challenging to explain the evolutionary stability of life cycles with isomorphic gametophytes and sporophytes because the two stages are expected to be ecologically equivalent. However, theoretical modelling has shown that a subtle ecological difference between stages is sufficient to stabilize the life cycle on evolutionary timescales. Here, we explore a suite of phenotypic variables in the red alga *Gracilaria vermiculophylla* which may help explain the persistence of three morphologically similar life stages at some sites and the systematic loss of gametophytes at others. Thallus morphology and composition are two types of phenotypes that might vary subtly among stages, leading to differences in survival, reproductive output, or both. We quantified size, composition (i.e., water and organic content), and architecture of thalli collected at three fixed and two free-floating sites. We found stage and site-specific differences that may manifest in ecologically relevant ways thereby contributing to life cycle stability or instability depending on the abiotic and biotic conditions.

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EMERGING HARMFUL ALGAL BLOOM ISSUES IN THE CALIFORNIA CURRENT: SHIFTING PATTERNS AND NEW ISSUES DRIVEN BY CLIMATE?

Blooms of harmful and toxic algae have increased in frequency and severity within the California Current System (CCS) during the past few decades. Many explanations have been proposed and investigated vis-à-vis the possible environmental driving forces for the observed patterns of harmful blooms in the CCS. The possibilities include hydrographic features that affect macro- and micronutrient availability (coastal upwelling, existence of retention/incubation areas, river and sewage effluent discharge) and biological aspects of the algae (e.g. light and nutrient competition, vertical migration, mixotrophy). While progress has been made, particularly regarding the annual occurrence of *Pseudo-nitzschia* blooms, the emergence of several new HAB problems in the last decade has raised new concerns. Dinoflagellates in particular have become an emerging, and increasing, issue. In addition to *Alexandrium*, California is susceptible to *Lingulodinium*, *Margalefidinium*, *Gonyaulax*, and *Dinophysis*. At the same time there is increasing recognition of HAB issues at the freshwater to marine continuum. These shifts in HAB problems within the CCS may be caused by a combination of decadal scale oscillations, coastal eutrophication, establishment of seed populations in new geographic regions, as well as secular trends in temperature and pH driven by climate change. Using examples from several recent large-scale HAB events, these patterns and mechanisms are explored with an aim towards establishing both ecological understanding of bloom dynamics and developing an effective monitoring and management approach towards HAB event prediction and response.

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BIOFOULING ADHESION BY FIELD-SAMPLED AND LABORATORY-CULTURED *ULVA* SPP.

Biofouling is a significant problem for long-term deployment of water quality sensors in marine environments. The marine algae *Ulva* spp. are commonly used as model organisms in biofouling experiments. We tested the biofouling capacity, attachment processes, and anti-fouling strategies for *Ulva* spp. spores on seawater sensors. However, limitations from relying on field samples were identified including uncertainty of species, seasonal variation, the inability to run experiments year-round, and a requirement to conduct studies in coastal regions with access to *Ulva* spp. To address these limitations, we developed a protocol for on demand development and release of *Ulva* zoospores. Mass spore release was induced in the laboratory for use in biofouling trials producing more than 50 million spores from laboratory cultured material. We compared the biofouling potential of wild collected *Ulva* spp. with laboratory cultured *Ulva* spp. DNA analysis indicated the laboratory cultures were all *Ulva* Clade C (LPP complex), whereas the field sampled *Ulva* were a diverse group of species including *Ulva* sp. Clade C (LPP complex), *Ulva compressa* clade I, and *Ulva flexuosa* clade D. Following spore settlement, a waterjet apparatus was used to test the spore adhesion. The results found less variation in spore adhesion with laboratory cultures than wild collected *Ulva* spp. This easily replicated protocol for on demand production of *Ulva* spores from wild collected or laboratory cultured specimens can improve currently used biofouling methods.

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KELP FORESTS AND RESTORATION ON AUSTRALIA'S GREAT SOUTHERN REEF

Kelp forests are the foundation of the Great Southern Reef, Australia's continent-wide temperate reef system that supports high levels of biodiversity, endemism, and economic value. Unfortunately, in Australia and elsewhere, kelp forests are declining due to climate change, overgrazing from herbivores, and coastal development and pollution. Habitat restoration is one tool for kelp forest conservation, but requires a multi-disciplinary approach to overcome diverse challenges in topics including ecology, genetics, physiology, and policy, and also the ongoing stressors of climate change that continue to drive kelp loss. Here I present a suite of work focused on kelp restoration in Tasmania, Australia, where we have used our ecological understanding of kelp forests to create a foundation for restoration knowledge and practice, including testing the deployment and efficacy of kelp planting methods at scale, ecological interactions of juvenile kelp, and the 'future-proofing' of restoration efforts through the use of warmwater-tolerant giant kelp (*Macrocystis pyrifera*) genotypes. I will also discuss how the physiology and genetics

of *Macrocystis* can inform restoration decision-making and ethics, and our collaboration with a Tasmanian Indigenous community for the restoration of their Sea Country. Ultimately, we are working to provide a foundation for efforts to maintain and restore kelp forest resilience in a global ocean-warming and biodiversity hotspot, and to provide risk-management to habitat restoration in a rapidly changing climate.

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KELPS MAY COMPENSATE FOR LOW NITRATE AVAILABILITY BY USING ALTERNATIVE FORMS SUCH AS UREA AND AMMONIUM

Macrocystis pyrifera and *Eisenia arborea* are important canopy forming kelps that act as foundation species along southern California coastlines. Nitrate, the form of nitrogen often linked to kelp growth, is typically low in summer during periods of high growth. More ephemeral forms, such as ammonium and urea, are much less studied as sources of nitrogen for kelp, despite the relatively high concentrations found in the Southern California Bight. To assess how nitrogen dynamics of kelps vary by species, site, and nitrogen form in southern California, we measured nitrogen uptake rates of *Macrocystis* and *Eisenia* blades collected from 4 regions: Orange County, San Pedro, eastern Catalina Island, and western Catalina Island during the summers of 2021 and 2022. Seawater samples were also taken at each location and showed that total nitrogen availability was low, but ammonium and urea were often more abundant than nitrate. We found that both kelps readily took up nitrate, ammonium, and urea, with *Macrocystis* taking up nitrate and ammonium more efficiently than *Eisenia*. Urea uptake efficiency for both species increased as total environmental nitrogen availability decreased. Our results indicate that lesser studied, more ephemeral forms of nitrogen can readily be taken up by these kelps, with possible upregulation of urea uptake as nitrogen availability declines.

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THE CURIOUS CASE OF CYANOBACTERIA: A TALE OF LIGHT AND DARKNESS

Toxic algal bloom-forming cyanobacteria are a persistent problem globally for many aquatic environments. Their occurrence is attributed to eutrophication and rising temperatures due to climate change. The result of these blooms is often loss in biodiversity, economic impacts on tourism and fisheries, and risks to human and animal health. Of particular concern is the poorly understood interplay between viruses and toxic species that form blooms because viruses may exacerbate their harmful effects. Concurrently, cyanobacteria are also a source of bioactive compounds other than toxins, which makes them good candidates for drug discovery. We show that virus infection of the cyanobacterium *Microcystis aeruginosa*, results in as high as a 40-fold increase in the toxin microcystin two days post virus infection (dpi), and predict that microcystin levels may remain high in a body of water up to 7 dpi, long after water discoloration and cell lysis. This implicates viruses as major contributors to toxin release from cyanobacteria and emphasizes the importance of taking them into account in predictive models and in the assessment of water safety. We also show that bioactive compounds of *M. aeruginosa* inhibit and delay infection of single stranded DNA and single stranded RNA viruses. This highlights the potential of cyanobacteria as an excellent source for the discovery of novel antiviral compounds, and the ease with which screening for cyanobacterial antivirals can be achieved.

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ALGAE FOUNDATION'S WORKFORCE DEVELOPMENT AND EDUCATION INITIATIVES: ALGAE TECHNOLOGY EDUCATIONAL CONSORTIUM (ATEC) AND THE ALGAEPRIZE 2022-2023

Algae Foundation is an American non-profit organization dedicated to all forms of algal-based workforce development, education and training by promoting the “Power of Algae” and its ability to transform human society and the environment upon which it depends. Approaching its eighth year, ATEC has served over 180,000 students and trainees from 100 countries. The ATEC initiatives are intended to develop algal-based bioeconomy workforce development and education programs including: 1. Collegiate curricula in Algal Cultivation and Biotechnology; 2. Algae Cultivation Extension Short-courses (ACES 2.0); 3. Algae Academy, K-12 STEM education programs; and 4. Algae Massive Open Online Courses. The AlgaePrize, launched 1/13/2022, is a U.S. Department of Energy sponsored student competition including high schools through doctoral programs to develop new algal technologies supporting gigaton scale algal cultivation. Originally 62 teams entered with 15 finalist teams selected in March 2022. The winners and grand champion were announced during the AlgaePrize 2022-2023 competition weekend, April 14-16, 2023 held at the National Renewable Energy Lab in Golden, Colorado. ATEC 2017-2023 accomplishments include: Algae Academy ~ 145,000 students in 50 states; Adoption of ATEC curricula by 41 academic institutions with more than 2000 students; Algae MOOCs #1 (Introduction to Algae), #2 (Algae Biotechnology), and #3 (Introduction to Seaweeds) have attracted > 34,000 students with a 98 % approval rating; ACES has been taken by more than 2250 students from 100 countries.

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DIVERSITY AND RELATIONSHIPS OF GRACILARIA SPECIES FROM THE PACIFIC COAST OF PANAMA

Gracilaria is a genus of red algae that is found in tropical and subtropical oceans around the world. It is an important resource for marine communities in the tropical Eastern Pacific, where it is used as a food source by many organisms, but the genus is poorly known. This research project aims to investigate the biodiversity and phylogenetic relationships of *Gracilaria* on the Pacific coast of Panama. Only one species of *Gracilaria* had been reported from Pacific Panama prior to 2017, when DNA sequence data revealed that at least three unidentified species are found on this coast. In the current study, sequences of *rbcL* were analyzed with five algorithmic species delimitation methods and the results of these analyses were compared to and visualized with an UPGMA cluster diagram. At 2% *rbcL* divergence, there are six genetic clusters, and at 1%, there are 10 clusters. However, the species delimitation analyses increased the partitioning of the dataset into at least 12 genetic clusters. Morphological comparisons of the species identified by the species delimitation found that the habits and internal anatomy of specimens in the six *Gracilaria* species clusters separated at 2% *rbcL* divergence showed clear differences among them. Maximum-likelihood and Bayesian analyses of these sequences in a *Gracilaria rbcL* data set demonstrated that most of the Pacific Panama species are sister to Caribbean - Tropical Western Atlantic species. Additional sampling and analysis of COI-5P sequences is being used to better resolve the number and relationships of Pacific Panama *Gracilaria* species.

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PHYTOPLANKTON ASSEMBLAGE STRUCTURE, DRIVERS, AND THRESHOLDS IN A LARGE, SHALLOW, AND EUTROPHIC LAKE IN FLORIDA, USA

Monthly samples were collected from March 2019-October 2021 at 21 sites in Lake Okeechobee and its two outflowing rivers to study phytoplankton assemblage structure over time and space and identify thresholds to significant environmental drivers. Phytoplankton assemblages were strongly spatially structured by deterministic processes while temporal patterns were noisier and likely driven by stochastic processes. The environmental variables explaining the greatest proportion of the spatial variation in assemblage structure individually were NO₃ (45%, $P=0.00$), alkalinity (37%, $P=0.00$), and orthoP (33%, $P=0.00$). Conditional tests revealed that after accounting for the variation explained by NO₃, the addition of total P, turbidity, SpConductivity, DO, alkalinity, depth, and orthoP cumulatively explained 92% of the total spatial variation ($P<0.05$). Unlike the robust spatial model, the

temporal model failed to explain over half of the temporal variability in assemblage structure. However, the temporal chl-a model performed better than the multivariate assemblage model with temperature, solar radiation, NH₃, and DO cumulatively explaining 75% of the total variation ($P < 0.05$). Thresholds to the dominant explanatory variables of spatial assemblage structure occurred at 179 µg/L along the NO₃ gradient, at 50 µg/L along the orthoP gradient, and at 92 mg/L along alkalinity gradient. Identifying algal assemblage patterns, drivers of those patterns, and thresholds to the drivers is essential to understanding harmful algal bloom dynamics and developing tools for prediction and management.

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PREDATION, COMMUNITY ASYNCHRONY, AND METACOMMUNITY STABILITY IN BENTHIC CYANOBACTERIAL MATS

The dynamism of ecological interactions in rapidly changing ecosystems can be understood only by linking community context to population dynamics. Here, we integrated observational, experimental, and theoretical approaches to unify local and regional ecological processes driving the dynamics of benthic cyanobacterial mats on coral reefs off the island of Bonaire, Caribbean Netherlands. Community and metacommunity dynamics of mats were tracked for 49 days alongside quantification of macropredation pressure from fishes. We tested the hypothesis that enhanced predation would result in decreased mat persistence *in situ*. Finally, we constructed a cellular automaton model to predict patterns in mat metacommunity dynamics across different scenarios of top-down and bottom-up control and dispersal. Cyanobacterial mat metacommunities were temporally stable across the study, stabilized by asynchrony in the dynamics of communities. Diverse reef fishes foraged on mats *in situ* and simulated predation decreased the instantaneous mortality rate of mat communities over natural mat communities in model simulations. Theoretical simulations suggested that dispersal conveys a rescuing effect on mat metacommunity abundance under scenarios of strong trophic control. These results establish critical baselines and generate hypotheses relevant to the processes maintaining cyanobacterial dominance of reefs.

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IMPLEMENTING THE IMAGING FLOWCYTOBOT (IFCB) WITHIN FLORIDA'S HARMFUL ALGAL BLOOM OBSERVATION NETWORK TO EVALUATE ESTUARINE DYNAMICS DURING *KARENIA BREVIS* BLOOMS

Blooms of the toxic dinoflagellate, *Karenia brevis*, initiate offshore on the West Florida Shelf and can be transported shoreward by currents. To better understand nearshore *K. brevis* bloom dynamics, an interdisciplinary network—of discrete sampling, high frequency *in situ* observations, remote sensing, and ocean circulation models—was implemented to focus on two estuaries (Tampa Bay, Sarasota Bay) and two bloom events (2021, 2023). Imaging

FlowCytobots (IFCBs) were deployed at fixed sites to capture phytoplankton image data, and classifiers for *K. brevis* morphotypes and other taxa were used to examine community assemblages at different bloom and tidal stages. *K. brevis* populations displayed varying degrees of morphological plasticity, with near mono-specific bloom periods sometimes observed. Differences in the timing of bloom onset, magnitude, and variability over diel to tidal time scales were also characterized, and diel vertical migration patterns were discerned. Estuarine introduction and persistence was influenced by the presence of a coastal bloom, as well as tides and currents. More short-lived *K. brevis* events occurred in estuaries (days to months) relative to the coast (months to years). Furthermore, circulation patterns that intermittently connect Tampa and Sarasota bays via coastal and/or estuarine pathways were recognized and may contribute to coastal and estuarine bloom longevity. Overall, this work contributes to a conceptual model of bloom dynamics and persistence in estuaries repeatedly impacted by blooms.

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A STICKY SITUATION: CHEMICAL AND CELLULAR INVESTIGATION OF ADHESION IN THE KELP *ALARIA MARGINATA*

Adhesion is a critical first step in the successful recruitment of seaweeds. Kelp sporophytes secrete adhesives from specialized rhizoid cells to anchor themselves to the ocean floor and withstand immense forces applied by waves. The composition of adhesive has primarily been described in the Fucales as a “modified extension of the cell wall”, but this description is ambiguous and insufficient for asking ecological questions about adhesion. Additionally, it is unclear whether kelp adhesives are compositionally similar to fucoids, and the cellular organization of the attachment interface is poorly understood. To address this, rhizoid cells and adhesive from developing *Alaria marginata* sporophytes were examined with light and electron microscopy to describe the structure and biochemical composition of adhesives and walls in the attachment interface of developing holdfasts. The primary holdfast is composed of elongated, thick-walled cortical cells and a meristoderm layer. New rhizoids differentiate from meristoderm cells by modification of the meristoderm outer wall and elongation by tip growth. Rhizoid cells measure 6-8µm in diameter and up to 150µm in length in juvenile holdfasts. Small spherical plastids are distributed evenly along rhizoids, and physodes and phenolic vesicles bodies accumulate in higher concentrations towards the rhizoid tip. Histochemistry suggests similar adhesive composition between fucoids and kelps, involving association of anionic polysaccharides and polyphenolics polymers which suggests adhesives likely assemble and function by similar mechanisms.

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A RECONSIDERATION OF THE GENUS *VISIA* (BATRACHOSPERMALES, RHODOPHYTA) WITH THE PROPOSAL OF NEW GENUS AND SPECIES

The genus *Visia* is distributed in tropical regions of Asia, Australasia and South America. This study evaluated the species level taxonomy and phylogenetic relationships within the freshwater rhodophyte of the genus *Visia* based on DNA sequences (*rbcL* and COI-5P) of samples from northern and midwestern Brazil. Concatenated analyses of *rbcL* and COI-5P sequences revealed that the genus forms a clade within the order Batrachospermales. But two sequences formed a distinct clade outside the genus allowing to propose a new genus. The *Visia* clade included four species: the generitype *V. cayennensis* with samples from Brazil and French Guiana; *V. cylindrocelularis* from Malaysia; and two undescribed species, one from Brazil and the other from Australia. All species recognizable from DNA sequence data, except *V. cylindrocelularis*, are cryptic. Analyses of *rbcL* and COI-5P separately are congruent with the concatenated analysis of both markers. The new genus to be described, provisionally named *Pseudovisia*, is also cryptic, with similar morphological characters of *V. cayennensis*. This is the third case of a cryptic genus within the Batrachospermales, after the recent proposal of the genera *Macrosporophycos* (undistinguishable of *Macrosporophycos*) and *Volatus* (similar to *Kumanoa*). Current data indicate that the genetic

diversity within the small genus *Visia* is comparable or higher than typically than observed in other genera of the Batrachospermales, e.g. *Kumanoa* (with 44 species). *Visia* and *Pseudovisia* are phylogenetically related to two other tropical genera: *Acarosporophycos* (Brazil) and *Macrosporophycos* (India).

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DOES ICE COVER IMPACT MACROALGAL CHEMICAL COMPOSITION IN THE WESTERN ANTARCTIC PENINSULA?

Sea ice in the Southern Ocean can profoundly influence photosynthetic organisms by altering subsurface irradiance. The patterns and timing of sea ice cover can vary on a monthly to annual timescale in sub-regions of the Western Antarctic Peninsula (WAP). Sea ice is susceptible to changes in the climate. During the latter part of the 20th century, sea ice coverage significantly decreased in the WAP, a trend that aligns with warming in this area. Macroalgal biochemical components are impacted by light availability, often showing a close relationship between photosynthesis and biochemical compositions. We used satellite imagery of annual sea ice duration/extent and water turbidity during ice-free periods to identify 14 study sites that differed in ice coverage but were similar in terms of turbidity along the central WAP between the Terra Firma Islands in Marguerite Bay (S 68° 41.5') and the Joubin Islands west of southern Anvers Island (S 64° 46.4'). Common macroalgal species were collected by scuba divers between 35 m and 5 m depth at each site they occurred and were frozen for later biochemical analyses. Overall percentages of major biochemical components were determined. Correlations were run between biochemical compositions and four different sea ice indices. Protein content was positively correlated with ice cover for *Himantothallus grandifolius* and *Sarcopeltis antarctica*. Protein, carbohydrate, and lipid percentages varied for the remaining two species, *Desmarastia menziesii* and *Iridaea* sp., and for *H. grandifolius* and *S. antarctica* for carbohydrate and lipid content.

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FUNCTIONAL REDUNDANCY AND METABOLIC ADAPTATION: INSIGHTS FROM GENOMIC AND TRANSCRIPTOMIC ANALYSIS

The *Mesodinium* genus of ciliates is widely distributed in coastal marine ecosystems, with some species forming non-toxic red tides. Despite lacking their own genetic plastid, members of this genus exhibit a range of trophic modes, from completely heterotrophic to nearly completely phototrophic. Some species, such as *Mesodinium rubrum*, are able to acquire organelles from cryptophytes and utilize their photosynthetic machinery. In *M. rubrum*, the ciliate steals and maintains a transcriptionally active nucleus of its prey, known as the kleptokaryon, which facilitates control and division of sequestered plastids and mitochondria. Through genomics and transcriptomics analysis of four members of this genus, we demonstrate that *M. rubrum* relies on its acquired metabolism not only for photosynthesis, but also for the basic biosynthesis of several amino acids, fatty acids, and nucleic acids. Many of the lost biosynthesis genes are encoded by the mixotrophic *M. chamaeleon* and heterotrophic *M. pulex*. Our findings suggest that by retaining a foreign nucleus in its cytoplasm, *M. rubrum* has rendered many of its own biosynthetic pathways functionally redundant, leading to their loss. Overall, our results highlight the remarkable evolutionary consequences of an organism acquiring foreign genetic material and utilizing it for their own metabolic needs.

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DO ECOLOGICAL DISTRIBUTIONS OF MICROBIAL SYMBIONTS HELP IDENTIFY PROBIOTICS?

Microbial symbionts influence many aspects of the biology of kelp and other macroalgae. Manipulating the microbiome through addition of probiotics may be a sustainable way to improve macroalgal productivity, health, and resilience for aquaculture and conservation. Identifying the microbes most likely to impact the host trait of interest out of the 10s to 100s of microbial symbionts is a major hurdle. Understanding the ecological distribution of microbes on kelp in the wild may enable us to select probiotic candidates more efficiently. Microbes that are consistently associated with a host (core taxa) are hypothesized to have a greater effect on host biology. Yet, many of the probiotics currently in use across sectors are common microbes that are easy to culture but are rarely found on the host in natural settings. Within this framework, we 1) identified the core taxa of sugar kelp (*Saccharina latissima*) from wild populations in British Columbia, Canada, 2) assessed the influence of 129 bacterial strains isolated from sugar kelp on growth and development of sugar kelp gametophytes and juvenile sporophytes in the laboratory. Frequency in natural populations (a measure of core) is positively correlated with the ability of isolates to increase growth and development rates, in support of the hypothesis that core taxa are more likely to influence function. However, this is a trend and variability is high. Isolates that most strongly increase the # of sporophytes range in frequency on host populations from 2% to 95%. High growth with low-frequency isolates highlights the need for broader testing.

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THE ROLE OF MACROALGAL MICROBIOMES IN THE UPTAKE OF MERCURY BY COASTAL AND ESTUARINE SEA LETTUCE (*ULVA* SPP.)

Most of the research on mercury cycling in marine environments has centered on pelagic food webs, and little is known about mercury cycling in macroalgal-based food webs. Seaweed from the genus *Ulva* have a global distribution throughout the world's marine and brackish habitats and accumulate metals and other toxins from the water column with little effect on the host macroalgae. Although the mechanism driving *Ulva*'s tolerance to marine pollution remains unclear, studies suggest the macroalgal microbiome may be responsible. This study investigates how differences in collection location influence mercury uptake and bacterial community composition in *Ulva* spp. Estuarine and coastal *Ulva* were exposed to 1, 50, and 200 ng/L of mercury during 6-day laboratory experiments. The taxonomic composition of the *Ulva* microbiome was estimated based on the V1-V9 regions of the 16s rRNA gene. Estuarine samples accumulated higher concentrations of mercury than coastal samples (ANOVA, $p = 0.02$) across all treatments. The microbial community structure varied between coastal and estuarine *Ulva* samples (PERMANOVA, $p = 0.1$) at the phylum, class, and genus taxonomic levels. Finally, the community composition of the estuarine microbiome is driving the increased mercury uptake (nMDS, stress < 0.01) at the phylum, class, and genus taxonomic levels. This study shows that the *Ulva* microbiome is shaped by habitat and is correlated to mercury uptake responses. The microbiome of *Ulva* from estuarine environments could be making the macroalgal holobiont more resistant to increased nutrient and toxin loads.

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GENE EXPRESSION ANALYSIS OF SEXUAL MATURITY TRANSITION IN *MACROCYSTIS PYRIFERA* GAMETOPHYTES

Germplasm conservation is essential for biodiversity preservation and domestication of crop species. Recently created kelp germplasm collections of gametophytes will ensure the preservation of diverse genetic traits selected using modern genomic tools. *Macrocystis pyrifera* is an ecologically and economically important species due to its high production and diverse biochemical composition, making it a promising candidate marine crop. However, the long-term maintenance of gametophyte germplasm breeding values or lack thereof will require a comprehensive understanding of the genetic pathways underlying all culture stages in a kelp nursery. This study analyzed the gene expression variation in male and female gametophytes at various developmental stages to identify genes involved in gametophyte sexual maturity. The differential expression analysis was conducted using a factorial design, comparing vegetative and sexual stages and sex. We found expression patterns for over 21,000 annotated features, with 19% associated with sex. Interaction analysis of differentially expressed genes (DEGs) indicates that more genes related to male maturity are upregulated during reproduction. Principal component analysis confirms that 62% of the variation is attributed to sex, while 11% is specific to the population. These findings support previous observations in other brown algae and heterogametic organisms, indicating that males possess more genes regulating male fitness. This study will help to elucidate the underlying molecular mechanisms that contribute to sexual dimorphism in biological traits such as growth rate and reproductive strategies giving insight into biological pathways and regulatory networks involved in sex-specific development and function.

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THERMOTOLERANT SYMBIODINACEAE ASSOCIATED WITH CORAL HOLOBIONTS MAY PROMOTE PERSISTENCE IN EXTREME ENVIRONMENTS AND AFFECT BACTERIAL COMMUNITY STRUCTURE

Symbiodiniaceae, the family of endosymbiotic dinoflagellates associated with cnidarians, are critical components of reef ecosystems, driving productivity. Coral holobionts are composed of the coral host, Symbiodiniaceae, microbes, viruses, and more. Semi-enclosed inland bays in Curaçao are uniquely extreme and variable, and semi-analogous to future ocean conditions. Studying coral holobionts in these multi-stressor environments will help us uncover mechanisms for resilience and understand how holobiont community dynamics may shift under climate change. This study aims to characterize and examine correlations between algal symbionts and bacterial communities to assess coral holobiont dynamics. *Siderastrea siderea* samples were collected from bays and reefs in Curaçao over three seasons. We show that thermotolerant Symbiodiniaceae *Durisdinium trenchii* is associated with more holobionts from inland bays, potentially allowing these corals to thrive in these more stressful environments. In contrast, holobionts from fringing reefs associate with two *Cladocopium* species. Bacterial analyses show no distinct patterns based on site differences. We hypothesize that there are correlations between bacterial communities associated with different algal taxa which may be driven by handoffs between algae and microbial members, and nutrient cycling within the holobiont. These results show how interactions between members of coral holobionts are affected by multi-stressor environments and may respond as anthropogenic climate change continues to exacerbate and intensify these stressors.

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PROTEOMIC AND PHOSPHOPROTEOMIC INVESTIGATION OF A *HAEMATOCOCCUS PLUVIALIS* MUTANT EXHIBITING INCREASED HETEROTROPHIC GROWTH

The green microalga, *Haematococcus pluvialis*, is desirable for industrial cultivation because it produces the highest amount of the powerful antioxidant, astaxanthin. Currently, heterotrophic cultivation of *H. pluvialis* shows a slower growth rate compared to other cultivation modes, preventing its widespread industrial use. To address this problem, this work aims to improve heterotrophic growth rate by targeting specific acetate/acetic acid metabolic pathways in *Haematococcus*. EMS-based chemical mutagenesis and screening work identified an *H. pluvialis* strain, KREMS 23D-3, that achieved an 18% higher cell density and 22% higher acetate consumption rate than the wild-type when grown heterotrophically. TMT-based and titanium dioxide enriched LC-MS/MS conducted on triplicate mutant and

wild type samples at 48 h under heterotrophy identified 6364 proteins and 6053 phosphorylated proteins total, and 374 and 709 significantly changed (p-value<0.05 and >1.5-fold up- or downregulated) proteins and phosphoproteins, respectively. An ASH-domain containing protein was identified as highly down-regulated in the mutant KREMS 23D-3 in comparison with the wild type and is associated with the GO term “negative regulation of cell population proliferation”, which may be related with the high cell density phenotype observed in the mutant. These data may not only reveal potential targets for strain engineering, but also contribute to the annotation of the *H. pluvialis* genome, which is still incompletely sequenced and annotated.

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FRENEMIES WITH PHYSIOLOGICAL CONSEQUENCES: ENVIRONMENTAL PERTURBATIONS SWAY CELLULAR CROSSTALK WITHIN MICROALGAL-BACTERIAL INTERACTIONS

Unions among microalgae and bacteria are fundamental contributors to large scale ecosystem processes including the ocean carbon pump, the evolutionary success of coral reefs, and the duration of algal blooms. My research evaluates how environmental stressors elicit shifts in cellular crosstalk of microalgal symbioses and the resulting eco-physiological consequences. In this talk, I overview two vignettes where bacteria interact with microalgal symbionts as antagonistic producers of ‘iron carrier’ ligands to endure metal deficiency and as antagonistic producers of an algicidal quinone capable of microalgal ‘zombification’. These vignettes highlight the importance of contextualizing microbial interactions within the biogeochemical seascape of ecosystem wide processes such as coral bleaching and algal blooms. Ultimately, my current and future work serves as a framework for how cell-cell interactions govern organismal physiology and cascade into shifts in functional ecology.

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CHARACTERIZATION OF NITRIC OXIDE SYNTHASES WITH DIVERSE EVOLUTIONARY ORIGINS IN DIATOMS AND OTHER SELECT ALGAL GROUPS

Nitric oxide (NO) is a key signaling molecule in both prokaryotic and eukaryotic organisms. Nitric oxide synthases (NOSs) are a family of oxidoreductases that catalyze the production of NO from arginine. Genome analyses have revealed that some diatoms lack NOS genes, while others have genes encoding one or two distinct NOS isoforms. This study investigates the evolutionary relationship among NOS genes with particular focus on diatoms, green algae, cyanobacteria, and dinoflagellates. Sequences used in this study were retrieved from publicly available databases, aligned, and used in phylogenetic analyses. NOS genes from eukaryotes and cyanobacteria resolved three distinct clades: (1) animals, (2) cyanobacteria, diatoms, and dinoflagellates (CDD) and (3) green algae and diatoms. Within the CDD group, diatoms and dinoflagellates formed a clade that was sister to the cyanobacteria. In the green algal/diatom clade, the diatoms were nested within the green algal NOSs. Several diatoms contained NOS genes from both clades. If the NOS genes in diatoms were derived from either cyanobacterial or green algal endosymbionts, numerous genes losses would have had to occur to produce the present-day gene distribution. Alternatively, if the genes arose via horizontal gene transfer, several independent transfers of the same genes would have been required. Further analyses of whole genomes are required to develop a better understanding of the distribution and evolution of NOSs in diatoms and other algal lineages.

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ECOPHYSIOLOGICAL ADAPTATIONS OF ABUNDANT MESOPHOTIC MACROALGAE IN THE MAIN HAWAIIAN ISLANDS: SHEDDING LIGHT ON MACROALGAL PHOTOSYNTHESIS

The intensity and quality of light changes exponentially with increasing depth, thus driving adaptations in photosynthetic organisms. Mesophotic coral ecosystems are low light environments from 30–150+ m depths, and

have a high abundance of macroalgae in the Hawaiian Archipelago. The classic theory of chromatic adaptation predicts that brown algal species are better adapted to lower depth ranges than green algal species depending on coastal water type. To test the variance in ecophysiological characteristics between fleshy Chlorophyta and Ochrophyta at mesophotic depths, 112 samples of abundant macroalgae were collected from O‘ahu and Maui during 2004–2011 from 51–125 m depths. Each sample was dark-adapted and analyzed using pulse amplitude-modulated (PAM) fluorometry, and a subset of the collections was frozen at -80°C for pigment analyses with High-Performance Liquid Chromatography. PAM photosynthetic efficiency measurements suggest that changes in photosynthetic parameters along an increasing depth gradient are genus/family specific and that Ochrophyta and Chlorophyta are utilizing similar physiological adaptations to low light conditions. Analysis of Chl *a* concentrations and accessory pigment to Chl *a* ratios provides further insight into the physiological differences between these two phyla. These findings shed light on the unique physiology of mesophotic macroalgae and the factors driving the persistence of these species in low light conditions, which will be important in future climate change scenarios of decreasing water clarity and algal phase shifts.

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THE BACTERIAL COMMUNITY OF *SACCHARINA LATISSIMA* IS STABLE ACROSS TIME, SPACE, AND STRESS GRADIENTS

Saccharina latissima is a commercially valuable marine foundation species that is threatened by climate change, including extreme low-salinity events. In the lab, moderately low salinity conditions reduce growth-rates and reproductive success of *Saccharina*. In the field, *Saccharina* populations have been killed by very low salinity. In addition, *Saccharina* is host to a diverse bacterial community, that are important to algal biology. Since salinity is also an abiotic filter for bacteria, we asked if salinity always alters the bacterial community of *Saccharina*. To address this question, we conducted a manipulative lab experiment (8 times) and field surveys at 4 sites (13 visits/site) of *Saccharina* populations near Vancouver, during the yearly low-salinity event (freshet) in 2021 and 2022. Salinity regularly drops below 15 in kelp beds during the freshet. Consistent with previous studies, we document effects of low-salinity stress in the lab, validating that our selected culturing conditions were stressful. Across both the lab and field, we find that while the overall bacterial community varies across the freshet and by salinity, we observe remarkable consistency and stability in *Saccharina* indicator ASVs (core microbiome). To test the robustness of our study, we re-analyzed already published *Saccharina* bacterial data and found exact sequence matches between those sequences and our indicator ASVs. These data suggest that the *Saccharina* bacterial community is strongly determined by host filtering and is resilient to abiotic stress.

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LIGHT IMPACT ON CRUSTOSE CORALLINE ALGAE FROM THE GREAT BARRIER REEF GROWING ON ARTIFICIAL SUBSTRATE IN AQUACULTURE

Crustose coralline algae (CCA) function as reef binding cement, and by providing species-specific mediation of larval settlement for corals and other invertebrate taxa. CCA are thus fundamental to the health of tropical marine ecosystems including on the Great Barrier Reef (GBR) in Australia. Although it is well established that light is an important driver in marine ecosystem processes, little is known about how light quality or intensity impact CCA communities, particularly in aquaculture. This study tested the influence of light spectra and irradiance and on the community structure and composition of tropical CCA growing in culture on artificial substrate. Settlement tiles were conditioned in a common garden flow-through tank at the Australian Institute of Marine Science (Townsville), then distributed across aquaria exposed to three different spectra (blue-dominated, full, or green-dominated) and

four distinct irradiance levels (5, 15, 60, or 160 $\mu\text{mol m}^{-2}\text{s}^{-1}$). CCA were identified using morpho-anatomy and DNA sequencing. Results indicated that light intensity had a greater influence than light spectrum on community composition and algal morphology. Communities were dominated by *Lithophyllum*, *Porolithon*, and *Mesophyllum* species. These results may assist with the selection of optimal light conditions for propagating target CCAs for the purpose of settling coral in aquaculture and reseeding coral populations on degraded reefs.

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ON EUROPEAN SPECIES NAMES BEING APPLIED TO WESTERN ATLANTIC MARINE MACROALGAE BY WORKERS IN THE 19TH CENTURY

Prior to 1900, macroalgal specimens collected from various sites around the world were collected by or simply sent for identification to European phycologists including the Agardhs, Harvey, Kützing and Montagne. Just as a comprehensive foundational literature of marine macroalgae was being written, the first specimens collected in the Americas were being identified by these and other workers. In many cases, the familiar morphologies of local species prompted the application of European binomials for their American look-alikes. In the 1850s, Harvey wrote the first flora for the Americas, *Nereis Boreali-Americana*, focusing on the east and west coasts of the United States. Despite his description of many new species, a great number of the binomials applied to American specimens were the same names as those ascribed to specimens from European waters. These names remained in the floras of North America for more than 150 yrs. The shift to DNA sequences as a tool to distinguish among species in the mid-1990s enabled researchers to test whether or not species were truly ampho-Atlantic, *i.e.*, the same species being found in Europe as well as in Northwest Atlantic. We detail examples of “amphi-Atlantic” species from eastern North America, Bermuda and the Caribbean that we have sequenced in genera from *Champia* to *Wrangelia* that required splitting into species different from those in Europe and are characterized by more narrow geographic distributions. Those taxa genetically shown to be truly ampho-Atlantic are mostly those found in the coldest North Atlantic waters of North America and Europe, but even in these waters overlooked species can be found.

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CLIMATE-DRIVEN EVOLUTION AT RANGE MARGINS OF MARINE FORESTS

Climate-driven range shifts that shape the geographical distribution of genetic diversity can drive different modes of speciation including divergence in allopatry or recombination at contact zones and allopolyploidy. Empirical evidence for these predictions in marine forests was discovered by analysing the geographical distribution of genetic variability and modelling species range shifts. This revealed novel recombined genomic diversity at recent expansion fronts that form contact zones, in addition to the more expected high and unique genetic diversity in ancient populations at estimated long-term persistence zones, some of them presently located in shrinking climatic refugia. Hotspots of diversity and evolution have also resulted from diversity and reticulation within lineages with clearly discernable ancestry and geographical distribution at sympatric contact zones. Phylogroup distributions compared with habitat suitability over time further demonstrate a role of cycles of isolation in disjunct persistence areas intercalated with ephemeral expansions and admixture at high-latitude contact zones. Multi-glacial cycles thus acted as a speciation pump for marine organisms otherwise exhibiting cosmopolite amphiboreal distributions.

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INVESTIGATING THE REPRODUCTIVE SYSTEM OF A MONOICOUS, HAPLOID-DIPLOID MACROALGA

The relative rates of sexual versus asexual reproduction govern the distribution of genetic diversity within and among populations. Most studies on reproductive variation focus on mating systems (i.e., selfing to outcrossing) using taxa with diploid-dominant life cycles (i.e., angiosperms). However, eukaryotic life cycles vary widely. Outcrossing should be associated with diploidy, while selfing and clonality should correlate with a prolonged haploid stage as deleterious mutations can be exposed to selection and purged. These correlations have not been systematically investigated across life cycle types due to a lack of population genetic data for many eukaryotes. To address this gap, we investigated the reproductive system of the monoicous, haploid-diploid alga *Batrachospermum gelatinosum*. We hypothesized that *B. gelatinosum* populations would exhibit (i) high levels of intragametophytic selfing due to the physical proximity of male and female reproductive structures on the thallus and (ii) partial clonality due to the haploid-diploid life cycle and the capacity for both sexual and asexual reproduction. We haphazardly sampled and genotyped 359 gametophytes from 21 eastern North American populations using 12 polymorphic microsatellite loci. We observed a high frequency of repeated genotypes, suggesting a combination of selfing and possible monopore production. The reproductive system seems to fit theoretical predictions for haploid-diploid life cycles, but there are inherent challenges to working with these algae for which novel population genetic theory are necessary.

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HISTORY OF THE GIRAFFE PIPE LOCALITY INFERRED FROM MICROFOSSIL REMAINS: A THRIVING SUBARCTIC LAKE ECOSYSTEM DURING THE WARM EOCENE

Giraffe Pipe fossil locality offers a deep time analog into the life of a thriving subarctic freshwater ecosystem during the early-late Eocene under wet Greenhouse conditions. The remains of an extensive deposit of microfossils, including photosynthetic (chrysophytes, diatoms and green algae) and heterotrophic protists (euglyphids, heliozoans, paraphysomonads and rotosphaerids) were used to reconstruct the history of the ancient waterbody. Concentrations and diversity of chrysophyte algae, including synurophyte taxa, were extensive throughout the core, accounting for over 70% of the microfossil remains and indicative of a paleo-hotspot for this eukaryote lineage. The high ratio of chrysophyte cysts to diatom valves further emphasized the dominance of chrysophytes. Based on the totality of fossil evidence, the waterbody represented a series of relatively shallow habitats, with changing physical and chemical conditions, and varying water depths. The initial habitat, which lasted for hundreds to thousands of years, was shallow, slightly acidic and nutrient poor. This phase shifted abruptly to one dominated with the diatom *Aulacoseira* and numerous synurophytes, indicating a deepening of the waterbody and increase in nutrient content. Subsequently, the waterbody became dominated with extensive remains of acidophilic diatoms and synurophytes, shifted to a eutrophic lake dominated by heterotrophic protists, eventually to a humic-stained, acidic wetland before transitioning to a terrestrial habitat. Numerous tropical taxa were recorded throughout the lake history.

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BIOPHYSICAL TRAPPING AS A DRIVER OF *DINOPHYSIS ACUMINATA* BLOOM DEVELOPMENT AND PERSISTENCE IN NAUSET MARSH

Blooms of the dinoflagellate *Dinophysis* cause diarrhetic shellfish poisoning and may be increasingly prevalent

globally. These are specialist mixotroph species that must feed on *Mesodinium* ciliates, whose plastids they sequester internally for photosynthesis in a process called kleptoplasty. Despite this, *Dinophysis* and *Mesodinium* seldom co-occur in situ. Here, the ecological, behavioral, and physical conditions associated with the development of *Dinophysis acuminata* blooms in Nauset Marsh (Cape Cod National Seashore, MA) were explored through field observations during two separate blooms. Field populations were observed through deployments of an Imaging FlowCytobot (IFCB) phytoplankton sensor and the collection of conductivity, temperature, fluorescence, and dissolved oxygen profile measurements within one of Nauset's terminal kettle holes. Very few *Mesodinium* were observed through either bloom. Division and fusion rates were estimated through a culture study that related frequencies of these behaviors to cell accumulation. Comparison to accumulation rates indicate that Nauset blooms developed through selective retention rather than in situ division. Retention was driven by thin layer formation at oxyclines that lied deeper than shallow outlets from the Nauset holes. Linkage of these thin layers to sub-oxycline regions suggests that blooms may become more frequent or intense with increasing coastal eutrophication. Blooms persisted for weeks in spite of low rates of division. The cause of termination remains to be determined but occurred as *Dinophysis* grew increasingly stressed by scarcity of their *Mesodinium* prey.

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VARIATION IN THERMAL TOLERANCE BETWEEN POPULATIONS AND LIFE STAGES OF THE BULL KELP *NEREOCYSTIS LUETKEANA*

Rising sea temperatures have been associated with declines in the bull kelp *Nereocystis luetkeana*. Despite its ecological importance, a comprehensive understanding of bull kelp thermal physiology remains lacking. In particular, patterns of variation in thermal tolerance between life cycle stages and populations exposed to different thermal regimes have only recently garnered significant research interest. In this study, we compared the thermal performance of bull kelp sporophytes and gametophytes from four sites in southern British Columbia, two with stable low temperatures year-round and two with seasonally high temperatures. Vegetative tissue discs were collected from blades at each site and exposed to eleven temperature treatments from 5°C to 20°C for four days, after which maximum quantum yield (Fv/Fm) and mass were measured. Gametophytes were cultivated from spores obtained by collecting sori from each site, then exposed to the same eleven temperatures for five weeks, after which growth was measured as percent cover. Preliminary data indicate that gametophytes were more tolerant of elevated temperatures than sporophytes. "Warm" site sporophytes tended to exhibit greater thermal tolerance than "cool" site sporophytes, whereas gametophyte thermal tolerance did not show overt differences between sites. Our findings suggest that bull kelp sporophytes may be especially vulnerable to warming compared to gametophytes. However, the observed variation in thermal tolerance between "warm" and "cool" sites hints at the possibility for mediating adaptive or plastic responses.

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CHARACTERIZING THE REPRODUCTIVE SYSTEM IN TWO INVASIVE *AVRAINVILLEA* POPULATIONS

The relative rates of sexual versus asexual reproduction influence the partitioning of genetic diversity within and among populations. During range expansions, such as biological invasions, a shift to uniparental reproduction (i.e., selfing, asexual reproduction, or both) can facilitate successful establishment through reproductive assurance. The invasive green macroalga *Avrainvillea lacerata* was first reported in Hawai'i in the early 1980's and has since rapidly expanded in distribution around the island of O'ahu and to two neighboring islands. Field observations suggest the alga is reproducing asexually through fragmentation due to no documented or anecdotal collections of individuals bearing gametangia. However, to our knowledge, population genetic analyses have never been used to

characterize the reproductive system of *A. lacerata*. We sampled two populations on O‘ahu – ‘Ewa Beach and Maunaloa Bay – over several successive years (2018, 2019, 2021). We developed microsatellite loci to determine the prevailing reproductive mode. Based on the microsatellite data, there is evidence that *A. lacerata* may be polyploid. In addition to this, multiple unique multilocus genotypes were found across the dataset, including within individual populations at a given time point. This work adds to the body of literature on the evolutionary ecology for *A. lacerata* and provides data for green algae which generally lack information on population genetic patterns. Additionally, these data will provide evolutionary predictions for invasive species management in Hawai‘i.

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PATCHY AND PINK: DYNAMICS OF A *CHLAINOMONAS* SP. (*CHALMYDOMONADALES*, CHLOROPHYTA) ALGAL BLOOM ON BAGLEY LAKE, NORTH CASCADES, WA

Snow algal blooms frequently occur throughout alpine and polar environments. While these phenomena are observed globally during spring and summer months, and often persist while there is suitable snow habitat, our understanding of bloom dynamics is limited. We tracked a bloom of *Chlainomonas* sp. on Bagley Lake in the North Cascade Mountains of Washington. We used algal physiology, amplicon sequencing, and observations of snow color intensity to track trends and dynamics through the course of the bloom. Over eight weeks, we found that overall algal physiology decreased throughout the bloom. This decrease in physiology was decoupled from a patchy distribution of pink snow and a heterogeneous mixture of algal cell morphologies with no clear temporal trends. Additionally, the proportional representation of *Chlainomonas* sp. remained consistent throughout the study. These findings suggest that the *Chlainomonas* sp. community on Bagley Lake is not simply a bloom – bust cycle as is often seen in aquatic systems, though there is a physiological trajectory and sensitivity to environmental stress. The patchy distribution of pink snow across the lake is indicative of small colonies of algae growing asynchronously, likely in response to a suite of conditions. As we continue to understand drivers of dynamic snow algal blooms, we will further our understanding of the capacity of these organisms in marginal and extreme environments for acclimation and adaptation.

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RESOLVING CRYPTIC *CORALLINA* SPECIES (*CORALLINALES*, RHODOPHYTA) ACROSS THE EASTERN PACIFIC, WITH COMMENTS ON BIOGEOGRAPHY

Corallina (*Corallinoideae*, *Corallinaceae*) is a cosmopolitan genus of geniculate coralline red algae common in nearshore temperate regions. Recent taxonomic progress in this genus has incorporated molecular data from contemporary and type collections, but several clades have yet to be formally described. To identify molecular limits of taxonomically unresolved clades, clarify species descriptions, and document biogeographic distributions of *Corallina*, we analyzed three genes from extensive collections and type specimens of species described from the eastern Pacific. An *rbcL* sequence from the type specimen of *C. bathybentha* from Santa Catalina Island, California matched sequences from recent collections from the subtidal and occasionally the low intertidal zones from Alaska to central California. Species delimitation analyses suggested that one unnamed clade, which has thus far been

treated as a single taxon, includes multiple cryptic species, one of which appears to occur anti-tropically: collections include samples from southern Chile, and samples collected southward from British Columbia through California. COI haplotype network construction for this taxon suggests that most haplotypes radiate from the genetically rich region of northern BC. Thus, members of *Corallina* may have been historically distributed northward as individuals associated with long-distance dispersing, buoyant kelp species. Additional population genetic study is needed to clarify the biogeography of and test further phylogeographical hypotheses for these species.

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RECENT HARMFUL ALGAL BLOOMS OF *PRYMNESIUM PARVUM* IN TEXAS CONSIST OF MULTIPLE CRYPTIC SPECIES

Prymnesium parvum is a type of unicellular, biflagellated, haptophytic algae. *P. parvum* forms toxic blooms around the world that are disruptive to local ecosystems. In the United States, *P. parvum* blooms are most concentrated in Texas. *P. parvum* is a cryptic species complex with at least three member species. These member species are referred to as A-, B-, and C-types based on the toxins they produce. Previously, all chemotyped strains (n=3) of *P. parvum* from Texas are A-types. However, the genetic and chemical diversity of Texas *P. parvum* is not well understood outside of these cases. We surveyed eight different *P. parvum* blooms in Texas that occurred from 2018-2020, resulting in 32 additional *P. parvum* Texas strains. Each strain was sequenced, and its genome size, heterozygosity, and ploidy was characterized. Phylogenetic analysis revealed that both A-types and B-types are currently found in Texas, and can even be found in the same bloom. Significant intraspecific genetic variation was also found in A-types, with haploids, diploids, and hybrids being identified. All B-types characterized were diploids, and are the first B-type diploids to be identified. Together, our analysis indicates that the genetic diversity of *P. parvum* in Texas is greater than previously known. Future work is needed on the behavioral and metabolic differences between the A-type and B-type *P. parvum* and the effects that the two cryptic species have on blooms in Texas.

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LASTING IMPACTS OF A HISTORIC MARINE HEATWAVE ON ROCKY INTERTIDAL SEAWEED COMMUNITIES

The increasing frequency, severity, and duration of marine heatwaves (MHWs) pose serious questions about population persistence and community stability in nearshore ecosystems. Using the 2014-2016 Northeast Pacific MHW as a case study, we explored population and community responses of intertidal seaweeds and invertebrates over a ten-year period on rocky coasts of Calvert Island, Central British Columbia, Canada. We found major shifts in abundance and elevational distribution among populations that substantially reorganized communities. Namely, warming caused many seaweeds to shift downslope and decline in cover. At higher elevations, seaweeds were partially replaced by mussels, but this was not consistent across sites: in some cases, loss of seaweed led to loss of total biological cover. Following return of cooler waters, community recovery was variable across sites and elevations, and communities have tended not to return to previous states. We documented a positive relationship between seaweed community stability and species richness. Given the intensity and duration of MHW conditions over several years that impacted populations across elevations, we suggest that the biodiversity-stability relationship is not simply explained by prevailing stress gradients paralleling elevation. Rather, areas of greater seaweed species richness also have greater capacity for resistance and rebound that may reflect niche partitioning and recruitment facilitation, both of which were likely weakened in species depauperate high-shore communities.

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RECENT ADVANCES IN SEAWEED AQUACULTURE IN THE USA: FROM THE FARM TO BLUE FOOD

Global seaweed aquaculture production is approximately 33 million metric tons with an annual value of > \$13.7 billion in 2020. Seaweed aquaculture production occupies approximately 25% of total world marine aquaculture production by weight, with upwards of 97% being produced in Asia. Seaweed aquaculture production is by several species: the kelps, *Saccharina japonica* & *Undaria pinnatifida*; and the red seaweeds including *Neopyropia/Pyropia/Porphyra* spp., *Kappaphycus alvarezii* & *Eucheuma striatum* and *Gracilaria/Gracilariopsis* spp. More than 50,000 tons of seaweed have been cultivated in the Americas and Europe with an annual value of >US \$74 million. Although seaweed aquaculture is a relatively new in North America, the demand by western markets is expected to increase rapidly due to growing consumer demand for new protein sources, healthy blue food supplements, food industry's interest in sustainable textural additives and food security. After more than \$62 million invested by the ARPA-E (US DOE) MARINER Program, seaweed aquaculture is developing new business opportunities in the USA. The cold-water brown seaweeds, *Saccharina latissima* and *S. angustissima*, have been successfully cultivated in open water farms in the Northeastern USA. Our selectively bred kelp grew 7.0 m in length and yielded up to 28 kg FW per meter. Typical commercial yields are 4 to 8 kg FW per meter. With improvements in productivity, kelp and other farmed seaweeds continue to build significant value as blue foods and could potentially be viable feedstocks for animal feeds, phycocolloids and biofuels.

POSTER ABSTRACTS (alphabetical by first author; the presenting author is underlined)

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PSEUDOCRYPTIC LINEAGES OF *GLOIOCLADIA* (FAUCHEACEAE, RHODOPHYTA) AND VERTICAL DISTRIBUTION OF THE GENUS IN HAWAIIAN MESOPHOTIC CORAL ECOSYSTEMS

Mesophotic Coral Ecosystems (MCEs) extend from 30 to >150 m below the ocean surface in tropical and subtropical waters, and are currently one of the main foci of modern marine biology biodiversity research. Here, we characterized nine Hawaiian mesophotic specimens of the red algal genus *Gloiocladia*, of which only one species has been reported from shallow water in the Hawaiian Islands. Phylogenetic analyses using plastidial (Rubisco large subunit gene, or *rbcL*) and mitochondrial (cytochrome oxidase subunit 1, or COI) markers delineated three distinct clades with full support, which differed in vertical distribution (i.e., depth range). The previously reported shallow water species (*G. iyoensis*) and one of the new lineages, to be described as *Gloiocladia laukuamoo sp. nov.*, are indistinguishable in gross morphology, but some anatomical differences can be observed with light microscopy (size and number of layers of medullary and cortical cells). These two species can be found throughout the Hawaiian Archipelago, including both the Papahānaumokuākea National Marine Monument and the Main Hawaiian Islands, and they share an identical distributional range. A third lineage, which is an intertidal species requiring further investigation before description, was also revealed in the phylogenetic analyses. This study confirms the known habitat range of *G. iyoensis* as including both the upper-mesophotic as well as shallower waters, and demonstrated the presence of a mesophotic-exclusive species, *G. laukuamoo sp. nov.* The results of this study are consistent with previous reports of taxonomic confusion between *Gloiocladia* and *Gloioderma*.

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MACROALGAL ASSEMBLAGES AND VERTICAL DISTRIBUTION ALONG A SEA ICE GRADIENT IN THE CENTRAL WESTERN ANTARCTIC PENINSULA

Macroalgal forests dominate hard, shallow benthos along the northern portion of the western Antarctic Peninsula (WAP). Macroalgal biomass and species richness decline dramatically between southern Anvers Island and northern Marguerite Bay and observations in this gap have been limited to a few qualitative reports from the 1970s. We hypothesized that this pattern is correlated with annual sea ice patterns that govern light availability. We used satellite imagery of annual sea concentrations as well as water turbidity during ice-free periods to identify 14 study sites that differed in ice coverage but were similar in terms of turbidity along the central WAP. Divers continuously video recorded benthic organisms on replicate vertical transects between 5 and 20-40 m depths with horizontal transects at every 5 m depth interval along each vertical transect. Macroalgae were also collected by hand along each horizontal transect component. Fleshy macroalgal cover ranged from around zero at high ice sites to 80% at the lowest ice sites. Nonparametric, multivariate analyses resulted in clustering of macroalgal assemblages across most of the northern sites of the study area although they differed greatly with respect to macroalgal percent cover and diversity. At most northern sites, macroalgal cover was similar across depths but macroalgal (and macroinvertebrate) distributions suggested increasing effects of ice scour in shallower depths towards the south. Crustose coralline red algae were observed at all sites and non-calcified crustose red macroalgae at all sites except for one.

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DIVERSITY AND DISTRIBUTION OF *ULVA* SPECIES IN LONG ISLAND SOUND

Algae in the species-rich genus *Ulva* are found globally and often form blooms. These species often have cryptic morphologies which makes their identification often difficult, requiring DNA sequencing to confirm species identity. Previous studies in New Haven Harbor and Rhode Island have suggested a prevalence of *Ulva compressa* in the area, with lower amounts of *U. flexuosa* and *U. linza*; however, the distribution of *Ulva* species in Long Island Sound is not well described. This project examines the species identities and distribution of *Ulva* species on Long Island and on the shores of Long Island Sound. For this project, 230 *Ulva* samples were collected during the summers of 2020 and 2021. Following *rbcL* sequencing of these samples, nine species were identified, which is more than expected for this region based on previous surveys. The bloom forming species *U. compressa* and *U. rigida* were widespread, with a higher incidence of *U. compressa* in 2021 and a shift in *U. rigida* distribution from the north shore of Long Island in 2020 to all Connecticut shore sites in 2021. A large number of specimens were identified as either *U. linza* or *U. prolifera*; these species were difficult to differentiate even with additional ITS sequence data and require further study.

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ASSESSING THE BENEFITS OF ANTIOXIDANT AND ANTIBIOTICS TREATMENTS FOR CRYOPRESERVATION OF THE MODEL ALGA *ECTOCARPUS SILICULOSUS* AND THE ENDEMIC ALGA *ACINETOSPORA ASIATICA*

Cryopreservation in liquid nitrogen is a suitable technique for preserving seaweeds, a group of photosynthetic organisms with many applications. To test the effect of 2-mercaptoethanol (antioxidant) and antibiotic mixtures on cryopreservation of the model alga *Ectocarpus siliculosus* and the endemic brown seaweed *Acinetospora asiatica* using low-tech passive rate cooler. 2-mercaptoethanol was added to the cryoprotectant (CPA) solution, while antibiotic mixtures were included in the culture medium during the recovery process. In addition, two CPA solutions were tested on *E. siliculosus*. After two weeks of recovery, the treatment comprising PSC antibiotic mixture (Penicillin G, streptomycin, and chloramphenicol) showed a significant increase in post-thaw viability. Antioxidant treatment did not improve viability. The highest viabilities for *E. siliculosus* and *A. asiatica* were 64-83%, and 83-87%, respectively, using 10% glycerol + 10% proline as CPA solution. *E. siliculosus* and *A. asiatica* were successfully cryopreserved using a low-tech passive rate cooler, 10% glycerol + 10% proline solution, and antibiotic treatment. The highest post-thaw viabilities (64-87%) reported for PSC antibiotic mixture suggest the potential benefits of using antibiotics during post-thaw recovery of marine macroalgae. This study is the first report on cryopreservation of *A. asiatica*.

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ASSESSING DESICCATION STRESS EFFECTS ON MORTALITY RATES AND COMMUNITY COMPOSITION OF DIATOMS RESIDING IN STREAMS PRONE TO DROUGHT

The intermediate disturbance hypothesis predicts that species diversity will be highest at levels of moderate amounts of disturbance. In line with this hypothesis, this study characterized chronic desiccation stress on the long-term diatom assemblage of a hard substrate. Diatoms collected from the Colorado and Bosque Rivers of Texas were cultured onto glass microscope slides in stream mesocosms, then exposed to varying lengths of desiccation stress at ~39°C punctuated by brief submersion over the course of 6 weeks. Mortality rates and community assemblage were assessed on a weekly basis to identify species-specific desiccation tolerance and to characterize long-term assemblage shifts in stressed assemblages.

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CRYPTOMONAS PYRENOIDIFERA ORGANELLAR GENOMES AND ESTIMATION OF ITS ITS2 SEQUENCE DIVERSITY USING LINEAGE DIRECTED BARCODE PRIMERS

Cryptomonas is a common metropolitan freshwater microalgal genus that is easily recognizable due to its distinctive asymmetric cellular morphology and swimming pattern. There are currently 71 recognized *Cryptomonas* species but these can be difficult to identify by cellular morphology alone. This makes estimation of *Cryptomonas* diversity from environmental samples challenging as it requires culturing of strains followed by sequencing of genetic markers for clear identifications. In this paper we describe the isolation and culture of *Cryptomonas pyrenoidifera* from a small ephemeral pool in Southwestern Virginia, USA, with an annual recurrent population of this genus. Genomic resources from this isolate, including complete chloroplast and mitochondrial genomes, and nuclear and nucleomorph rRNA regions, were completed and archived. Metabarcoding, using lineage-directed primers designed to amplify the ITS2 region of *Cryptomonas*, was used to estimate an intra-specific variation of 99.3% for the *C. pyrenoidifera* ITS2 barcode from this natural environment. Metabarcoding also revealed that at least twelve phylogenetic species were present in this body of water. Our results provide new genomic resources for *C. pyrenoidifera* and suggest that metabarcoding with the ITS2 marker is a feasible approach to estimating *Cryptomonas* diversity and identification.

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CHARACTERIZATION OF *CHLAINOMONAS SP.* IN SEDIMENT CORE SAMPLES FROM BAGLEY LAKE IN CORRELATION WITH SEDIMENT COMPOSITION AND GLACIAL HISTORY

Alpine lake sediments can preserve biological records of organisms that live in or on seasonally snow-covered lakes whose biomass sinks and is deposited over time. These organisms include snow algae that grow on the surface of alpine lakes in the late spring and early summer. Bagley Lake in the North Cascade Mountains is a site that has regular recurring snow algae blooms. By collecting sediment cores from Bagley Lake we were able to examine changes in snow algae diversity and abundance over the past few millennia. Microfossils in the laminated sediments of the cores include snow algae, diatoms, testate amoebae and other unidentified cells. Our results indicate that both abundance and diversity of all these groups of microfossils has varied substantially over the past 2700 years. Historic photos and sedimentologic evidence (e.g., clastic laminae) indicate that a small cirque glacier likely existed in the Bagley Lake Basin for nearly the entire record, only disappearing in the last ca. 70 years. This glacial history may allow us to reconstruct the ecological history of snow algae in this area as well their response to the demise of the glacier historically.

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VIABILITY DETERMINATION OF THE HCT-116 COLORECTAL CANCER CELL LINE TREATED WITH FUCOIDAN EXTRACTED FROM SARGASSUM SPP. IN PUERTO RICO

Over the years, various treatments have been developed that have proven to be effective in preventing the proliferation of cancer cells in cancer patients. However, such treatments usually cause serious effects such as burns or severe inflammation; this referring to radiotherapies and chemotherapies. In this investigation, the HCT-116 colorectal cancer cell line was treated with a sulfated polysaccharide called “fucoidan”, which inhibits the growth of these cells and induces apoptosis. This compound can be extracted from various macroalgae and some marine invertebrates. Therefore, it was extracted from the Sargassum genus of brown algae that accumulates on the coasts of Puerto Rico, since it can cause many problems for marine species. Once the fucoidan was obtained, the cancer cells were exposed to this compound prepared at 125 µg/mL, 150 µg/mL and 175 µg/mL. To validate its anticancer potential, two MTT assays were performed, which consisted of culturing the cells in multiwell dishes with these different fucoidan concentrations to later determine their viability colorimetrically and measuring their absorbance at 570 nm. The extracted fucoidan turned out to be highly effective in inhibiting cell growth, lowering their viability percentage to around 40% in all concentrations used. However, it was not purified. Therefore, it cannot yet be established that fucoidan extracted from Sargassum in Puerto Rico is an effective anticancer agent.

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LIVING SNOW PROJECT: ENGAGING THE COMMUNITY IN ALGAE RESEARCH AND EDUCATION IN A CHANGING CLIMATE

The Living Snow Project works towards engaging communities and students in community supported science (often called citizen science). Outdoor recreators in alpine environments often see pink snow and are not sure what it is. We aim to educate communities on snow algae life cycle and influences by encouraging citizen science through citizen sampling. Through citizen and scientist sampling, we gain more data to form the characterization of pink snow algae biodiversity and its impact on snowmelt dynamics. In addition to engaging community scientists in sampling efforts, the Living Snow Project collaborates with regional partners (Mt. Baker Ski Area, Northwest Avalanche Center, Mount Baker- Snoqualmie National Forest, and Western Washington University) in Mt Baker Snow School, a snow ecosystem education program for middle school students. Snow School invites secondary students from local school districts to the Mt. Baker Ski Area to experience a day of data observation, collection, and analysis through a snowshoe-powered outdoor exploration. Students explore snow systems in an alpine environment via creating connections between mountain snowpacks and watersheds through hands-on data observation, collection, and analysis. Student engagement does not stop at the mountain, students are invited to Western to showcase projects highlighting snow algae life cycles through the scientific method.

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EPIBIOTIC DIATOM ASSEMBLAGES ON TEXAS FRESHWATER TURTLES

Turtles (Testudines) often host epibiotic floral communities on their shells, of which diatoms can be a major component. Turtle ecology varies across age, sex, and species, and the basibiont habitat conditions provided by their shells vary accordingly. This undergraduate study evaluated the degree to which epiphytic diatom assemblages vary across turtle sizes, sexes, and/or species. Turtles were surveyed in the upper Guadalupe River of Texas in June 2021 and March 2022. Diatom samples were scrubbed from the entire carapace of each turtle, as well as rocks collected at the study site to provide environmental reference points. Up to 200 cleaned diatom valves were counted per sample; diatoms were identified to genus level. Non-metric multidimensional scaling was used to create 2-dimension ordination of the observed relative abundance data of assemblages found on rocks, Texas cooters (*Pseudemys texana*), stinkpots (*Sternotherus odoratus*), and Cagle’s map turtles (*Graptemys caglei*). ANOVA testing showed significant differences in assemblage between turtles and environmental substrate (rocks), as well as between Texas cooters and stinkpots. No significant differences were found between sexes. Linear correlation showed a significant relationship between log-corrected turtle mass and NMS axes 1 and 2. These results imply that diatom assemblage

differs in correlation with turtle size and species, supporting the potential of turtle ecology studies based on carapacial diatom assemblages.

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HALIMEDA DISCOIDEA MICROBIOME DIVERSITY IN THE HAWAIIAN ARCHIPELAGO: LOCATION AND TIME MEAN EVERYTHING

Marine bacteria form complex and mutualistic relationships with macroalgae and are important to their health, physiology, and ecology. Thus, spatial and temporal variability in macroalgal microbiome community composition and diversity may have profound impacts on community-level processes. The objective of this study was to determine spatial and temporal differences in the microbiome diversity of *Halimeda discoidea* from two locations in the Hawaiian Archipelago and across years. Samples of *H. discoidea* were collected from Manawai Atoll in the Papahānaumokuākea Marine National Monument in 2019 (n=12) and 2021 (n=13), and from ‘Ewa Beach, O‘ahu, HI in 2019 (n=3). DNA was extracted and amplified via PCR methods using Illumina primers targeting the V3V4 variable region of the 16S rRNA gene. Products were sequenced via Illumina MiSeq using v3 chemistry (2 x 300 bp). Microbial communities of *H. discoidea* were primarily composed of Alphaproteobacteria, Gammaproteobacteria, and Cyanobacteria. The microbiome diversity at Manawai in both 2019 and 2021 was significantly different from the diversity observed at ‘Ewa in 2019. Samples from Manawai had differences in microbiome diversity based on depth; differences in community composition among sites at Manawai were observed in 2019 but absent in 2020. The temporal and spatial characterization of macroalgal microbiome diversity is key to understanding differences in these mutualistic communities and may also reflect anthropogenic influences amongst regional locations and the influence of invasive algae.

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EPIZOIC DIATOM DIVERSITY OF GULF OF MEXICO SEA TURTLES

Many diatom taxa are specialized to live on animals as epibionts. Previous research has found diverse and unique diatom taxa on the carapace and neck skin of sea turtles. This undergraduate research aims to characterize the assemblage of diatom genera found on sea turtles inhabiting the Gulf of Mexico that were either in rehabilitation or residing at the Texas State Aquarium from 2019-2022. Diatoms were collected by the aquarium veterinary team during inpatient procedure by scrubbing quarter-sized sections of tissue with a toothbrush that was then rinsed into a vial and stored in ethanol. Cleaned valves were enumerated and identified to genus. Initially, this study compared the epizoic diatom assemblages between the carapace and skin of individual Kemp’s ridley sea turtles (*Lepidochelys kempii*). *Nitzschia* was dominant on the carapace whereas *Tursiocola* was dominant on the neck skin. Even so, there was no statistically significant difference in overall diatom assemblage between the carapace and neck skin due to other genera held in common by both locations. This study will continue to compare seasonal differences in diatom assemblages of the same species of sea turtle and differences in diatom assemblages among the four sea turtle species common in the Gulf of Mexico.

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FIRST INSIGHTS INTO GREEN ALGAE FROM NEW MEXICO SOILS

Microscopic green algae are severely understudied, compared to their plant relatives. Terrestrial algae inhabiting gypsum substrates are especially poorly understood. Our study was the first to investigate the diversity of green algae in the gypsum soil crusts of White Sands National Park (WSNP). In addition, we characterized new algal isolates from another desert area, the Organ Mountains-Desert Peak National Monument (OMDP). We used light microscopy and DNA barcoding to classify the newly obtained algal strains. We also conducted an experiment to determine whether strain isolation could be aided by the addition of anhydrite to the growth media. We isolated 24 green algal strains, spanning twelve genera in two classes. There was no overlap in taxa between localities or samples. The most common taxon was *Bracteacoccus minor*, a species with a near-worldwide distribution. The WSNP samples also harbored two genetically unique algae from the family Oocystaceae, which may represent species new to science. The OMDP samples were overall more diverse than the WSNP material and contained species belonging to common soil-dwelling genera. Our growth experiment did not support our hypothesis – the growth of colonies was significantly inhibited by the addition of anhydrite to culture media. Overall, our study shows high potential of novel biodiversity in the soil crusts of New Mexico. Additional sampling and isolation will likely reveal more algal diversity in both localities and will further enrich our knowledge of the New Mexico microflora, which to date remains largely unknown.

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LIGHTING THE WAY TO IDENTIFYING THE COMMUNITY COMPOSITION OF BIOLUMINESCENT DINOFLAGELLATES IN THE SALISH SEA

Bioluminescence is a natural phenomenon that occurs all over the world in coastal waters. In the Salish Sea, located in Washington State and British Columbia, bioluminescent plankton are widely present however they are not well studied. Bioluminescent plankton can include both single celled plankton and larger zooplankton. Dinoflagellates are single celled plankton that are well known to be contributors to bioluminescence. *Noctiluca scintillans*, is one of the most widely known bioluminescent dinoflagellates in the world but unexpectedly, may not emit bioluminescence in the Salish Sea even though it does so elsewhere. The objective of this study was to identify the community composition of potential bioluminescent dinoflagellates in the Salish Sea with microscopy and eDNA data. We took samples from Bellingham Bay in the summer of 2022 during known bioluminescent events and carried out microscopy to identify the dinoflagellates present in each sample. We compared those results with ones we received from DNA extractions and sequencing of the 18s gene to identify the diversity of dinoflagellates that may have not been identified in our microscopy. We collated this with the known bioluminescent dinoflagellates identified in the literature to define the diversity of potential bioluminescent dinoflagellates in the Salish Sea. This project was completed in collaboration with the Community Boating Center as part of a citizen science initiative to engage with the Bellingham community about bioluminescence.

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PHYCOCOSM: JGI ALGAL GENOMICS IN 2023

PhycoCosm (<https://phycocosm.jgi.doe.gov>) is the algal multi-omics portal developed in 2020 by the US Department of Energy Joint Genome Institute (JGI) to support analysis and distribution of algal genome sequences and other 'omics' data. JGI has continued to focus on algal sequencing and analysis projects in support of the DOE's Biological and Environmental Research program mission focus on bioenergy, the global carbon cycle, and biogeochemistry. In particular, algae are one of the focus areas of the Community Science Program call for proposals for high-throughput sequencing and other genomics projects (<https://jgi.doe.gov/user-programs/program-info/how-to-propose-a-csp-project/>).

Alongside JGI's own sequenced genomes, PhycoCosm also hosts externally sequenced algal genomes and their structural and functional annotations, providing one of the most comprehensive tools for algal comparative genomics. BUSCO is a respected and useful tool for assessing genome completeness at many well-studied taxonomic levels. However, recent genome sequencing efforts have outpaced algal representation in BUSCO in several key lineages. We discuss the current state of algal genomics and our understanding of algal phylogeny, using clustering of orthologous proteins as a proxy for genome completeness in previously less well represented taxonomic groups, including Rhodophyta, Streptophyta, and Bacillariophyta.

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DETERMINING THE UPTAKE OF INORGANIC NITROGEN IN MARINE PHYTOPLANKTON ASSEMBLAGES THROUGH THE ¹⁵N-TRACER TECHNIQUE AND METATRANSCRIPTOME

The availability of inorganic nitrogen is considered one of the limiting factors for primary production in the ocean. However, different phytoplankton possess unique strategies to take up and assimilate nitrate and ammonium to cope with environmental changes. To investigate the nitrogen uptake characteristics of different size-fractionated phytoplankton in natural assemblages, three research cruises were conducted in the southern East China Sea in 2018 and 2019. The nitrogen uptake characteristics of two size-fractionated natural assemblages, microphytoplankton (20-200 μm) and pico-nanophytoplankton (<20 μm), were measured using the ¹⁵N-tracer technique. At most of the stations, significantly higher potential maximum uptake rates of ammonium than of nitrate were detected in the pico-nanophytoplankton, indicating that small phytoplankton possess a relatively superior capacity to take up ammonium. In contrast, comparing the potential maximum uptake rate for nitrate between microphytoplankton and pico-nanophytoplankton showed that microphytoplankton have the capacity to take up nitrate as a nitrogen source. However, repressed uptake rates for ammonium and nitrate in microphytoplankton were sometimes found in the coastal station even when ambient nitrate concentrations remained high. Metatranscriptomic analysis of nitrogen transporter genes in microphytoplankton suggested that most diatoms should utilize regenerated ammonium prior to nitrate to maintain their populations at the end of blooms.

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PHYLOGENOMICS AND TAXONOMIC REVISION OF RHOPALODIALES - DIATOMS WITH OBLIGATE CYANOBACTERIAL ENDOSYMBIONTS

Symbiosis, the tight association of separate organisms living together, is a common phenomenon in nature. From the ancient organelles inside of our cells to lichens and corals, the integration of life forms from disparate backgrounds to form new organisms is found across the tree of life. What are the mechanisms that allow this to happen? What are the costs and benefits of these relationships? In one group of eukaryotic microorganisms called diatoms (which form the base of the food chain in aquatic ecosystems and generate more oxygen by photosynthesis than all rainforests

combined), symbioses are formed with cyanobacteria that “fix” nitrogen. We explore how these organisms came together, whether that happened once or many times, the impacts of the association on host, symbiont and the ecosystems in which they live, and how these partners coordinate their life activities. The project will carry out a taxonomic revision of the Rhopalodiales, on the species and subspecies level, for over 700 named taxa. Preliminary results from SEM observations highlight the diversity of valve ultrastructure among several *Epithemia* species, showing variation in raphe position and structure, areolar morphology and presence/absence of a central nodule. These data point to several morphologically distinct groups within the genus. Molecular data on the genome of SB symbionts indicate core gene composition and variation among their genomes. Phylogenetic analysis of SB genomic data support the hypothesis that acquisition of the SB symbionts within the Rhopalodiales was through a single event.

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UNDERSTANDING THE CELLULAR AND MOLECULAR CHANGES OF CHOREOCOLAX POLYSIPHONIAE AND VERTEBRATA LANOSA IN RESPONSE TO INFECTION

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

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NUISANCE *DIDYMO* BLOOMS - EXPLORATION OF DYNAMIC MICROBIAL COMMUNITY COMPOSITION AND FUNCTION

Didymosphenia geminata, also called didymo or rock snot, is a species of diatom that is composed of an external silica cell wall and produces a mucilaginous stalk material. Like most diatoms, didymo also consists of a consortium of microbes—a “phycosphere”. Nuisance growths of didymo form thick mats adhering to rocks and stream bottoms, typically within colder, oligotrophic rivers and streams. These blooms are seasonal but can last for months at a time, covering long stretches of stream beds, altering stream conditions, outcompeting native algal species, and suffocating aquatic organisms. In September 2022, a combined field and lab study was conducted using samples from South Holston River, TN. The objectives were to (1) explore niche partitioning of didymo mat microbial communities across a diurnal cycle, (2) explore mat metabolic products, and (3) explore changes in mat physiology during senescence. Field sampling occurred over a 24-hour period, with multiple sampling times (n=5). Environmental parameters were measured at each sampling time: dissolved organic carbon (DOC), photosynthetic active radiation (PAR), water temperature, pH, and conductivity. Live biomass was collected for quantification of oxygen dynamics (photosynthesis vs. respiration) and DOC release across mat senescence. The blooms consisted of

both didymo and *Diatoma ehrenbergii*, which dominated the bloom biomass in a secondary bloom. In lab experiments, photosynthesis and respiration rates were found to be significantly different during early senescence stages compared to later stages (ANOVA, $p = .016$).

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THE MACROALGAE HERBARIUM CONSORTIUM PORTAL, PAST AND FUTURE

In 2013, a consortium of museums and universities began a collaborative Thematic Collections Network funded by the National Science Foundation (DBI-1304924). Our initial goal was to digitize the algal collections in North American herbaria and provide an Internet portal to document collections and facilitate research. Since 2013, the Macroalgae Herbarium Consortium Portal (MHCP; <https://macroalgae.org/portal/index.php>) has expanded to include more institutions and the number of digitized specimens has grown dramatically. The MHCP now contains specimens from approximately 60 institutions housing almost 950,000 algal specimens! The MHCP is now hosted and managed by the Symbiota Support Hub (<https://symbiota.org/>). Herbaria with algal collections are encouraged to join the consortium and catalog their specimens through the portal. With support from the Symbiota Support Hub, the Macroalgal Portal offers many resources to member collections. For Collection Managers, there are tools to facilitate data entry; management, and sharing; access to the Symbiota Support Hub; flexible data import/export options; crowdsourcing georeferences, data entry, and annotations; taxonomic data cleaning tools; and easy data publishing to GBIF and iDigBio directly from the portal. When you Live-manage your collection in the portal, you can do all of the above, plus access following: a web-based CMS that can be accessed anytime, anywhere; tiered user permissions and edit tracking; more nimble integration with ongoing portal development; and faster and even easier data publishing to other aggregators. Visit and join the Macroalgae Herbarium Consortium Portal today at <https://macroalgae.org/portal/index.php>.

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FINDING *EUASTROPSIS* (SPHAEROPLEALES, CHLOROPHYCEAE)

Molecular studies of the green algal family Hydrodictyaceae (Sphaeropleales) over the last two decades have revealed new lineages, a diversity of chloroplast and mitochondrial genomes in size and architecture, and aided in resolving evolutionary relationships not supported in morphological studies. In these previous studies, representatives of all genera within Hydrodictyaceae have been included with the exception of *Euastropsis* Lagerheim 1895. This study incorporates *Euastropsis* after isolating it from a pond in Drawa National Park in Poland. Phylogenetic analyses place *Euastropsis* as a sister lineage to *Stauridium* spp., and its plastome architecture is characteristic of Hydrodictyaceae. The addition of *Euastropsis* in analyses offers insight into the trends of plastome and morphological evolutionary patterns in the family.

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OPTIMIZATION OF DISINFECTION METHODS FOR *CITRUS AURANTIFOLIA* AND *CITRUS SINENSIS* MICROPROPAGATION

Studies show how the production of *Citrus aurantifolia* and *Citrus sinensis* has been in decline throughout the years. An alternative for this problem is the technique known as micropropagation; “propagation of plants in closed vessels under aseptic conditions” (Roberts, Schum, 2003). The disadvantage of this technique is the rapid state of how the contamination may present in the medium or plant tissue. In past investigations, *Sargassum* spp. has been used as a sustainable biofertilizer. This research aims to optimize disinfection methods for the micropropagation of *Citrus aurantifolia* and *Citrus sinensis* to obtain viable plants without contamination utilizing *Sargassum* spp. as biofertilizer. The methods employed consisted of three variations: method #1 commercial Clorox (50%), method #2 commercial Clorox (30%) and Bacdown disinfectant detergent (10%), method #3 commercial Clorox (25%) and Bacdown disinfectant detergent (10%). Preliminary results showed that method #3 was more optimal for the disinfection of plant tissue, with a 79% of viability without presenting microbial growth. Media supplemented with *Sargassum* extract helped the plant heal much faster and increased in growth by size, and leaf number compared with the negative control. Hormone induced media was the best result for leaf and stem number. Method #1 presented 22.5% of viability, while method #2 42% of viability. As the research continues, further improvements are being made toward a better understanding of *Citrus aurantifolia* and *Citrus sinensis* micropropagation.

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CHARACTERIZATION OF THE MICROBIAL COMMUNITY ASSOCIATED WITH THE GREAT LAKES INVADER, *BANGIA ATROPURPUREA* (BANGIALES, RHODOPHYTA)

Many factors contribute to algal function and growth, such as the chemistry of their aquatic environment as well as interactions with other organisms through symbiotic relationships, including those between an alga and the microbial community that inhabits its surface or intercellular space. This study examines the microbial community compositions of *Bangia atropurpurea* and *Cladophora glomerata* from the Laurentian Great Lakes to understand bacterial diversity and compositional changes between species and different collection times. Microbial taxonomy was determined through sequencing of the V4 region of 16S rRNA gene and phylogenetic analyses were constructed using MEGA. Comparisons of algal microbiota isolated from different host species or geolocations demonstrated that bacterial communities likely assemble in alga-specific and environment-specific patterns. Sequencing of the microbiota of *B. atropurpurea* from samples taken 14 years apart showed a significant decrease in bacterial diversity over this time. In addition, the core microbial community consisted of genera with functions that may drive strong associations with the alga, such as degradation of cell surface polysaccharides agar and carrageenan, or protection against oxidative stress. Future studies can use these data to inform larger metagenomic surveys and further investigate the relationships between bacteria and their algal hosts. This will provide valuable insight into the microbial effect on algal function which may contribute to the mitigation of further invasions that impact local ecosystems.

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MORPHOLOGICAL ANALYSIS OF *CORALLINA* SPECIES IN THE NORTHEAST PACIFIC

Coralline algae play significant roles in coastal ecosystems, providing habitat for animals and recruiting invertebrates and kelps, yet they are predicted to be sensitive to ocean acidification and warming. Studying the current and future ecology of coralline algae, especially species-dependent processes, requires accurate species identifications. However, corallines are difficult to identify without molecular tools. Here, we investigated the taxonomic value of morphological characters for four northeast Pacific coralline species in the genus *Corallina* (*C. bathybentha* and three undescribed, genetically distinct species). We aimed to: (1) determine if morphological data support phylogenetic species concepts for these taxa, and (2) evaluate morphological and habitat traits that would allow for accurate identification of these species in the context of other *Corallina* species found in British Columbia. Using specimens whose species identities were confirmed using molecular barcoding, we measured and compared

physical traits of intergenicula and conceptacles, in combination with habitat data from collection records. When compared exclusively with each other, the four focal species could be differentiated morphologically. However, in the context of the greater *Corallina* diversity, not all British Columbian *Corallina* species could be consistently distinguished using the measured traits. One complicating factor is the wide variation in morphology exhibited by *C. vancouveriensis*. These findings highlight the need for molecular methods for reliable coralline species identifications.

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INSIGHTS ABOUT A COLLECTION OF CALOGLOSSA FROM A FRESHWATER STREAM IN PUERTO RICO

The red alga *Caloglossa* typically occurs in brackish water or mangroves, but also can be collected in tropical freshwater rivers. We found *Caloglossa* growing in the Los Negro river in Corozal, Puerto Rico. We visualized samples using the light microscope and scanning electron microscope (SEM) to examine the morphology. In order to confirm the species identity, DNA extraction, PCR and sequencing of the *rbcL* gene was performed. Morphological examination showed some plants to have clusters of tetrasporangia, which may be the first report of these structures from a freshwater collection. Results of the sequencing data placed this collection in *C. lepriurii* which has been previously reported from the Caribbean. We performed flow cytometer analysis to measure the ploidy level of *Caloglossa*. Also, we used ICP (Inductively Coupled Plasma) to measure the elemental composition of trace and heavy metals. Our preliminary suggests that *Caloglossa* can be used as a phycoremediator of heavy metals. To the best of our knowledge, the current work is the first report of characterization of *Caloglossa* species from Puerto Rico.

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TWO NEW SPECIES OF ENDOPLURA (RALFSIALES, PHAEOPHYCEAE) FROM KOREA

Endoplura gyeokpoensis sp. nov. and *E. limpeticola* sp. nov. from Korea are newly described based on molecular and morphological analyses. The crustose brown algal genus, *Endoplura* comprises three species: *E. aurea*, *E. jejuensis* and *E. koreana*. Our phylogenetic analyses of the *rbcL* and COI-5P genes reveal that *E. gyeokpoensis* sp. nov. and *E. limpeticola* sp. nov. are placed in the *Endoplura* clade with strong bootstrap supporting values. *Endoplura gyeokpoensis* is characterized by small crustose thalli, irregular outline of thalli, lighter margin, and 2–4 plurangia terminated by 2–3 sterile cells. *Endoplura limpeticola* is distinguished by epizoic crustose thalli on limpets, thick thalli up to 751 µm, darker margin, multicellular rhizoids, and 2 plurangia terminated by 2–3 sterile cells. Our study shows that the two new *Endoplura* species are molecularly and morphologically distinguished from each other as well as from the congeners.

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POPULATION DYNAMICS OF SNOW ALGAE, *CHLAINOMONAS* SP., THROUGHOUT A BLOOM CYCLE

Annually, snow algae in alpine environments across the globe experiences a bloom during the summer months as the snow melts. A unique sub-habitat within the alpine systems that hosts algae blooms is snow-on-lake habitats. This habitat commonly is dominated by the genus *Chlainomonas*, a green algae that produces red blooms in this wet snow. Over the course of several weeks in the summer of 2022, we characterized the biological and physical dynamics of a *Chlainomonas sp.* bloom on Bagley Lake in the North Cascade Mountains in Washington State. For this study we characterized populations of algae growing in patches on the lake, due to findings the previous year that suggested that the bloom was highly heterogenous. We characterized the snow habitat by measuring snowmelt, temperature, and chemical conditions throughout the bloom. To assess the biological community, we use microscopy to assess biodiversity, cell abundance, cell size, and infection status, as *Chlainomonas* cells in this environment are often infected by chytrids. Our data also suggests that total cell density and photosynthetic efficiency is relatively consistent but cell abundance cell size, and infection status are dynamic and are variable by pates. Cell size distributions are significantly different weekly across the bloom, and but is also, like abundance and infection status variable from patch to patch.

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CAN A PHYCO-SPHERE ASSOCIATED BACTERIUM BE USED AS A BIOLOGICAL CONTROL FOR THE *MICROCYSTIS AERUGINOSA* (CYANOBACTERIA)?

Freshwater harmful algal blooms (HABs) are a global water quality issue. One potential line of investigation is the employment of biologicals controls. Algae, especially cyanobacteria, are integrally associated with complex microbial assemblages, which cycle nutrients, provide micro-anaerobic environments, breakdown potentially harmful molecules, etc. However, these same microbial consortia are competitors or even inhibitors to algae in these systems. One potential biological control is *Rhodospirillum rubrum*, a Gram-negative, purple non-sulfur, motile proteobacterium. To test the capacity for HAB mitigation, 14 mesocosms (55 gallon) were inoculated with a native assortment of algae and *Microcystis aeruginosa* and half of the tanks inoculated with *R. rubrum*. Relative Fluorescence Units (RFU), Ash Free Dry Mass (AFDM), percent coverage, and bacterial (16S rDNA) and eukaryotic (23S rDNA) metabarcoding was conducted. The RFU was influenced by treatment (Kruskal-Wallis, $p < 0.001$, Mann-Whitney, $p < 0.001$) and which mesocosm it was collected from (Kruskal-Wallis, $p < 0.05$). Analyses of the meta-barcoding data are underway, but water clarity was clearly different in the two groups. Thus, employment of *R. rubrum* may be a potential control in some HAB scenarios.

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INTRIGUING INTRODUCTIONS: DO INTRODUCED *LITTORINA LITTOREA* AND NATIVE *L. OBTUSATA* PREFER NATIVE OR INVASIVE MACROALGAE?

Introduced species are considered a significant threat to global biodiversity. The introduced gastropod, *Littorina littorea*, is a dominant, generalist grazer whose herbivory has shaped macroalgal diversity and abundance patterns along northwestern Atlantic coastlines. This species broadly consumes ephemeral species, such as *Ulva* spp. while native *L. obtusata* has fairly restricted habitat and food preferences. We investigated grazing preferences of these gastropods for native vs. introduced macroalgal species as well as for ephemeral vs. perennial species occurring in New England. *L. littorea* showed a clear preference for native species, i.e., *Ulva* spp., *Gymnogongrus griffithsiae*, *F. vesiculosus*, and *Chondrus crispus*, over introduced *Bryopsis maxima* and *Grateloupia turuturu*, likely due to herbivore deterrent compounds produced by these introduced species. Similarly, *L. littorea* preferred native macroalgae collected from an N-enriched site. Again, an introduced species from this site, *Gracilaria vermiculophylla*, produces potent herbivore deterrents. Notably, *L. littorea* did not always select ephemeral species over structurally complex algae. *L. obtusata* strongly preferred the native algal species, especially *Fucus* spp., in paired-choice tests over all other macroalgae. Neither herbivore selected introduced species, and we observed tidepools filled with *G. turuturu* and thick mats of *G. vermiculophylla* at the N-enriched site. Such releases from herbivory could result in introduced species outcompeting native algae, disrupting coastal ecosystems.

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THE GLOBAL DISTRIBUTION OF DIVERSITY IN GIGARTINALES (RHODOPYTA)

The order Gigartinales includes a large number of species with great ecological importance, serving as habitats and food for a vast diversity of marine life. Several species are also economically important, being widely used in food and cosmetics industries. However, we lack biogeographical knowledge of the clade, and spatial patterns of diversity have yet to be assessed across global scales. Using data from the literature and GBIF across all Gigartinales, we quantify global patterns of species diversity and examine its potential environmental determinants, such as temperature, salinity, and insolation. Our results indicate that the diversity of this clade is high across tropical regions, and that the influence of different environmental factors varies across regions. We identified that species tend to generally have larger geographic ranges at lower latitudes compared to those at higher latitudes. Our results provide a clearer understanding of the global distribution diversity within Gigartinales, identifying hotspots of richness, which will improve predictions of global change effects on the biodiversity of this economically and ecologically relevant order of red algae.

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CONTRASTING NATIVE AND INVASIVE ALGAL PHYSIOLOGY TO UNDERSTAND COMPETITIVE ABILITIES BETWEEN DIFFERENT HABITATS OF CHARLESTON, SC

Macroalgal invasions are increasing in coastlines throughout the world. A better understanding of the physiological traits that enhance successful invasions may allow for an increase in predictive modeling to improve management. This study compared the physiological responses of the invasive *Gracilaria vermiculophylla*, native *Gracilaria tikvahiae*, and native and bloom-forming *Ulva* spp. within different habitats in Charleston, South Carolina. Seven sites were selected based on South Carolina's Department of Health and Environmental Control (DHEC) shellfish monitoring program, which classifies sites as "prohibited" or "approved" based on bacteriological and water quality analyses. Sites classified as "prohibited" by DHEC had the highest $\delta^{15}\text{N}$ values (7.03-11.27‰ vs. AIR) and % tissue nitrogen (2.72-3.66%), while the sites labeled "approved" had significantly lower values. Generally, *Ulva* spp. had the highest photosynthetic efficiency, with high yield and alpha. These results support the use of *Ulva* spp. as a bioindicator of water quality in estuarine environments. In comparison, the invasive *G. vermiculophylla* and native *G. tikvahiae* had similar photosynthetic rates across sites, suggesting these species are equally competitive physiologically. Other ecological processes, such as substrate preference and association with the decorator worm *Diopatra*, may be influencing the invasion success of *G. vermiculophylla* in estuaries.

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NOVEL FLORA OF DIATOMS ASSOCIATED WITH A MESIC EDWARDS PLATEAU CLIFF COMMUNITY IN TEXAS

In Bosque County, Texas, in the West Cross Timbers ecoregion, is a limestone cliff community that has tentatively been identified as a Mesic Edwards Plateau Cliff (MEPC), which is rare in Texas. The MEPC includes vegetation like the chatterbox orchid (*Epipactus gigantea*) and the maidenhair fern (*Adiantum capillus-veneris*). Little is known about these communities, but they have similarities to other cliff communities such as Western hanging gardens. These are typically small communities of ferns and mosses as well as other, often rare, plants that grow

from shallow soil of bedrock located near a spring or a seep. We are examining the algal and plant species composition of the MEPC since little is known about the ecosystem. Here, the diatom flora of this cliff community is described.

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CYANOBACTERIAL CONTRIBUTION TO ANNUAL CYCLES OF PHYTOPLANKTON IN LAKE MURRAY, SC

Lake Murray, near Irmo, SC, is a source of municipal water, hydroelectric production, and recreation. Freshwater cyanobacterial blooms have been increasing in both frequency and severity in recent years, and the importance of monitoring such blooms and indicating factors has become a priority for lake managers. The purpose of this study was to monitor and quantify the cyanobacterial contribution to phytoplankton biomass in Lake Murray, SC. Understanding seasonal cycles of cyanobacterial contributions to the local phytoplankton community can provide insights into the conditions that may initiate and sustain blooms. Weekly to biweekly phytoplankton collections and measurements of water quality were obtained using a YSI sonde, LiCor spherical quantum sensor, secchi disk. HPLC quantified photopigments that were converted to algal group relative abundances using ChemTax. Cyanobacterial contributions to the phytoplankton community range from 5-40% of the total phytoplankton biomass throughout the year, the highest of which occurs in the late summer and early fall seasons. A paired comparison t-test was utilized to compare samples taken from surface water and a depth of 4m, and although values show statistical significance, the values showed little potential for ecological relevance when comparing cyanobacteria at each depth. Cyanobacterial abundance varied seasonally, and the cyanobacterial contributions were considered within range of a healthy water system. The data ultimately provided insights into the baseline cyanobacterial contribution to the phytoplankton community.

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CHARACTERIZING INVERTEBRATE COMMUNITIES ASSOCIATED WITH THE CRYPTOGENIC ALGA *CHONDRIA TUMULOSA* IN THE PAPAĀNAUMOKUĀKEA MARINE NATIONAL MONUMENT, HAWAII

The availability and structural complexity of coral reefs strongly influence invertebrate community composition. Habitat alteration by a newly established species can change community abundance and diversity, especially in relatively undisturbed ecosystems such as the Papahānaumokuākea Marine National Monument (PMNM). A cryptogenic alga, *Chondria tumulosa*, was discovered in the PMNM at the atolls Manawai and Kuaihelani in 2016 and 2021, respectively. This alga forms dense mats up to 20 cm in height that overgrow native corals and macroalgae. Satellite imagery and field surveys suggest *C. tumulosa* can spread rapidly, thus altering the habitat available for invertebrates. The goals of this study were to characterize and compare invertebrate abundance and diversity in *C. tumulosa* mats between the two atolls. *C. tumulosa* samples were collected at Manawai (n=624) from five sites in August 2019 and eight sites in July 2021 and at Kuaihelani (n=275) from eight sites in July 2022. Invertebrates from each sample were sorted to the lowest identifiable taxon using a dissection scope, and DNA barcoding was used to identify representative specimens. The most abundant classes were Gastropoda, Amphipoda, and Polychaeta. Gastropoda was the most diverse taxon with 14 distinct morphotypes. This is the first study to describe invertebrate communities in native and invasive-like algae in the PMNM and establishes a baseline to understand how the continued spread of this habitat-altering alga will influence invertebrate community structure.

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LONG-TERM MONITORING OF MACROALGAL BIODIVERSITY IN STANLEY PARK, VANCOUVER, BRITISH COLUMBIA

Macroalgae are marine foundation species in rocky intertidal ecosystems. Although they are critical to the health of our aquatic ecosystems, we lack data regarding their historical abundance in many regions, including British Columbia. This lack of data prevents researchers from convincingly making claims regarding the impacts of severe weather events (e.g., 2021 heat dome), invasive species, and other disturbances on algal diversity in the region. To fill this data gap, we started a collaborative effort in September 2021 to collect monthly macroalgal biodiversity data at a highly biodiverse site in Stanley Park, Grouse in a Wetsuit, to categorize the macroalgae present throughout the year. We identify all the macroalgal species present in a 1 m x 1 m quadrat, which we place every 5 m along three consistent transect lines, once a month, at low tide. This sampling scheme allows us to capture the seasonal changes in algal abundance within the same 1 m x 1 m area throughout the year. Our goal is to make these data freely available to the public and work with other researchers to coordinate monitoring efforts to increase the utility and richness of the collected dataset.

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DIFFERENCES IN PHYTOPLANKTON POPULATIONS IN AGRICULTURAL IRRIGATION PONDS BASED ON SAMPLING TIME AND DEPTH AS REVEALED BY CELL AND PHOTOSYNTHETIC PIGMENT CONCENTRATIONS

Irrigation water quality can have substantial implications on crop, soil, human, animal, and environmental health due to the presence of harmful cyanobacteria. While studies exist on larger water bodies, little is known about the spatiotemporal dynamics of phytoplankton in small, shallow waterbodies often used for agricultural irrigation. This work evaluated the significance of sampling time and depth on common phytoplankton metrics in two Maryland, USA, agricultural irrigation ponds over the 2019 and 2020 growing seasons. Water was sampled at 9 am, 12 pm, and 3 pm at multiple depths and locations in each pond. The phytoplankton community was examined through several metrics including photosynthetic pigments (chlorophyll-a and phycocyanin) and microscopy-based enumeration and identification of diatoms, chlorophytes, and cyanobacteria. In-situ and fluorometric water quality parameters were also measured. A two-way analysis of variance indicates that time and depth had significant relationships with pigment concentrations, whereas no significant relationships were observed between time, depth, and microscopy-based cell counts. Correlations were found between phytoplankton metrics and water quality parameters. However, cell concentrations rarely correlated with pigment concentrations. This work indicates that selection of sampling time and depth when assessing phytoplankton communities in irrigation ponds may alter analysis outcomes because pigments and microscopy-based work may not always correspond to each other, and distinct spatiotemporal phytoplankton communities exist.

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KELPS ON DEMAND: CLOSED-SYSTEM PROTOCOLS FOR CULTURING LARGE BULL KELP SPOROPHYTES FOR RESEARCH AND RESTORATION

Kelp culture for commercial, conservation and scientific purposes is becoming increasingly widespread. However, traditional culture methods (e.g., ocean-based farms) face numerous constraints, which may limit smaller scale

cultivation efforts common in research and restoration. Growing kelps in closed, recirculating culture systems address many of these constraints, but closed system methods have remained largely undescribed. Extensive declines of the bull kelp *Nereocystis luetkeana* have received widespread attention and prompted numerous research and conservation initiatives. Here, we detail two approaches for cultivating *N. luetkeana* sporophytes in recirculating systems. *N. luetkeana* thalli were reared on ceramic tiles in custom flumes and freely floating in tumble culture. Careful control of stocking density, water motion, aeration, and nutrient levels allowed for rapid growth and normal morphogenesis of lab-grown kelp. A stocking density of up to 3 kg/m³ was achieved, and individual thalli attained lengths of up to 6m. Cultivated kelps exhibited substantial developmental sensitivity to flow conditions, highlighting promising avenues for future research. Our results demonstrate key advantages of recirculating culture systems over traditional culture methods. Recirculating systems enable the precise control of culture conditions, improving biosecurity and facilitating cultivar development and other research. Kelps can be grown away from the ocean or outside their native ranges, and seasonal or annual species can be produced year-round.

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CHARACTERIZING THE REPRODUCTIVE SYSTEM OF *FUCUS VESICULOSUS* ALONG THE EASTERN SHORE OF VIRGINIA

The reproductive system describes the relative rates of sexual and asexual reproduction and therefore partitions genetic diversity within and among populations. Population persistence is thus influenced by the prevailing reproductive mode. However, as compared to angiosperms, we know much less about reproductive system variation in the ocean. To date, one of the most well studied genera is the brown macroalga *Fucus*. *Fucus* spp. are also well known for forming ‘ecads’, or free-living thalli with morphological variability linked to persistence in estuaries and salt marshes. We are exploring the prevailing reproductive mode in *Fucus vesiculosus* populations along the Eastern Shore of Virginia (ESVA). Many thalli are fixed to oysters or mussels but have variable morphology with few vesicles, spiraling, or both. All thalli in ESVAs appear to be *F. vesiculosus* using a combination of *rbcL* sequencing and an RFLP assay. Second, we used temporal sampling and microsatellite genotyping to determine the relative rates of sexual versus asexual reproduction and the relative connectivity of populations sampled along the ESVAs. These data will enhance our knowledge about macroalgae in the Chesapeake for which in-depth studies broadly across algal taxa are lacking. We will also further our understanding of this genus – an emerging model of reproductive biology. Finally, these data are integral to conservation efforts in ecosystems where macroalgae are important ecosystem engineers.

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CHARACTERIZATION OF MACROALGAL ABUNDANCE, DIVERSITY, AND SEASONALITY AT POTENTIAL FORAGING SITES IN SOUTH CAROLINA

Macroalgae are commonly consumed world-wide and are a potential resource for local harvesting and the aquaculture industry in South Carolina. However, knowledge of edible macroalgal species diversity, abundance, and distribution is limited in this region. This study characterized seasonal trends in macroalgal diversity, abundance, and water quality to provide a baseline for potential macroalgal foraging sites and promote subsequent consumption. Macroalgal abundance was quantified every meter along a 10 m transect using the DACOR method at seven sites during Fall 2022 and Spring 2023. Water temperature, salinity, and dissolved oxygen concentration were recorded to characterize water quality conditions. Species identifications were verified based on morphological and microscopic examination. Twenty-seven macroalgal species of Rhodophyta (70%), Chlorophyta (19%), Ochrophyta (7%), and cyanobacteria (4%) were recorded at all sites. The spring had a higher abundance and diversity of macroalgae, with hard substrates such as docks hosting a higher diversity than estuarine and jetty environments. However, soft sediment environments hosted the highest abundance of edible *Gracilaria* spp. and *Ulva* spp. Only two species of Ochrophyta were recorded in the spring months. These data suggest that spring months may be the optimal time

period for foraging a diversity of species from hard substrate (jetty and dock) environments. Future studies should compare this diversity with summer months and conduct nutritional analyses across species from sites with different water quality conditions.

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NOVEL USE OF THE COVARIS ML230 FOCUSED-ULTRASONICATOR FOR RECOVERING DNA FROM ARMORED DINOFLAGELLATES

The success of many HAB monitoring programs lies in the ability to identify and quantify toxigenic species so resource managers can make timely decisions that safeguard environmental and public health. The co-occurrence of similar species, that may be non-toxic, makes microscope-based cell counts alone unreliable and has led to the development of quantitative, species-specific molecular assays. This process relies on accurate species identification, which is more easily achieved when clonal cultures can be established. However, many HABs are difficult to culture so data must be curated from cells found in preserved field samples. This often means working with single cells to obtain information (morphological via microscopy and genomic via sequencing). Probe-tip sonication is often used to lyse cells, but previous work on armored dinoflagellates had a DNA amplification rate of less than 20%. This study used the Covaris ML230 Focused-ultrasonicator to obtain DNA from armored dinoflagellates. Species-specific lysis parameters were determined using cultures of *Dinophysis acuminata* and *Gambierdiscus belizeanus* and were fine-tuned for the recovery of DNA from single cells of cultured *G. belizeanus* and *D. acuminata* cultures and preserved field samples. When using focused-ultrasonication the DNA amplification rate increased to 46%. The improved amplification rate and ease in which sonicated material can be processed and delivered to high-throughput applications may increase the speed and accuracy in which barcodes and species-specific molecular assays can be developed.