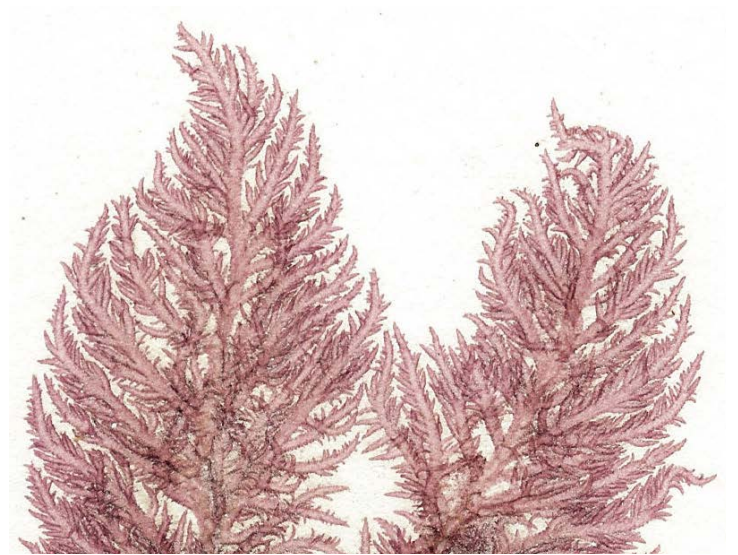


NEAS 2021 Program April 10 (online)



- Welcome and thanks, p. 1-2
- Meeting code of conduct, p. 2
- Overview of schedule with links, p. 3-4
- Detailed schedule of presentations, p. 5-9
- Abstracts, p. 10-45
- Index, p. 46-47
- Auction donors and sponsor p. 48

Welcome to NEAS 2021

This year has been like none other, especially to those impacted directly by COVID-19 and those with first responders and health providers in their family. Our regular lives, our routines, classes, research, and the opportunities to interact and exchange ideas, have been highly modified. When the pandemic hit in spring 2020 we were very close to the date of our spring meeting, but were unable to switch to a virtual meeting on such a short time frame (given that everyone was also adapting their lives at the same time).

So, the NEAS executive committee really wanted to hold a virtual meeting this year. We got such strong support for this meeting – over 120 participants giving 36 talks and posters! We are grateful to each of you, and optimistic about NEAS, because you adapted to and perhaps even embraced this meeting format! Thank you!

In the future we hope to see one another in person again. If things go as predicted, the 2022 meeting will be in Burlington, VT (the original venue of the missed 2020 meeting). A brief overview of the meeting will be given during today's business meeting (a short one--I promise!).

In the mean-time some general points about this year's meeting. Please read the code of conduct on page 2. We assume that by participating in this meeting you agree with these policies. Also on page 2 is a (surely incomplete) list of people we wish to thank. Then, there is a quick guide to the schedule and links on pages 3-4. Subsequent pages show more details about the schedule. The morning will be devoted to oral student presentations, and there will be two poster sessions in the afternoon. Don't miss the special topics sessions that will allow for more interaction. Lastly, we will have a quick business meeting followed by the social event. Highlights will certainly be the announcement of student awards, the virtual auction, and getting to see you all!

Warm regards,

Louise Lewis and Peter Siver (co-organizers)

Check out our and other fantastic auction items!



Meeting Code of Conduct

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

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

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

Thank You

A heart-felt *thank you* to all who provided assistance for this meeting! First, the NEAS executive committee who generously offered their feedback, often on short notice. Sarah Whorley and Karolina Fučíková always jumped in with ideas. Chris Neefus, our webmaster, builder of the registration / submission portals, and fielder of many questions. Treasurer Lindsay Green-Gavrielidis seems unflappable! Dale Holen and Hilary McManus provided great feedback on the scientific program. Brian Wysor, is our most excellent membership director! We also thank those who eagerly stepped up to lead the exciting special topics sessions (Karolina Fucikova, Hilary McManus, Amanda Savoie, Jessica Muhlin). We recognize and thank those who volunteered as session moderators (Morgan Vis, Patricia Thibodeau, Karolina Fučíková, Hilary McManus, Amanda Savoie, Susan Brawley), and the large number of judges who stepped up. You are much appreciated especially as the format for posters and talks were so different this time. We thank Craig Schneider for again leading the auction so skillfully, and for those who were generous with items for the auction. Craig and the rest of the development committee ensure that NEAS can continue to provide resources to students. So, support the auction! We highlight the kind donation of Ron Hoham, who also supports student awards. Lastly, we thank you for your energy and participation!

NEAS 2021 Schedule and Links

Mon April 5 – Fri April 9, 2021

Pre-recorded videos and files are available by going to this link

(<https://drive.google.com/drive/folders/1BqNgkTj4HRFF-tfeQ-Cj5AHSRvk6LnVz?usp=sharing>).

Saved files are located in the following folders, organized by session.

- Oral Session 1 – President's Award (undergrad) and Wilce Award (graduate)
- Oral Session 2 – Wilce Award (graduate)
- Oral Session 3 – Wilce Award (graduate)
- Poster Session 1 – Trainor Award (graduate)
- Poster Session 2 – President's Award (undergraduate) + Professionals
- Auction items (place your bid during the evening social event on April 10)

Sat April 10, 2021

All sessions use this link unless indicated:

<https://us02web.zoom.us/j/81610756104?pwd=WS9zODBMUDgvdGNNam1laTdHM1ZvUT09>

Meeting ID: 816 1075 6104

Passcode: 6pzAxE

8-9 AM Breakfast (optional) - BYO NEAS mug!

9-9:10 AM Opening Remarks, Louise Lewis and Peter Siver

9:15-9:57 AM Session 1, Moderators: Morgan Vis, Patricia Thibodeau

Presenters, please be in attendance. Moderator shows recorded videos during the session, followed by Q&A for each talk.

10:00-10:15 AM BREAK

10:15-10:57 AM Session 2, Moderators: Karolina Fučíková, Hilary McManus

Presenters, please be in attendance. Moderator shows recorded videos during the session, followed by Q&A for each talk.

11:00-11:15 AM BREAK

11:15-11:56 AM Session 3, Moderators: Amanda Savoie, Susan Brawley

Presenters, please be in attendance. Moderator shows recorded videos during the session, followed by Q&A for each talk.

12-1 PM LUNCH (on your own)

1:00-2:00 PM POSTER SESSION 1: use main meeting zoom link

(4 breakout rooms, 2 presenters each)

Presenters: enter your assigned room and be sure to have your presentation open and ready to share.

2:00-2:15 PM BREAK

2:15-3:15 PM POSTER SESSION 2: use main meeting zoom link

(3 breakout rooms, 2-3 presenters each)

Presenters: enter your assigned room and be sure to have your presentation open and ready to share.

3:15-3:30 PM BREAK

3:30-4:15 PM AFTERNOON DISCUSSIONS

(a) Translating teaching innovations developed during COVID to non-COVID times

Moderator: Karolina Fučíková and Hilary McManus

<https://assumption.zoom.us/j/93020244846?pwd=SHdPQ282NURqZStuWStjeHZBeEp1Zz09>

Password: 101315

(b) Blood, sweat, and (maybe) some tears: sharing no secrets for success but definitely some steps to avoid a research quagmire [note: for students]

Moderators: Amanda Savoie and Jessica Muhlin

<https://mainemaritime.zoom.us/j/92114751873?pwd=VUNNaFRSWFA2QitSVXNHVIVqM1lydz09>

Meeting ID: 921 1475 1873

Passcode: 021378

(c) Open session. Enter using main meeting zoom link.

4:30-4:55 PM Business meeting - use main meeting zoom link

Brief remarks.

NEAS 2022 (Vermont: Sarah and Karolina)

NEAS 2023 (Likely CT: Louise and Peter)

NEAS 2024 (We welcome ideas!)

Opportunities to get involved.

5:00-6:30 PM Awards, Social and Auction - use main meeting zoom link

Student Awards: judging teams present awards.

Auction (Craig Schneider): Preview items ahead of time using link provided for stored presentations; auction will happen via the zoom chat.

Socialize, network and relax!

Oral Session 1 - President/Wilce Award Candidates: Marine/ Macro
9:15-9:57 AM

Presenter	Title	Award Category	Abstract #
Gabriella Pantoni	Assessing changes in kelp and rockweed in Narragansett Bay	President	1
Margaret Cassidy	Molecular-Assisted Alpha Taxonomy of the Genus <i>Dasya</i> (Delesseriaceae, Rhodophyta) from the Euphotic and Mesophotic Zones off Bermuda	President	2
Evan Dunn	An Overview of the Algal Collections in the University of Maine Herbarium (MAINE)	President	3
Justine Rivera	Presence of <i>Labyrinthula</i> sp., the causative agent of seagrass wasting disease, on San Salvador Island, the Bahamas	President	4
Winter Shymko	Antibiotic Properties of Invasive Algae in Long Island Sound, CT.	President	5
Marie Dankworth	Update on Seaweed diversity in the Lower Bay of Fundy, New Brunswick, Canada	Wilce	6
Megan Fass	<i>Fucus serratus</i> (Fucaceae) in Nova Scotia forms a new pattern of intertidal zonation in the Western Atlantic	Wilce	7

Oral Session 2 - Wilce Award Candidates: Microalgae

10:15-10:57 AM

Presenter	Title	Award Category	Abstract #
Molly Erickson	Seasonal Variability of Phytoplankton Population Dynamics in Coastal New Hampshire	Wilce	8
Erin Borbee	Abiotic drivers of protist community structure in coastal marine ecosystems across Indonesia	Wilce	9
Michael Kausch	Influence of Nitrogen on Cyanobacteria Bloom Species Composition and Nutrient Stoichiometry in Mesotrophic Lake Mesocosms	Wilce	10
Rachel Cray	Effects of Oxidative Stress on the Astaxanthin Biosynthesis Pathway of <i>Haematococcus pluvialis</i>	Wilce	11
Imran Ahmad	Versatility of Extremophilic microalgae: A study based on <i>Galdieria sulphuraria</i>	Wilce	12
Kristina Terpis	A Phylogenomic investigation into Photosynthetic stramenopile evolution	Wilce	13
Kira Turnham	Species-specific toxicity in symbiotic and non-symbiotic dinoflagellates	Wilce	14

Oral Session 3 - Wilce Award Candidates: Chlorophyceae & Cyanobacteria

11:15-11:56 AM

Presenter	Title	Award Category	Abstract #
Emily Neuman	Using a random forest algorithm to predict suitable habitat for starry stonewort (<i>Nitellopsis obtusa</i>)	Wilce	15
Amanda Szinte	Morphological and Molecular Characterization of Cyanobacteria Present in the Gypsum Soils of White Sands National Park, New Mexico	Wilce	16
Mildred Akagha	Novel freshwater and subaerial cyanobacteria from tropical sites in Lagos, Nigeria	Wilce	17
Chelsea Villanueva	Elucidating the genomic compliment of rRNA operons inherent to a genus, for taxonomic application	Wilce	18
Ryan Owens	Physiological response to environmental stressors in <i>Ulva compressa</i>	Wilce	19
Ryan Assini	Genetic diversity of <i>Ulva</i> species on and around Long Island	Wilce	20
Alex Goodridge	Dynamics of Chaperone Expression in Green Seaweed under various combinations of intertidal stress	Wilce	21

Poster Session 1 – Trainor Award Candidates

1-2 PM

Breakout room	Presenter	Title	Award Category	Abstract #
1	Sarah Shinker	Freshwater red algae as eco-evolutionary models	Trainor	22
1	Zachary Muscavitch	Patterns in the diversity and specificity of <i>Trebouxia</i> and the lichenized fungus <i>Niebla</i>	Trainor	23
2	Josephine Crichton	An Analysis of DNA Metabarcoding Techniques on Rhodophyta (Red Algae) Biodiversity and Phenology in the Bay of Fundy	Trainor	24
2	Brandon O'Brien	Seasonal Recruitment Patterns of <i>Dasysiphonia japonica</i>	Trainor	25
3	Mikaela Hoellrich	Biocrust community composition and implications for carbon flux under timed light incubation	Trainor	26
3	Elizaveta Terlova	Two desert species of <i>Tetrademus</i> (Sphaeropleales, Chlorophyceae) demonstrate distinct metabolomes during a desiccation-rehydration cycle	Trainor	27
4	Joshua Evans	Genetic signatures from glass houses deposited millennia ago: metabarcoding of sedimentary ancient DNA (<i>seadDNA</i>) to reconstruct diatom diversity in the North Water polynya (Pikialasorsuaq) during the last c. 3800 years	Trainor	28
4	Caleb Butler	The recognition of host-generalist and host-specialist species of 'zooxanthellae' and their relative prevalence in reef coral communities of the Pacific	Trainor	29

Poster Session 2 – President’s Award Candidates and Professionals
2:15-3:15 PM

Breakout room	Presenter	Title	Award Category	Abstract #
1	Hannah Parson	Examination of the 23S rRNA gene in cyanobacteria: variation in secondary structure of the 23S rRNA molecule and its impact on sequence alignment	President’s	30
1	Emily Palmer	Novel cyanobacteria from biological soil crusts In Canyonlands National Park, Utah	President’s	31
1	Alexander Geragotelis	A comparison of desmid communities in two New Hampshire wetlands	President’s	32
2	Katherine Doiron, Allen Lyon	Paleolimnology to understand blooms of <i>Didymosphenia hullii</i> , <i>Didymosphenia geminata</i> , and <i>Cymbella janischii</i> : nuisance stalk-forming diatoms in the West Branch of the Farmington River, Connecticut, USA.	President’s	33
2	Sophia Wells	Novel cyanobacterial genera from Martinique	President’s	34
3	Toko Mori	15,000-year-old Charophyte Oospores in New Jersey Sediment	N/A	35
3	Patricia Thibodeau	Elucidating long-term trends from a 60-year time series in Narragansett Bay: implications for plankton dynamics and nutrient cycling	N/A	36

ABSTRACTS

Session #1

Presenters: Pantoni, Cassidy, Dunn, Rivera, Shymko, Dankworth and Fass

1) Assessing changes in kelp and rockweed in Narragansett Bay.

Gabrielle Pantoni¹, Lindsay Green-Gavrielidis², Niels-Viggo Hobbs¹, David Taylor³, Giancarlo Cicchetti⁴ & Carol Thornber²

¹Biological Sciences, University of Rhode Island, Kingston, RI; ²Natural Resources Science, University of Rhode Island, Kingston, RI; ³Marine and Natural Sciences, Roger Williams University, RI; ⁴Atlantic Ecology Division, Environmental Protection Agency, Narragansett, RI

Narragansett Bay contains a variety of important seaweed ecosystems that are home to diverse fish and invertebrate communities. Rockweed, *Fucus* spp., in the intertidal, and kelp, *Saccharina latissima* and *Laminaria digitata*, in the subtidal have historically been prevalent in the bay. Surveys conducted in the 1970s and 1980s have provided historical data on the location and abundance of rockweed and kelp habitats. In order to monitor changes in these habitats, video surveys on SCUBA were conducted at 24 sites chosen for their previous abundance of rockweed or kelp from historical studies in Narragansett Bay. Video surveys were conducted in both the fall and summer using a metal ski mounted with GoPro cameras, underwater lasers, and lights along a 30m transect in order to document seaweeds, invertebrates, and fishes at all sites. Current percent cover of rockweed and kelp at all 24 sites was determined by analysis of the seaweed videos based on the total time that rockweed or kelp was seen along the transect. Additionally, subsamples were collected during surveys to determine rockweed and kelp density and biomass at each site. The results from these surveys will highlight the current abundance of kelp and rockweed habitats in the bay, as compared to the historical record, and determine which invertebrates and fishes are associated with these habitats. As the ocean climate continues to change, these seaweed habitats will also be subject to change, and subsequently their associated invertebrate and fish communities. Continuing to survey these vital habitats in the future will create a better understanding of the importance and abundance of diverse seaweed habitats in Narragansett Bay.

2) Molecular-Assisted Alpha Taxonomy of the Genus *Dasya* (Delesseriaceae, Rhodophyta) from the Euphotic and Mesophotic Zones off Bermuda.

Margaret M. Cassidy¹, Craig W. Schneider¹ & Gary W. Saunders²

¹Department of Biology, Trinity College, Hartford, CT 06106, U.S.A.; ²Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, New Brunswick E3B 5A3, Canada.

Examination of the genus *Dasya* in Bermuda reveals at least two new species. Deep water collections from 60–90 meters by technical divers and submersibles resulted in the identification of two new species unique to these waters. Genetic sequences (COI-5P, *rbcL*) and morphological characteristics show that *D. sylviae* sp. nov. is distinct from other known pseudodichotomous *Dasya* spp. worldwide. The mesophotic offshore collections also allowed us to take a closer look at the *D. 'baillouviana-pedicellata'* complex in the western Atlantic by comparing inshore specimens from Bermuda presently known as *D. baillouviana*. Molecular sequencing and morphological comparisons demonstrated that the mesophotic collections, despite their similarities to *D. baillouviana*, represent a new species, *D. bathypelagica* sp. nov. Inshore collections presently known as *D. baillouviana* (type locality, Mediterranean Sea) are compared with the generitype, *D. pedicellata* (type loc., New York). Our genetic results uncover a complex of species residing under these two names that calls for clarification.

3) An Overview of the Algal Collections in the University of Maine Herbarium (MAINE).

Evan S. Dunn¹, Kyle Capistrant-Fossa¹, Anne C. B. Davison¹ & Susan H. Brawley¹

¹School of Marine Sciences, Orono, ME, 04469, USA

Algae held by the University of Maine Herbarium include collections of historical importance (Algae Boreali-Americanæ, Flora Universalis) and multiple specimens dating back to the mid-1800s. The oldest specimen was collected in 1864, and the median age of herbarium specimens is 1977 (1864-2020; > 8000 specimens). Phycological holdings expanded rapidly in the 1960s after Professor Emeritus Robert S. Vadas joined the faculty. Collections are from many continents including Asia (China, Japan, Jordan, Lebanon), Australia, Europe (Denmark, Germany, Ireland, Italy, Isle of Man, Norway, Russia, Spain, Sweden, the UK), and North America (the Bahamas, Bermuda, Canada, Greenland, Jamaica, Nicaragua, the USA). MAINE collections document the origin and spread of non-indigenous species and have been used by companies interested in historical levels of trace elements in aquaculture species. Laminariales, Fucales, and Bangiales are especially prominent in MAINE. Some collections (*Fucus* spp., *Porphyra* spp.) are curated to permit future studies on how long the natural microbiome persists on herbarium specimens. Replicated collections of several *Fucus* spp. and *Porphyra* spp. from locations across the North Atlantic have potential to advance studies on the effects of climate change on genetic diversity. Our recent focus is to finish identification, repair, and labeling of specimens, their accession and databasing, and the curation of companion digital photographs. The digital database and photographs will be submitted to public archives later this year.

4) Presence of *Labyrinthula* sp., the causative agent of seagrass wasting disease, on San Salvador Island, the Bahamas.

Justine Rivera¹, Jonathan Gilbert^{1,2}, & Amy Carlile¹

¹Biology and Environmental Science, University of New Haven, West Haven, CT, 06516, U.S.A.

²Molecular and Cellular Biology, University of Connecticut, Stamford, CT, 06901, U.S.A.

Seagrass beds are critical habitats for a variety of fauna and serve important ecological functions. As such, identifying threats and concentrating conservation efforts for these habitats is of significant importance. The species *Labyrinthula zosterae* has been linked to significant occurrences of seagrass wasting disease, and has caused the greatest loss of seagrass habitats recorded to date on the Northwest coast of the Atlantic Ocean. *L. zosterae* has been documented extensively in both the northern and southern hemispheres; however, metabarcode data from recent samples collected from algal turf communities on San Salvador Island, the Bahamas has provided the first evidence of *Labyrinthula* sp. present in the Caribbean. Amplification of 18S rRNA sequences using taxon specific primers will confirm and identify the species of *Labyrinthula* present in the algal turf samples. The occurrence of *Labyrinthula* sp. in environmental samples will provide information regarding its spatial distribution throughout the island and confirm the first record of this taxon in the Bahamas. Results of this study will assist in the development of future studies aimed at identifying *Labyrinthula* in seagrass beds and potential source populations in surrounding communities on San Salvador Island. This study will also provide data that may be used to predict potential areas susceptible to seagrass wasting events and require future monitoring.

5) Antibiotic Properties of Invasive Algae in Long Island Sound, CT.

Winter Shymko & Amy Carlile

Department of Biology and Environmental Science, University of New Haven, CT, 06516, U.S.A.

The improper and repeated usage of antibiotics has decreased their efficiency, making them less reliable. A critical component of antibiotic synthesis is having the resources to create them in abundance, quality, and efficiency. Therefore, new unconventional sources are being used to replace them, including algal species. Previous studies on *Ulva lactuca* showed antibiotic activity against several bacterial species, including *Escherichia coli*. Other studies focused on the utilization of invasive *Caulerpa* sp. as an antibiotic. Although studies on the antibiotic properties of invasive algae are limited, more research will aid in the identification of these properties. This will in turn contribute to the removal of excess biomass for medical purposes and limit the impact of the invasive species on the environment. *Codium fragile*, *Dasysiphonia japonica*, *Agarophyton vermiculophylla*, and *Grateloupia turuturu* are invasive algal species found in abundance along the coastline and rocky intertidal of Long Island Sound. This study aims to assess the antibiotic activity of these species by using the extraction solvents methanol, ethanol, acetone, and water to isolate antibiotic compounds of each species against *E.coli*. *E.coli* is a commonly used bacterium in antibiotic studies due to its prolific growth and prevalence in human diseases. Results of this study will identify which invasive algal species in Long Island Sound show antibiotic activity against *E. coli*. Preliminary data show some inhibition of *E. coli* in methanol extractions of *Codium fragile* and ethanol extractions of *Grateloupia turuturu*.

6) Update on seaweed diversity in the lower Bay of Fundy, New Brunswick, Canada.

Marie Dankworth & Gary W. Saunders

Centre For Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

Changes in seaweed biodiversity in the Bay of Fundy have been recorded in detail and have been associated with changes in sea surface temperature, irradiance, sedimentation, seawater quality, and the arrival of introduced species. These abiotic and biotic factors are acting in complex systems, which make it difficult to correlate changes to a specific stressor. Specific to the lower Bay of Fundy, there have been published accounts suggesting that increased aquaculture production, through eutrophication and oxygen depletion, was likely influencing water quality and consequently marine benthic vegetation. The surveys on which those assertions were based ended in 2006 with some changes in aquaculture practices having occurred in the intervening ~15 years. Therefore, we have completed the same surveys at two keys sites from those earlier studies, Letete and Lepreau, in 2020 to provide an update on seaweed richness and composition. Previous data from 2000-2006 merged with present data from 2020 revealed no overall changes in the species richness in the lower Bay of Fundy, but a significant increase in richness at the Letete site were uncovered. As well, significant changes in species composition occurred in the lower Bay between 2000 and 2020 (e.g in 2000 there was a higher percent coverage of *Fucus*, *Chondrus*, *Ulva* and *Palmaria* and a lower percent coverage of rock and coralline crust compared with 2020) which could be caused by natural variation and or be associated with other abiotic stressors e.g., aquaculture.

7) *Fucus serratus* (Fucaceae) in Nova Scotia forms a new pattern of intertidal zonation in the Western Atlantic.

Megan P. Fass¹, David J. Garbary¹, Herb Vandermeulen¹ & Carolyn Bird²

¹*Jack McLachlan Laboratory of Aquatic Plant Resources, Department of Biology, St. Francis Xavier University, Antigonish, Nova Scotia, B2G 2W5, Canada*

²*P.O. Box 9, Chester Basin, Nova Scotia, B0J 1K0, Canada*

Fucus serratus is a non-native species in Nova Scotia that, since its introduction in the 19th century, has become widely distributed, and is known primarily as a subtidal species. New observations starting in August 2020 showed a pattern of *F. serratus* in which the species had become a dominant canopy-forming species in the low intertidal zone. Here it was replacing the previously characterised zone-forming species, *Chondrus crispus*, and was becoming a dominant in parts of the lower shore that would have been occupied by *Ascophyllum nodosum*. Qualitative evidence in the form of photographs and the occurrence of *F. serratus* in wrack demonstrated abundant populations along sites examined over 30 km and 40 km stretches of outer coast in Yarmouth and Lunenburg Counties, respectively. Quantitative estimates of cover based on transects at Chebogue Point and Kingsburg indicate dramatic changes in intertidal zonation along the Atlantic coast of Nova Scotia in which 10–15 m of intertidal zone comprising 15% to 40% of the horizontal extent of the shore had 75% to 100% cover of *F. serratus*. Further surveys are needed to confirm the overall distribution and impact of this invasive fucoid on intertidal communities.

Session #2

Presenters: Erickson, Borbee, Kausch, Cray, Ahmad, Terpis, Turnham

8) Seasonal Variability of Phytoplankton Population Dynamics in Coastal New Hampshire.

Molly Erickson & Elizabeth Harvey

Department of Biological Sciences. University of New Hampshire, Durham, NH.

Phytoplankton population dynamics are significant indicators of ecosystem health and marine food web structure. Given the stochastic nature of marine ecosystems, particularly coastal systems, predicting alterations in primary productivity and phytoplankton populations remains complex. Phytoplankton population dynamics are impacted by a variety of biotic and abiotic factors such as temperature, salinity, biogeochemical nutrient cycling, and predator-prey interactions. Additionally, these factors vary spatially and temporally, making it challenging to correlate one particular factor with driving phytoplankton population dynamics using observations from a single point in space and time. In order to better understand the factors that drive phytoplankton variability in marine ecosystems, especially in coastal ecosystems, time series have proved to be invaluable. Here, we present data from an on-going time series initiated in October 2020 from two locations in coastal NH, located centrally in the Gulf of Maine. An initial look at the data reveals significant differences in abundance and community composition between the sampling station in Great Bay, NH and the sampling station along the outer coast. Additionally, our data captures episodic bloom events of non-harmful phytoplankton species, and the wintertime community of phytoplankton in this region. Future work will compare the observed phytoplankton biodiversity and community structure to the characteristics of these coastal ecosystems. By understanding phytoplankton population dynamics, particularly how they change over time, the development of marine ecosystem models can be improved, especially in the face of climate change.

9) Abiotic drivers of protist community structure in coastal marine ecosystems across Indonesia.

Erin Borbee¹, Austin Humphries², Hawis Madduppa³ & Christopher Lane¹

¹Department of Biological Sciences, The University of Rhode Island, Kingston, RI, 02881, U.S.A.;²Department of Fisheries, Animal, & Veterinary Sciences, The University of Rhode Island, Kingston, RI, 02881, U.S.A.;³Department of Marine Science and Technology, Institut Pertanian Bogor (IPB), Bogor, Indonesia 16680.

Protists exhibit immense morphological and ecological diversity while facilitating ocean processes such as primary production and biogeochemical cycling. Despite the increased use of high throughput sequencing in sampling efforts across the globe, our knowledge of protist communities in the Indo-Pacific is largely limited to visual surveys, which have shown to vastly underestimate diversity in these groups. The Indo-Pacific poses an interesting setting for studying protist communities, because it is both home to some of the most biodiverse ecosystems in the world and is a region where two oceans converge through associated currents. These features allow us to characterize various biotic and abiotic drivers of protist community structure in regions across Indonesia spanning from the Pacific to Indian Oceans. A major finding from our data shows an increase in diatom diversity in the easternmost sampling region, while overall protist diversity and diversity other abundant groups like dinoflagellates drop in that region. This shift in diversity is potentially being driven by surface current patterns across this region creating either: (1) a chokepoint in circulation at the Indonesian Throughflow resulting in lower diatom diversity in the westernmost regions; (2) increase in nutrient availability at the edge of the Halmahera Eddy in the easternmost region leading to increased diatom diversity; or (3) seasonal variations in these communities potentially in line with seasonal variations in the velocity of the Indonesian Throughflow. These results demonstrate the importance of dispersal limitation in shaping protist community structure across the Indo-Pacific and enable future research into identifying the specific mechanisms driving these shifts in diversity across major protist groups.

10) Influence of Nitrogen on Cyanobacteria Bloom Species Composition and Nutrient Stoichiometry in Mesotrophic Lake Mesocosms.

Michael E. Kausch & John D. Wehr

Louis Calder Center - Biological Station and Department of Biological Sciences, Fordham University, Armonk, NY, USA.

Harmful algal blooms (HABs) are a global water quality concern in freshwater lakes that degrade ecosystems, impair drinking water supplies, and impact economies. Recent water quality monitoring of lakes in the New York metropolitan area suggests that nitrogen supply may have a critical role in cyanobacteria bloom development and species composition. We tested the influence of forms and concentrations of nitrogen in 24 large-scale (5400 L) outdoor mesocosms containing mesotrophic lake water at Fordham University - Louis Calder Center's Experimental Lake Facility. Replicated mesocosms were supplied with surplus phosphorus and amended with different forms (nitrate, ammonium nitrate, urea) and concentrations (+15 μM , +50 μM N) of nitrogen in a factorial design. Experiments were run for 27 days with a second nutrient pulse mid-experiment. We collected samples weekly for dissolved nutrients, particulate C:N:P, pigments (chl-a, phycocyanin), and phytoplankton taxonomic diversity. Cyanobacteria blooms dominated by *Aphanizomenon flos-aquae* were observed in all +N treatments. While *A. flos-aquae* was the dominant species of cyanobacteria at the start of the experiment, other bloom-forming taxa (*Microcystis*, *Woronichinia*, *Dolichospermum*) were present, suggesting that *A. flos-aquae* was a stronger competitor for nitrogen. Chl-a concentrations in +P-only treatments did not differ significantly from controls, suggesting that, at least at the time of our experiment, productivity was not limited by P alone. Particulate N:P ratios in +urea and +NH₄NO₃ treatments increased significantly, but decreased in the nitrate-treatments, suggesting a strong preference for incorporation of urea and ammonium. Nitrate uptake was significantly reduced in experiments replete with ammonium. Our results highlight the importance of N in the development of cyanobacteria blooms, and that management strategies to combat HABs should include efforts to reduce N loading concurrently with the reduction of P loads.

11) Effects of Oxidative Stress on the Astaxanthin Biosynthesis Pathway of *Haematococcus pluvialis*.

Rachel Cray

Biology, University of Southern Maine, Portland, ME, 04101, U.S.A.

Astaxanthin is a key carotenoid pigment produced primarily in nature and industrially by the unicellular microalga *Haematococcus pluvialis*. This potent antioxidant is produced in response to environmental stressors, such as high light, upon which reactive oxygen species (ROS) are produced. While the presence of ROS has been established in this cascade via carotenogenic genes, its effect has not been clearly defined. The overall goal of this study was to quantify the effect of ROS on the astaxanthin biosynthesis pathway within *H. pluvialis*. Cellular ROS concentrations and astaxanthin output were quantified in response to environmental variables, redox-sensitive compounds, and ROS-scavengers. All environmental and redox-sensitive conditions led to encystment and an increase in astaxanthin output. Initial astaxanthin production rates over days 0-5 were highest in the redox-sensitive variable group, with a later rate peak at days 5-10 for environmental test groups. Cellular ROS concentrations similarly peaked over days 0-5 and 5-10 for redox-sensitive and environmental test groups respectively, however showed significant decreases in concentration by days 10-15 for all groups. Furthermore, application of an ROS-scavenger decreased cellular ROS concentrations and induced germination. By determining and quantifying a relationship between cellular ROS concentration and *H. pluvialis* astaxanthin production and germination behavior, this work aims to highlight the important role of ROS in the astaxanthin biosynthesis pathway. Further application of this knowledge could be used to design a cost and resource efficient method of natural astaxanthin production in industrial settings.

12) Versatility of Extremophilic microalgae: A study based on *Galdieria sulphuraria*.

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Microalgae are often used in bioremediation. One of the categories of microalgae based on their growing conditions is extremophilic microalgae. Extremophilic microalgae are then classified based on the parameters that exert extreme but necessary growing conditions to the microalgae. The parameters include temperature, pH, salinity, and pressure. Microalgae are evolved to adapt and survive under extreme conditions. Applications of extremophilic microalgae have made positive impacts to the world of biotechnology and environmental studies. Since, the characteristics of wastewater is varying in terms of pH (2.0-8.0), temperature (>40°C) and organic load (>100 g/l). Therefore, its composition, acidic and thermophilic nature, and its metabolism make it a potential microalga in treating wastewater having high temperature, COD, and low pH. *Galdieria sulphuraria* is an extremophilic species of red algae that survives in acidophilic and thermophilic conditions. It is found in acidic hot springs and polluted environment with pH ranged 0-4 and temperature up to 56 °C. Cell wall of *Galdieria sulphuraria* is rigid and made up of protein. It is metabolically flexible as it can be grown photo-autotrophically, heterotrophically or mixotrophically on more than 50 carbon sources. Its extremophilic properties minimize the contamination and invasion by common parasites. Its wide range of environmental habitat has made it possess novel characteristics that interest researchers on discovering its unique capabilities in application of biotechnology. Novel applications of *Galdieria sulphuraria* in recovering rare earth metals and detoxification of heavy metal make it to have the potential to be the microalgae strain used for bioremediation. Furthermore, it is effective in removing phosphorus, nitrogen, and carbon from wastewaters. This study will provide an insight about the growth and potential of *Galdieria sulphuraria* under adverse environment.

13) A Phylogenomic investigation into Photosynthetic stramenopile evolution.

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The photosynthetic stramenopiles (Ochrophyta) are an incredibly diverse clade including members ranging in complexity from 30m, multicellular kelp, to unicellular protists, <20 µm in size. They are found in marine, freshwater, and terrestrial habitats and the range of morphology, life history, ecology, and diversity, provides an ideal framework for exploring the evolution of traits. However, the lack of a resolved phylogeny representing the diversity of the group significantly hinders the ability to make meaningful inferences about ochrophyte evolution. Here we expand the taxonomic sampling for ochrophytes by generating 22 novel transcriptomes, focusing on classes lacking genome-scale data and species of uncertain taxonomic affiliation. By combing these data with other publicly available data, we constructed the most taxonomically comprehensive ochrophyte phylogeny comprised of 17 previously described classes. Within this robustly resolved evolutionary framework, we place historically difficult to resolve taxa and have improved phylogenetic resolution among ochrophyte lineages. An apparent rapid radiation early in the evolutionary history of ochrophytes remains problematic for resolving deep branches within the clade, and will likely require additional taxa and methodological advances to extract a reliable phylogenetic signal from these ancient events.

14) Species-specific toxicity in symbiotic and non-symbiotic dinoflagellates.

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Rapid ocean warming is causing the demise of coral reef ecosystems by disrupting the mutualism between corals and endosymbionts in the family Symbiodiniaceae. Host-symbiont signaling via exchange of secondary metabolites may be an important component in dysbiosis, but is largely unexplored. Some free-living symbiodiniacean species produce secondary metabolites that appear to be toxic, however, no species capable of forming symbioses with animal hosts have been examined. Dinoflagellate toxin production typically varies with nutrient availability, temperature, and light; parameters that also influence maintenance of functioning symbioses. We sought to test whether five symbiotic and two non-symbiotic species from four genera of cultured Symbiodiniaceae exhibited toxicity under nutrient replete conditions, and whether production changed with nutrient availability, thermal stress, and light stress. We use hemolysis as a proxy for toxicity, and describe the functional activity and efficiency of photosystem II throughout each experiment. Both non-symbiotic species showed toxicity in each treatment, while species-specific responses were observed for those which are symbiotic. Our results showcase the diversity in response to stress of species within the Symbiodiniacean family, and make the case for future study in the function of these compounds as they pertain to cell survival and proliferation (i.e. allelopathy, defense, signaling or heterotrophy) outside of or within a host.

Session #3

Presenters: Neuman, Szinte, Akagha, Villanueva, Owens, Assini, Goodridge

15) Using a random forest algorithm to predict suitable habitat for starry stonewort (*Nitellopsis obtusa*).

Emily Neuman¹, Sean Woznicki¹, Kenneth G. Karol², James N. McNair¹ & Sarah E. Hamsher^{1,3}

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Since 1974 when *Nitellopsis obtusa* was first reported in the St. Lawrence River, rapid population expansion in Michigan and seven other U.S. states has been recorded. This invasive macroalga has become a nuisance for native plants, animals, and recreational activities. Because eradication of invasive species is more difficult after establishment, early detection plans are an important tool in preventing and slowing the spread of invasive species. Macroscale data analyses have improved our ability to predict changes in freshwater ecosystems, and these types of data analyses are therefore becoming increasingly important in efforts to assess and control the rapid expansion of invasive species. The random forest algorithm was used to analyze occurrence records of *N. obtusa* from the New York Botanical Garden C. V. Starr Virtual Herbarium (NY) and the Global Biodiversity Information Facility coupled with landscape and water quality variables from the Lake multi-scaled GeOSpatial and temporal (LAGOS) database, the U.S. Water Quality Portal, and a global dataset of bicarbonate concentrations in lakes and streams. From the variables tested, bicarbonate concentration and road density around lakes served as the most important predictor variables for *N. obtusa* occurrence. The results from the model indicated further spread of *N. obtusa* in Michigan, Minnesota and Wisconsin. Additional preliminary results will be discussed.

16) Morphological and Molecular Characterization of Cyanobacteria Present in the Gypsum Soils of White Sands National Park, New Mexico.

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Biological soil crusts are important components of desert ecosystems that contain a diverse array of taxa and provide ecosystem services such as nutrient cycling and soil stability. One crucial component of biological soil crusts is cyanobacteria, which can stabilize the soil, increase water retention, provide UV protection, and fix nitrogen. Research on cyanobacteria in biological soil crusts has become increasingly prevalent in arid to semi-arid biomes. In North American drylands, soil collections from the Great Basin, Colorado Plateau, Mojave Desert and Chihuahuan Desert have all had some cyanobacterial strains sequenced. There are still many sites that have been understudied, including the unique gypsum soils at White Sands National Park. Only a few morphological descriptions of cyanobacteria are currently presented in the literature for this location, but no designated study has been done in this area. Other research in North American deserts has shown the need for molecular research on soil cyanobacteria to identify true taxonomic relationships. Therefore, this study aims to characterize the diversity of cyanobacteria in biological soil crusts at White Sands morphologically and molecularly from 16S and 16S-23S ITS sequence data. Thus far, eight cyanobacterial strains have been sequenced belonging to three genera: *Trichocoleus* and *Leptolyngbya* in the Synechococcales and *Scytonema* in the Nostocales. Phylogenetic analyses indicate that we have multiple species of *Trichocoleus* and one new species of *Leptolyngbya*.

17) Novel freshwater and subaerial cyanobacteria from tropical sites in Lagos, Nigeria.

Mildred Akagha¹ and Jeffrey R. Johansen¹.

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Soils, tree bark, and rivers were sampled for cyanobacteria in Lagos and Imo, Nigeria. Samples were plated on enrichment agar and ~30 cyanobacterial strains were isolated from those plates into unialgal cultures. The algae were morphologically characterized in photomicroscopes with Nomarski DIC optics and then sequenced for the 16S rRNA gene and associated 16S-23S ITS region. Preliminary results from the largest group isolated, the Synechococcales revealed rich diversity and novel species. Two *Arthronema* (Leptolyngbyaceae) species were found, *A. africanum* and a new species of *Arthronema*. The reference strain of *A. africanum* is incompletely characterized, and we have plans to obtain the culture, conduct analyses, and then describe this new species which represents only the second time this genus has been isolated into culture. We also collected seven new species from the recently described genera *Albertania* (Oculatellaceae), *Tildeniella* (Oculatellaceae), and *Nodosilinea* (Prochlorotrichaceae). The most original and exciting find was a new genus and species with uncertain placement near the Prochlorotrichaceae and Synechococcaceae. This taxon resembles the loosely defined genus *Leptolyngbya*, and is therefore a cryptic genus quite distant from the Leptolyngbyaceae. These few samples illustrate the great diversity we can expect to find in tropical regions and in Africa, both of which are sparsely sampled at present. We will propose naming this interesting new genus *Imonema*.

18) Elucidating the genomic compliment of rRNA operons inherent to a genus, for taxonomic application.

Chelsea D. Villanueva¹, Markéta Krautová² and Jeffrey R. Johansen³

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Many genera of cyanobacteria are paraphyletic or polyphyletic. There is also clear evidence that 16S rRNA gene sequence data, used to designate novel prokaryotic species, lacks resolution at the species level. Establishing innovative methods to accurately identify cyanobacterial genera and species is vital. Analysis of the noncoding, intergenic, and potentially regulatory sequence, the 16S-23S ITS region, could provide species-level phylogenetic resolution. The ITS regions in thirty-two putative species within *Brasilonema*, were analyzed. *Brasilonema*, a tropical, heterocytous genus in the Scytonemataceae (Nostocales), varies on average less than 2% in 16S rRNA coding genes. Through intensive cloning and sequencing, we attempted to establish how many different rRNA operons are present in each putative species and the genus as a whole. For each putative species, 16S rRNA genes and associated 16S-23S ITS regions were amplified via PCR. Amplicons were subsequently cloned, and 12 clonal replicates were sequenced. Consensus sequences, from multiple clonal replicates, were determined for each operon copy, from all strains. Operon types were designated as having either 2 tRNAs present or none. Both sequence alignment and folded structures were analyzed to further classify variable operons within each category. Three distinct operons were found to be inherent to *Brasilonema*. Only one operon with no tRNAs was recovered from sequenced genomes. However, two different operons containing two tRNA genes were found to be distributed amongst several putative species. Establishing the genomic compliment of rRNA operon types is crucial to developing this tool for use in taxonomy, because paralogous operons have separate evolutionary histories, and therefore should not be compared.

19) Physiological response to environmental stressors in *Ulva compressa*.

Ryan Owens & Amy Carlile.

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Ulva compressa is one of the green algal species common in Long Island Sound that can form nuisance blooms. These blooms form large mats across estuaries and coastal marine waters and can cause a dramatic shift in the ecosystem, altering food web dynamics, fishery resources and potentially impacting human health. In understanding what regulates the growth of blooms, we can better predict and mitigate these blooms' formation. Studies suggest that gene regulation could be responsible for the rapid growth and success of *Ulva* species. DNA methylation is commonly studied in determining gene expression and will be used in this study to test the hypothesis that there is an epigenetic response in *U. compressa* to environmental stressors. This research examines the physiological and molecular response of *U. compressa* to the environmental stressors temperature, salinity, and copper. Lab experiments were used to test a single stressor at a time for one - two week periods, with the physiological response measured using Pulse Amplitude Modulation fluorometry (PAM).). The molecular response will be determined using methylation sensitive amplification polymorphism (MSAP) protocol, a widely used method for DNA methylation due to its ability to provide genome-wide methylation without the need to know which genes are being targeted. Current data shows a broad physiological tolerance to both higher and lower ranges in temperature and salinity, while copper data shows tolerance in concentrations under 12ppm. *U. compressa* is broadly tolerant and we predict that methylation patterns will correspond to the rapid response to different temperatures and salinities.

20) Genetic diversity of *Ulva* species on and around Long Island.

Ryan Assini & Amy Carlile

Biology and Environmental Science, University of New Haven, West Haven, CT, 06516, USA.

Algae that belong to the species-rich genus *Ulva* are found globally. These species often have cryptic morphologies causing their species identification to be extremely difficult based on their morphology alone. Genetic sequencing is required to confirm species identity for this genus. Species distributions for this genus can be mapped in specific regions. Previous work in New Haven Harbor and Rhode Island has 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 the region of Long Island, and the coast of Long Island Sound, is not well classified. 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, 115 *Ulva* samples were collected in the region of interest. Following *rbcl* sequencing of these samples, it has been found that there are more species present in the region of interest than predicted, with eight species identified so far. Preliminary results have shown much lower incidence of *Ulva compressa* than anticipated and large numbers of *Ulva rigida* on the north shore of Long Island.

21) Dynamics of Chaperone Expression in Green Seaweed under various combinations of intertidal stress.

Alex Goodridge & Dr John Bothwell

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Chaperone proteins maintain protein homeostasis in cells under stress by monitoring, stabilising, and inducing refolding of denatured proteins. Chaperones are also involved in more specialised responses, for example, mitochondrial and endoplasmic reticulum (ER) unfolded protein responses and protection of the chloroplast photosynthetic machinery in algae and plants. However, compared to model land plants and microalgae, chaperone dynamics in intertidal macroalgae are poorly understood. Regulating chaperone activity is most likely crucial for the survival of intertidal seaweeds such as *Ulva mutabilis* (Chlorophyta), exposed to dynamic environmental conditions and high stress at low tide. To address this, we identified representatives of the heat shock protein (HSP) family of molecular chaperones within the *Ulva mutabilis* genome, including representatives from the well-characterised SHSP (small heat shock protein), HSP40 (DnaJ), HSP60, HSP70, HSP90, and HSP110 families. Using subcellular localisation prediction tools, we identified *U. mutabilis* HSPs localised to the cytosol, ER, mitochondria, and chloroplast. We confirmed an expansion in HSP families in *Ulva* through phylogenetic analysis compared to closely related freshwater and unicellular chlorophytes. To assess the role of the HSPs in the intertidal stress response, we exposed seaweed to various combinations of heat, light, and dehydration stress, and gene expression analysis was performed on genes of interest using quantitative PCR (qPCR). We observed a clear response to heat stress in cytosolic and ER-localised proteins, with additional dehydration or light stress having an additive effect on expression. No response to sole dehydration or light stress was observed. Chloroplast and mitochondrial HSPs exhibited a different expression profile, where significant upregulation in expression was only observed following combined heat and light stress. This work offers preliminary evidence indicating that the expansion and specialisation of *Ulva* HSPs may have facilitated adaptation to intertidal habitats.

Poster Session #1

breakout room 1: Shinker, Muscavitch

room 2: Crichton, O'Brien

room 3: Hoellrich, Terlova

room 4: Evans, Butler

22) Freshwater red algae as eco-evolutionary models.

Sarah J. Shinker¹, Roseanna M. Crowell², Morgan L. Vis² & Stacy A. Krueger-Hadfield¹.

¹University of Alabama at Birmingham, ²Ohio University.

The relative frequency of sexual versus asexual reproduction governs the distribution of genetic diversity within and among populations. As a consequence, the reproductive mode affects a population's ability to track environmental change through phenotypic evolution. Most studies of the consequences of reproductive variation focus on the mating systems (i.e., outcrossing to selfing) of diploid-dominant taxa (i.e., angiosperms). Outcrossing results in greater genetic diversity, while selfing results in lower genetic diversity. Asexual reproduction has similar evolutionary consequences as selfing. Many eukaryotes are partially clonal, undergoing both sexual and asexual reproduction, but we understand less about the consequences of partial clonality. Moreover, reproductive modes should also correlate with life cycle types. Outcrossing should be associated with diploidy, while selfing and clonality should correlate with a prolonged haploid stage as deleterious mutations are exposed to selection and can be directly purged. However, these correlations have not been systematically investigated because eukaryotic reproductive mode variation is poorly described. We advocate for filling these gaps through the simultaneous investigation of life cycle and reproductive mode evolution using freshwater red macroalgae. Selfing is possible in both monoicous (hermaphroditic) and dioicous taxa (separate sexes) and asexual reproduction may result in the temporary or permanent loss of a ploidy stage. These eco-evolutionary consequences are unique for organisms with haplodiplontic life cycles, such as many freshwater reds. Understanding the evolutionary consequences of selfing and asexual reproduction will aid in our understanding of eukaryotic evolution generally and of the evolutionary ecology of freshwater red algae specifically.

23) Patterns in the diversity and specificity of *Trebouxia* and the lichenized fungus *Niebla*.

Zachary M. Muscavitch, Louise A. Lewis & Bernard Goffinet

University of Connecticut, Storrs, CT, USA.

Lichens are a dominant terrestrial mutualism comprised of an alga or cyanobacterium (photobiont) and a fungus (mycobiont). We know a great deal about the evolution, distribution, and diversity of the mycobionts, but much less is known about the photobiont diversity, taxonomy, distribution, or specificity with which they interact with their better characterized mycobiont partner. Because of this uneven characterization and the non-monophyly of both symbionts, we know little about the evolution of symbiosis in lichens. Given this extreme phylogenetic range, multiple evolutionary origins and different mechanisms likely govern symbiont specificity. While lichens containing cyanobacterial photobionts display a range of specificity between their symbionts, 90% of lichens, those containing green algal photobionts, escape comparable academic scrutiny. The high dispersal potential of cryptogams inherently complicates their study, as taxonomic sampling for widespread genera is challenging and endemic lineages are rarely speciose. Our study profiles the diversity of *Trebouxia* species that associate with species of *Niebla*, endemic to the west coast of North America. While they all rely on coastal fog, the associations are distributed along broad climatic, and ecological gradients. We seek to delimit taxonomic diversity of algal and fungal symbionts, to develop the foundation for understanding the evolution of their mutual specificity. We have uncovered a diversity of *Trebouxia* lineages, including several putatively new taxa, within the larger so-called clade A. Overall, photobiont-mycobiont specificity is more labile between *Trebouxia* and *Niebla*, than the stronger specificity exhibited in some cyanolichen symbionts (e.g. *Peltigera* and *Nostoc*). In addition to phylogenetic specificity between *Trebouxia* and *Niebla*, the diversity of both symbionts seems strongly correlated to substrate (e.g. wood or rock). Existing analyses are based on limited select loci, but pending phylogenomic analyses will likely provide new and deeper insights into symbiont specificity between these charismatic organisms.

24) An Analysis of DNA Metabarcoding Techniques on Rhodophyta (Red Algae) Biodiversity and Phenology in the Bay of Fundy.

Josephine Crichton and Gary W. Saunders

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The Bay of Fundy remains a region of active focus among marine biologists owing to its diverse marine life and large tidal range. Seaweed phenology (periodicity of biological life cycles) and biodiversity are no exceptions and have been studied relatively extensively. Techniques employed in these studies, though useful, have been limited in sampling capacity, study length, invasiveness and cost due to their laborious nature. There is an additional barrier to our understanding of seaweed phenology and diversity in this flora, especially for the Rhodophyta. Reproductive features can be easily overlooked in the field due to their cryptic nature, notably the male and tetrasporangial structures. Further, biodiversity estimates for many species with heteromorphic alternations of generations are incomplete as they can be limited to the more identifiable stage. This project aims to fill these gaps by using metabarcoding methods (eDNA sampling) alongside traditional morphological survey techniques to detect red algae in all their life stages. To meet these aims, DNA will be acquired from intertidal scrapes and nearshore plankton tows and used for metabarcoding analyses. Traditional morphology-based surveys will also be completed for both phenological and diversity estimates. The efficacy of these two methods will be compared relative to one another. If metabarcoding proves as, or more effective than traditional methodologies, the use of this approach could improve the accuracy, efficiency and cost-effectiveness by which scientists and organizations (e.g. Fisheries and Oceans Canada) can obtain seaweed biodiversity data; it may also outperform traditional sampling techniques in terms of repeatability and standardization. The data generated during this study will establish a robust baseline for future comparisons as climate change continues to alter seasonality and species composition in the Bay of Fundy.

25) Seasonal Recruitment Patterns of *Dasysiphonia japonica*.

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An ongoing field study, started in summer 2019, aims to elucidate the seasonal recruitment patterns of the invasive red alga *Dasysiphonia japonica*. Introduced to New England in 2007, this species has rapidly become one of the most abundant species in subtidal ecosystems of the southern Gulf of Maine. *Dasysiphonia* is known to have wide thermal tolerances and initial observations have shown that it is common year-round, even through harsh New England winters. However, the finer details of this species' seasonal reproduction patterns in New England are unknown. It was hypothesized that *Dasysiphonia*'s success could possibly be attributed to active year-round reproduction. To test this hypothesis, sets of settlement plates have been deployed subtidally at multiple coastal sites. The plates are retrieved and replaced every three months to capture seasonal patterns. The algae community that has grown on each plate over that time is then analyzed. For comparison, a benthic photo quadrat survey is being conducted simultaneously to record the algae community in the surrounding area near the settlement plates. Preliminary results indicate that while *Dasysiphonia* is commonly encountered on most settlement plates in most seasons, it is rarely dominant on them, contrary to the original hypothesis. More often, it is present in small quantities, coexisting with numerous other species on the plates. In contrast, the photo quadrat surveys show *Dasysiphonia* as a consistent and dominant part of the seascape year-round. The puzzling disconnect between the settlement plate results and the observed community raises further questions. What then are the reproductive tendencies of *Dasysiphonia japonica* in this ecosystem, and how does it continue to thrive despite its apparently lackluster recruitment? This study will continue into summer 2021, and will hopefully shine light on these questions.

26) Biocrust community composition and implications for carbon flux under timed light incubation.

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Biological soil crusts (biocrusts) are living soil aggregates hosting diverse communities of cyanobacteria, eukaryotic algae, lichens, bryophytes, and other microorganisms in the uppermost millimeters of dryland soils. Biocrusts array along a gradient of structural complexity, each biocrust type being distinguished by the dominant photoautotrophic community member. Consequentially, each type hosts a unique microbial community with different associated biogeochemical processes. This project aims to 1) assess the carbon fixation capacity of biocrust types under varying incubation times and light intensities; and 2) link maximal fixation rate of each crust with their associated microbial community composition and microbial biomass. Five biocrust types (light cyanobacterial, dark cyanobacterial, cyanolichen, chlorolichen, and moss crust) were collected from four locations in the Chihuahuan Desert. Carbon fixation rates were quantified using a LI-6400XT portable photosynthesis system. Measurements were taken after biocrust wetting and light incubation at five different time periods (30min, 2hr, 6hr, 12hr, 24hr). Microbial biomass and community composition were assessed using phospholipid fatty acid assays. Additionally, amplicon Illumina MiSeq sequencing of 16S rRNA gene is currently underway to more deeply investigate microbial community composition. Preliminary data showed that different biocrust types display a different response to light exposure. Generally, carbon fixation and respiration were greater in thinner crusts, and net fixation increased over time for most crust types. Moss dominated crusts resulted in the lowest net fixation, while dark cyanobacterial and cyanolichen crusts were greatest carbon fixers despite not hosting greatest total microbial biomass or highest diversity at most sites. This project will provide new insights into the dynamics of carbon flux within biocrust communities in the context of their respective microbial communities.

27) Two desert species of *Tetradismus* (Sphaeropleales, Chlorophyceae) demonstrate distinct metabolomes during a desiccation-rehydration cycle.

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Desert algae are not monophyletic and diverse taxa possess the ability to recover from extreme dehydration without forming specialized resting structures. The green algal genus *Tetradismus* (Sphaeropleales, Chlorophyceae) contains aquatic, temperate terrestrial, and desert species. A recent ancestral states analysis indicates multiple habitat switches in the genus and a possible common origin of the terrestrial species. In physiological studies, the habitat of origin is predictive of a desiccation tolerance phenotype, with terrestrial, but not aquatic species, recovering their photosynthetic activity upon rehydration after desiccation. Close phylogenetic relationships of these algae and their responses to desiccation provide a unique opportunity to pinpoint specific physiological adaptations of terrestrial algae to their habitat. We used liquid chromatography tandem mass spectrometry (LC-MS/MS) methodology to study changes in composition of small water-soluble molecules in two desert *Tetradismus* species under desiccation (11% RH) followed by rehydration. We assessed if the expression pattern of the most important metabolites is similar in the two desert congeners supporting the hypothesis of a single transition to land in *Tetradismus*. We examined how the metabolomic profiles changed during the desiccation-rehydration treatment. Our analysis showed that each of the sampled cell hydration states (hydrated, dehydrated, desiccated, rehydrated 15 min, rehydrated 24 hours) is characterized by a distinct metabolite profile, indicating that even 24 hours of rehydration does not return the metabolome to its original hydrated state. Preliminary analysis of the most important metabolites showed differences between the focal species, suggesting distinct underlying mechanisms of desiccation tolerance in these two terrestrial species. To be able to state this definitively we will annotate the metabolomes and carry out pathway analysis, then integrate these data with corresponding transcriptomic data.

This project was supported by a 2020 NEAS Graduate Research Grant.

28) Genetic signatures from glass houses deposited millennia ago: metabarcoding of sedimentary ancient DNA (*sedaDNA*) to reconstruct diatom diversity in the North Water polynya (Pikialasorsuaq) during the last c. 3800 years.

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The North Water (NOW) polynya (Pikialasorsuaq) in northern Baffin Bay is the largest Arctic polynya. Each year, formation of the polynya provides ideal open-water conditions for massive spring phytoplankton blooms that promote the regional biodiversity. Diverse assemblages of diatoms play a key role in this productivity and are the dominant photosynthetic eukaryotes in planktonic and ice-associated (sympagic) habitats. Little is known regarding the response or potential adaptations of these organisms to large-scale climatic changes, and the multifaceted significance of the NOW polynya ecosystem requires continued investigation of climate-driven environmental changes. Sedimentary ancient DNA (*sedaDNA*) metabarcoding can be a powerful tool to increase the detection and resolution of taxa over long temporal periods. In addition, the development of *sedaDNA* in conjunction with other multi-proxy datasets developed for the NOW polynya can provide new insights regarding long-term changes to surface ocean conditions and primary productivity. However, metabarcoding can be limited by quality of reference sequence databases and taxonomic resolution of the markers employed. We aim to perform *sedaDNA* metabarcoding of diatoms on sediment core samples collected in the NOW with a temporal archive of ~3800 years. The focus of this presentation will be an overview of the methodology used to curate a robust reference database for a short, variable region of *rbcl*, and results of *in silico* tests for two primer pairs designed to amplify fragments of 75 or 148 bp.

29) The recognition of host-generalist and host-specialist species of ‘zooxanthellae’ and their relative prevalence in reef coral communities of the Pacific.

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In symbiotic systems, variation exists between symbionts and hosts in flexibility and fidelity of associations. Some symbiont species are generalists and are able to associate with a wide range of host taxa, while others are more specialized to a small group of hosts. The nature of the ecological relations cannot be thoroughly investigated without first delimiting species boundaries. In many symbiotic systems, trade-offs have been documented between host-generalist and host-specialist symbionts, and further, this can have an effect on the host physiology. However, this phenomenon has not been thoroughly investigated in coral-algal symbioses. In this study, we used molecular, ecological, and morphological evidence to describe two closely related lineages of *Cladocopium* (formerly *Symbiodinium* Clade C) that display contrasting host-specificity strategies in Palau. *Cladocopium 40* is a locally-adapted host-generalist that can associate with more than forty genera of reef-building coral (order: Scleractinia), but appears as a host-specialist in different locales. In contrast, *Cladocopium 21* sp. nov, is a host-specialist that is specific to one coral genus *Acropora* across Palau and other Indo-pacific reefs. Once formally described species, investigation into the trade-offs of different symbiotic strategies and the consequences on the host-coral physiology may help provide insight into the coral bleaching process and long-term community health as ocean temperatures rise.

Poster Session #2

Breakout room 1: Parson, Palmer, Geragotelis

room 2: Doiron, Wells

room 3: Mori, Thibodeau

30) Examination of the 23S rRNA gene in cyanobacteria: variation in secondary structure of the 23S rRNA molecule and its impact on sequence alignment.

Hannah Parson, Emily Palmer & Jeffrey R. Johansen

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While there has been extensive research utilizing sequence data of the 16S rRNA gene in cyanobacteria for phylogenetic analysis, there has been very little research on the 23S rRNA gene and the impact of phylogenies based on this gene on the classification of cyanobacteria. In examining ClustalW alignments, we observed extensive regions in which long series of indels prevented reliable alignment of the sequence data. In this project, we studied the 23S rRNA sequence in regards to its secondary structure from over 50 different cyanobacterial taxa and determined the secondary structures of six variable regions that did not align properly in ClustalW. These 23S rRNA gene regions differed to a much greater extent than any similar regions in the 16S rRNA gene, and even differed in the number of helices present between distantly related taxa. Only one species of cyanobacteria has a published 23S rRNA full molecular sequence secondary structure diagram (*Scytonema hyalinum*) and it was used as a guide for constructing secondary structure in this set of sequences. Structures differed significantly, and in particular the H8-H11, H16-H20, and H56-H59 structures were notably different among taxa. We used secondary structures to correctly align our sequences and these realigned sequences were then used to determine the phylogeny of the cyanobacteria based on the 23S rRNA gene. The phylogeny of the 16S rRNA gene was also determined and compared with the 23S rRNA gene results. When alignments were corrected for secondary structure, phylogenetic analyses had greater resolution of polytomies and had greater nodal support. While inclusion of secondary structure in alignment and analysis is not commonly completed due to its difficulty, we recommend that future workers align their cyanobacterial sequences of ribosomal genes with a secondary structure cross-check.

31) Novel cyanobacteria from biological soil crusts In Canyonlands National Park, Utah.

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Canyonlands National Park, a remote wildlands park accessible primarily by 4WD vehicles only, was sampled nearly 20 years ago for biological soil crusts. Numerous algal isolates were made at that time, but no publications followed from these collections. We have recently sequenced cyanobacterial cultures from the isolates still maintained in the Algal Culture Collection at John Carroll University. Strains were characterized morphologically in Olympus photomicroscopes with Nomarski DIC optics and characterized genetically by sequencing the 16S rRNA gene and associated 16S-23S ITS region. We found new species belonging to the recently described genera in the Synechococcales, including *Timaviella* (Oculatellaceae), *Nodosilinea* (Prochlorotrichaceae), and *Phormidesmis* (Leptolyngbyaceae). In addition, two strains belonging to the recently described species, *Myxacorys californica*, were also found. Morphological characterization of the strains indicates that additional taxa will be indicated once molecular sequencing and analysis are complete.

32) A comparison of desmid communities in two New Hampshire wetlands.

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Desmids are a group of morphologically diverse green algae and occur frequently in freshwater wetlands. While desmids are rarely abundant, numerous species can co-occur in a single body of water. Several European studies have suggested that desmids may be indicative of the overall ecological value of a wetland, its maturity and basic water chemistry. This approach has not been widely tested in the Americas, but because the North American desmid flora has been thoroughly studied and synthesized, it may be possible to adapt the desmid indicator system to this continent as well. In this study, we selected two ponds in New Hampshire, both known for their diverse desmid communities but differing in the amount of disturbance and pollution affecting them. We cataloged the desmid species occurring in each pond, calculated simple community-structure metrics for them, and attempted to apply the European desmid index method to these data. While species richness was higher in the more pristine Pratt Pond (46 species), Simpson and Shannon diversity indices were higher in the more urban Round Pond (37 species), because of a more even representation of the species in the community. Only twelve species occurred in both ponds. Pratt Pond flora contained more indicator species, including three red-list species, compared to one in Round Pond. The present study suggests that using desmids as indicators in New England may be possible and potentially useful. However, much more data will be needed to adapt the method fully, and to add North American species to the indicator list.

33) Paleolimnology to understand blooms of *Didymosphenia hullii*, *Didymosphenia geminata*, and *Cymbella janischii*: nuisance stalk-forming diatoms in the West Branch of the Farmington River, Connecticut, USA.

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Recently, nuisance stalk-forming diatoms are believed to have expanded their global range. This expansion and other unknown processes have triggered prolific blooms with thick mats of filamentous stalk material causing habitat deterioration and loss of biodiversity to river ecosystems, and significant negative impacts on the sport fishing industry. Until recently, these nuisance diatom species have not posed problems for rivers in Connecticut. However, three especially problematic and nuisance stalk-forming species are now actively growing in the West Branch Farmington River: *Cymbella janischii*, *Didymosphenia hullii*, and *Didymosphenia geminata*. *Didymosphenia* taxa are known to grow in stable flowing, regulated, cold, oligotrophic waters. Our project will use, coring, morphological analysis of sedimented cells, and DNA analysis of currently-growing cells to determine species affinities to sequences from other geographic locations, and to determine whether these taxa historically have been present in the river, but rare, or represent new arrivals. Coring has been widely used to examine paleo-records of diatom frustules from lakes, though this approach has not been frequently employed in active river corridors due to the possibility of erosion and discontinuous sedimentation. In 2020, manual-driven core methods and vibracoring were used to successfully retrieve sediment samples from the floodplain of the Farmington River, which are now the subject of microscopic examination. This work may provide enough information to determine the historical extant of these stalk-forming diatoms in Connecticut.

34) Novel cyanobacterial genera from Martinique.

Sophia L. Wells & Jeffrey R. Johansen

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Algal samples were collected from subaerial habitats from the Island of Martinique, a protectorate of France in the Caribbean Sea. Cyanobacterial isolates were made from these samples, and seven of these strains were sequenced for both the 16S rRNA gene and the 16S-23S ITS region. Phylogenetic analysis with other thin filamentous forms in the Synechococcales indicated that these strains likely belong to a new family level clade containing six species in four genera. The family level clade falls between family Trichocoleusaceae and a clade containing four families, Leptolyngbyaceae, Oculatellaceae, Prochlorotrichaceae and Synechococcaceae. Morphologically the strains resemble *Leptolyngbya*, and so would be described as cryptogenera not morphologically distinct from *Leptolyngbya* or members of the family Leptolyngbyaceae. An additional two strains discovered were new species in the genera *Oculatella* (Oculatellaceae) and *Nodosilinea* (Prochlorotrichaceae). These discoveries support the contention that the Synechococcales likely contains a wealth of undescribed diversity.

35) 15,000-year-old Charophyte Oospores in New Jersey Sediment.

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Charophytes are macroscopic green algae that live in oligotrophic freshwater worldwide and are important ecological indicators. Their vegetative thalli are often not preserved in sediments, but their sexual spores (oospores) have a hard covering containing sporopollenin often coated with calcium carbonate, and as a result the group has a rich fossil record of preservation extending as far back as the Silurian. But they also occur in more recent deposits, such as those we studied from an ancient bog in southern New Jersey near the Pine Barrens. Oospores of *Nitella* sp. were found in a ~3.5 m sediment core at a depth approximately 13,000-15,000 years of age (2.3-2.7m). These ages are based on ¹⁴C values in the sediment. Interestingly, there were some segments of the core within this range where no oospores were found, which suggests a constant change in the freshwater habitat. Although some oospores were cracked or slightly deformed, most were still intact, and we obtained light microscopic and SEM images that we identified to the genus *Nitella*. Although the oospores appeared much like those found on living thalli, preliminary attempts to germinate the spores in water or defined media were not successful.

36) Elucidating long-term trends from a 60-year time series in Narragansett Bay: implications for plankton dynamics and nutrient cycling.

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Long-term ecological time series research provides a unique perspective on environmental processes, population dynamics, and emergent properties of ecosystems. Due to their relatively short generation times, limited mobility, and sensitive physiology, plankton can be particularly responsive to climate change and important indicators of ecosystem shifts within time series. The Narragansett Bay Long-Term Plankton Time Series, one of the longest in the world, provides a unique opportunity to explore long-term trends in phytoplankton and nutrient dynamics within a regional estuary experiencing long-term warming. Analysis of the 60-year dataset (1959-2019) reveals a significant decrease in chlorophyll a, ammonium, and phosphate as well as a decline in the magnitude of winter and summer chlorophyll a. Chlorophyll a and nutrient phenology (i.e., timing of annually occurring events) were characterized by large variability, but no long-term, directional trend. Bloom frequency remained stable overtime with significantly more summer blooms than winter blooms. These observations in nutrient and phytoplankton dynamics indicate that strong variability in phenology may aid in buffering the system from observed warming trends in Narragansett Bay, which has important implications for food web interactions in the region.

INDEX (pages for abstracts)

A	G
Abdullah, 21	Garbary, 16
Ahmad, 21	Geragotelis, 41
Akagha, 26	Gilbert, 13
Arsenault, 44	Goffinet, 32
Assini, 29	Goodridge, 30
	Green-Gavrielidis, 10
B	H
Bailey, 22	Hamilton, 42
Barcyté, 22	Hamsher, 24
Bird, 16	Harðardóttir, 37
Borbee, 18	Harvey, 17
Borkman, 45	Hobbs, 10
Bothwell, 30	Hoellrich, 35
Brawley, 12	Humphries, 18
Brown, 22	
Butler, 38	
C	J
Callomon, 44	Johansen, 25, 26, 27, 39, 40, 43
Capistrant-Fossa, 12	
Carlile, 13, 14, 28, 29	
Cassidy, 11	
Cicchetti, 10	
Cray, 20	
Crichton, 33	
Crowell, 31	
D	K
Dankworth, 15	Karol, 24, 44
Darrouzet-Nardi, 35	Kausch, 19
Davison, 12	Kemp, 38
Delwiche, 44	Khan-Bureau, 42
Dijkstra, 34	Koji, 21
Doiron, 42	Kolisko, 22
Dunn, 12	Krautová, 27
	Krueger-Hadfield, 31
E	L
Eliáš, 22	LaJeunesse, 23, 38
Erickson, 17	Lane, 18, 22
Evans, 37	Lewis A, 38
	Lewis L, 32, 36, 42
	Limoges, 37
	Luknis, 40
	Lyon, 42
F	M
Fass, 16	Madduppa, 18
Fucikova, 41	McCourt, 44
	McNair, 24
	Mohamad, 21
	Mori, 44
	Muscavitch, 32

	N	Selgjakaj, 40 Shainker, 31 Shymko, 14 Siver, 42 Strock, 45 Szinte, 25	
Neefus, 34 Neuman, 24			
	O		
O'Brien, 34 Ouimet, 42 Owens, 28			T
	P	Taylor, 10 Terlova, 36 Terpis, 22 Thibodeau, 45 Thornber, 10 Turnham, 23, 38	
Palmer, 39, 40 Pánek, 22 Pantoni, 10 Parson, 39 Perrino, 25 Pietrasiak, 35 Puggioni, 45			V
	R	Vandermeulen, 16 Verbruggen, 22 Villanueva, 27 Vis, 31	
Ribeiro, 37 Rivera, 13 Rynearson, 45			W
	S	Warner, 38 Wehr, 19 Wells, 43 Woznicki, 24	
Salomaki, 22 Santiago, 35 Saunders, 11, 15, 33, 37 Schneider, 11			Y
		Yuzir, 21	

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