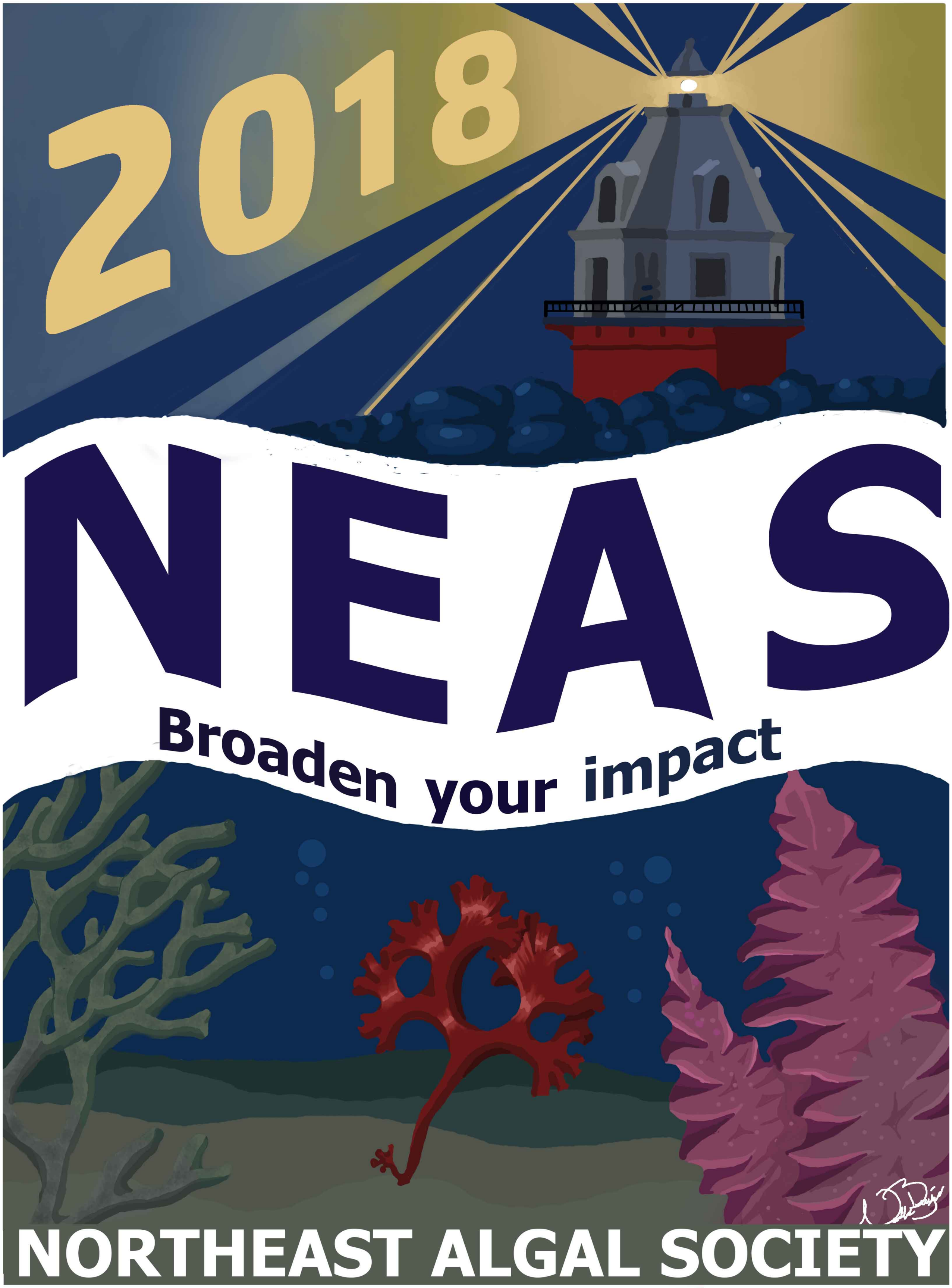


2018

NEAS

Broaden your impact

NORTHEAST ALGAL SOCIETY

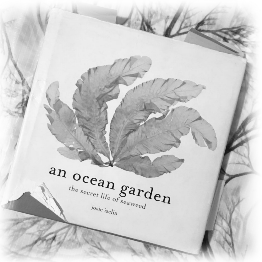
57th Annual Symposium
April 13-15, 2018
University of New Haven

Table of Contents & Acknowledgements

The co-conveners would like to acknowledge the generous support of our sponsors for this meeting, the College of Arts and Sciences at the University of New Haven, the Feinstein School of Social & Natural Sciences at Roger Williams University, and Dominion Energy Charitable Foundation. We are grateful to Nicholas Bezio for designing our fantastic meeting logo (see the cover page of this program), and Jim Lemire at RWU for printing numerous large format posters and images for this meeting. We thank Ken Hamel and University of New Haven students Sabrina Foote, Jonathan Gilbert, Kyla Kelly, and Marissa Mehlrose for their assistance with registration and meeting support. We thank award judges for the Wilce Graduate Oral Award Committee (Dale Holen, Diba Khan-Bureau, Sarah Whorley), Trainor Graduate Poster Award Committee (Dion Dunford, Lindsey Green-Gavrielidis, Ursula Röse), and President's Undergraduate Presentation Committee (Oral: Ken Dunton, Jessie Muhlin, Deb Robertson, Poster: Thea Popolizio, Eric Salomaki, John Wehr). We thank our session moderators: Anne Lizarralde, Morgan Vis, Susan Brawley, and Karolina Fučíková and our intrepid auctioneer Craig Schneider. We thank our vendors Scott Balogh (Balogh International Inc.) and Micro-Tech Optical Inc. We are particularly grateful to our distinguished guests Sunshine Menezes, Josie Iselin, and Bruce Barber for helping us scientists communicate more effectively.

We are pleased to welcome you to the 57th Northeast Algal Symposium!

This year's theme is ***Broaden your Impact***, a nod to the National Science Foundation's grant proposal evaluation criterion to document the broader impacts of scientific research. We hope to generate discussion on how we can communicate our work to the public, which is especially important in this era of "fake news" and suspicion of science. To this end, we have invited three distinguished guests, each with their own area of expertise, who will help us to share the merits of our work with a wider audience. We have special events scheduled for every day of the conference that will allow you to interact with this theme and learn from our guests. We hope that you will take away plenty of ideas and some tangible tools on how you can communicate your high quality science to the public as you *broaden your impact*!



This year's meeting will begin with the Friday evening welcome reception in the Seton Art Gallery on campus and will feature an exhibition and gallery talk (9:00 PM) by Josie Iselin. Josie is a photographer, author of books focused on forms in nature, and winner of the Phycological Society of America's Tiffany Award for her book *Ocean Garden: The Secret Life of Seaweed* (http://www.josieiselin.com/books/). This exhibition will feature Josie's seaweed images and some phycologically inspired artwork and outreach products contributed by some of our society members. Marine Photographer Bob Rattner (Lecturer, University of New Haven) has also contributed some of his local seaweed images.

On Saturday morning, we will hear from Dr. Sunshine Menezes. Sunshine is Director of the Metcalf Institute for Marine & Environmental Reporting (http://metcalfinstitute.org) and an expert on training scientists to be effective communicators. We will finish our afternoon session with a unique panel discussion with our three distinguished guests: a pitch slam! **Please bring your ideas for outreach activities and science communication strategies to pitch to our panel and they will give you feedback. This is a great opportunity to test-run your ideas!**

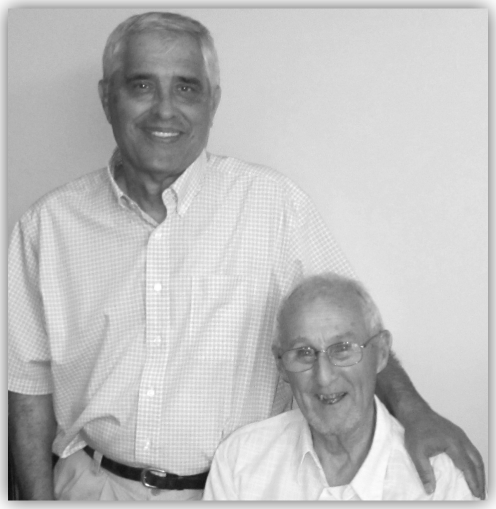
We will kick off Sunday morning with a workshop by Bruce Barber on crafting a high-impact podcast. Bruce is the radio station manager at the University of New Haven's WNHU and an avid podcaster (http://wnhu.org/bruce-barber/). He is also currently teaching the university's first course on an *Introduction to Podcasting*.

In addition to these exciting events, we will have our usual Phycological presentations, including talks by students and a poster session sponsored by Dominion Energy. We will also have our banquet on Saturday night, which will be followed by the infamous auction! We encourage all to stay through the NEAS business meeting, which will close the annual symposium.

We look forward to a truly engaging and inspirational meeting!

Amy Carlile & Brian Wysor
NEAS 2018 co-conveners

Milan Keser



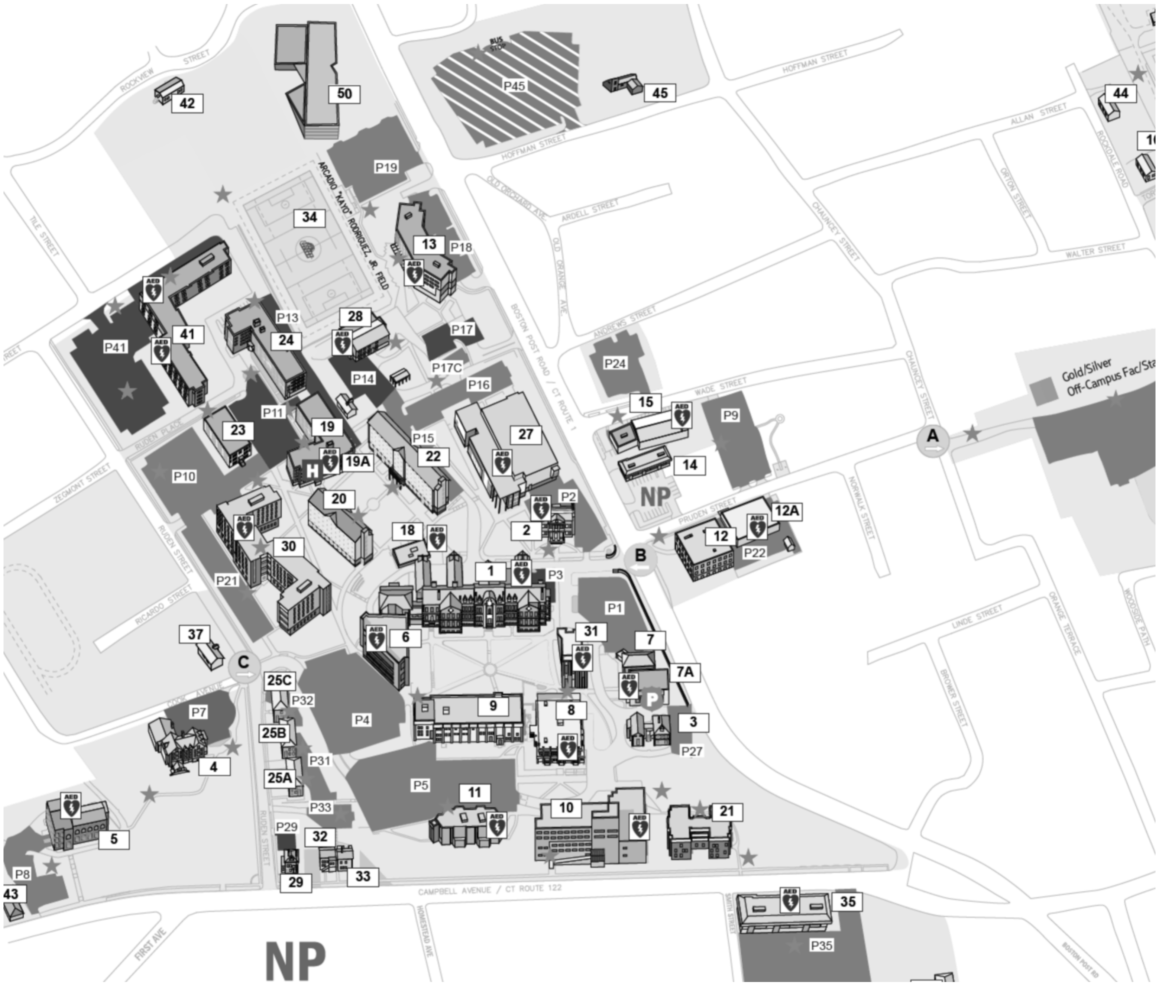
This 57th NEAS symposium is dedicated to our dear friend and colleague Milan Keser, who passed away this past December in East Lyme, Connecticut at the age of 79. Milan was a long-standing member and contributor to our society and this symposium since the mid-1970s. It is fitting that the theme of this year's meeting is "Broaden Your Impact" as Milan was a strong advocate for applied science. He passionately promoted rigorous science, in both industrial and public policy settings, as the best pathway to protecting and improving our environment and world. Milan grew up in war-torn Yugoslavia, surviving imprisonment at a concentration camp where his younger sister perished. He came to the U.S. at age 19 with no money and a limited grasp of the English language, so he joined the U.S. Air Force and then put himself through school. He received a B.S. from Westfield State College, a M.Ed. in science education, a M.S. in botany, and finally, a Ph.D. in plant sciences from the University of Maine under Bob Vadas.

Milan was hired by Millstone Power Station (then owned by Northeast Utilities, now by Dominion Energy) in 1978 to develop, staff, and supervise an in-house ecological monitoring program. He was instrumental in designing studies of algae and intertidal organisms to incorporate into the comprehensive monitoring program, and to complement studies of lobster, eelgrass, finfish, subtidal benthic infauna and aquatic toxicity. A testament to his foresight, the Millstone monitoring program continues to this day, 40 years later. He authored or co-authored dozens of scientific papers, not only on marine algae (*Ascophyllum* and *Fucus*), but other diverse organisms including lobsters, sea urchins, *Spartina*, eelgrass, oysters, and Asiatic clams. He was particularly proud of his first publication on the influence of aluminum ions on the developmental morphology of sugarbeet roots in Agronomy Journal, a publication known for its high acceptance standards. He was an adjunct professor and then an associate professor in the Department of Marine Sciences, University of Connecticut, Avery Point. He also served as a member of the Connecticut Institute of Water Resources, the Long Island Sound Study Science and Technical Advisory Committee, and was elected into the Connecticut Academy of Scientists and Engineers in 2012. Throughout his life, Milan was actively involved in soccer, as a player of distinction at Westfield State and as a youth soccer promoter, organizer, and coach. More recently, Milan returned to his homeland in the former Yugoslavia several times to interview family members and friends as part of research for a book documenting his family history. The book, written in both English and Serbo-Croatian, was published after his retirement in 2010.

More than anything, Milan was a devoted family man who cherished his wife Karen, his sons Milan, Adam, and Aleksander and especially his grandchildren. But Milan's family extended beyond his relatives, as he was fiercely loyal to many colleagues, coworkers and friends. He is dearly missed by many.

University of New Haven Campus Map

For your GPS, the address of campus is 300 Boston Post Road, West Haven. There are entrances to campus from Boston Post Road and Ruden Street (from Campbell Ave.). You may park anywhere on campus that doesn't have a sign for special parking; the most convenient lot for the meeting is lot P5 on the map below. There is also street parking on Campbell Avenue.



Meeting locations:

- Seton Gallery in Dodds Hall (building 10): opening mixer, poster session
- Alumni Lounge, upstairs in Bartels Hall (building 8): all talks on Saturday only, Saturday lunch, banquet, auction items
- Moulton Lounge in Bartels Hall (building 8): on Saturday only – coffee breaks, development table, and vendors Balogh books and Micro-Tech Optical Inc.
- Student Dining Room, downstairs in Bartels Hall (building 8): Executive Committee meeting during Saturday lunch
- Westside Hall (building 41): on Sunday only – talks, coffee, and Balogh books
- Marketplace Dining Hall in Bartels Hall (building 8): lunch on Sunday

Nominations for the NEAS Executive Committee 2018

Candidates for Member-at-Large

Karolina Fučíková is an assistant professor in the Natural Sciences Department at Assumption College in Worcester, MA. Her research focuses on evolution, systematics and biodiversity of terrestrial and freshwater green algae, but she has also dabbled into genomics and evolution of other critters including amoebas and oomycetes. Karolina's interest in biodiversity finds an outlet in outreach events as well – she has participated in and organized a number of BioBlitzes and manages an iNaturalist project on freshwater algae of New England.

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

Eric Salomaki: I first attended NEAS in 2011 where I presented my masters research on molecular systematics of freshwater red algae in the Batrachospermales as a member of the Vis lab (Ohio University). I attended the University of Rhode Island for my PhD in Chris Lane's lab, studying organellar and nuclear genome evolution in red algae that have transitioned from a photosynthetic to a parasitic life strategy. Currently, I am a Postdoctoral Fellow in the Department of Cell and Molecular Biology at University of Rhode Island using a metatranscriptomic approach to investigate diatom community composition and physiology across a natural nutrient gradient which makes up three oceanic provinces (Sargasso Sea, Gulf Stream and Coastal) in the North Atlantic. Additional research interests include eukaryotic biodiversity and changes in parasite abundance and physiology across the North Atlantic oceanic provinces.

Candidate for Treasurer:

Lindsay Green-Gavrielidis: I am currently a postdoctoral researcher at the University of Rhode Island. I teach seaweed ecology and seminar courses that explore the intersection of ecology and society. My research focuses on seaweed aquaculture and the causes and impacts of seaweed blooms. Over the past two years, I have worked closely with the shellfish farming industry to add sugar kelp to their existing lease sites in Rhode Island. I am also interested in how seaweed blooms will respond to climate change and recent regulations regarding nutrients released from wastewater treatment plants. In 2016, I joined the Kelp Ecosystem Ecology Network and have participated in yearly monitoring of kelp beds in Rhode Island since then. I joined NEAS in 2010 when I was a graduate student studying under Dr. Chris Neefus at the University of New Hampshire. I completed by Ph.D. in 2014, which focused on the aquaculture of nori (*Pyropia* and *Porphyra* species). In addition to conducting research and teaching, I also mentor undergraduate students and have brought several of them to NEAS. I enjoy the studentfriendly environment of NEAS and look forward to attending the annual meetings. I would be honored to serve and represent the society.

Candidate for Nominations chair-elect:

Dale Holen is an Associate Professor of Biology at Pennsylvania State University – Scranton Campus. He's been at PSU for 24 years and teaches courses in Microbiology, Lake and Stream Ecology, Evolution, Cell Biology and a non-majors course in Genetics, Ecology and Evolution. He is originally from Wisconsin where he went to UW Stevens Point and UW Milwaukee. His research interests are in mixotrophic algae, particularly chrysophytes, and the tradeoffs associated with having both phagotrophic and phototrophic capabilities. Currently he's studying a freshwater mixotrophic ciliate, *Prorodon viridis*, that harbors chlorella-like endosymbionts. He is also interested in the environmental cues behind cyst formation in chrysophyte algae. Dale is married, has one daughter, twin grandchildren and a crazy bloodhound.

Senjie Lin is a Professor of Biological Oceanography at University of Connecticut where she teaches in the Department of Marine Sciences. His research interests focus on molecular ecology and ecological genomics of marine phytoplankton, including dinoflagellate biodiversity, nutrient ecology, symbiosis biology, and harmful algal bloom ecology. Senjie is actively involved in public education on DNA tools for algal research and harmful algal bloom monitoring. He is committed to promoting public awareness of algae and the environment.

Please cast your vote using the removable ballot at the end of the program. Please return ballots to the registration table by the end of the first coffee break on Sunday.

General Program: 57th Northeast Algal Symposium University of New Haven

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Friday, April 13th, 2018

7:00 – 10:00 PM	Evening Registration, Gallery Opening & Poster Setup Session I Speakers load presentations on computer, *Dodds Hall*
9:00 – 10:00 PM	Gallery Talk & Keynote Address: *Josie Iselin: Art & Algae*

Saturday, April 14th, 2018

7:30 – 8:00 AM	Coffee & Pastries, *Moulton Lounge*, Bartels Hall Auction Drop off & Preview, *Alumni Lounge* Speaker Presentation File Upload, *Alumni Lounge* Poster Set-up, *Dodds Hall* Balogh Books, *Moulton Lounge* Micro-Tec Optical, *Moulton Lounge*
8:00 – 8:15	Group Photo
8:15 – 8:30	Welcome & Opening Remarks
SESSION I	***Student Presentations,* Moderator – Anne Lizarralde**
8:30 – 8:45	*President's Award Candidate* **Kyla Kelly**, Amy Carlile & Gary Wikfors· Measurement of *Pseudo-nitzschia*'s (Bacillariophyceae) physiological adaptations in between blooms. (Abstract #16)
8:45 – 9:00	*President's Award Candidate* **Sabrina Foote** & Amy Carlile. Molecular identification and distribution of *Halimeda* spp. (Chlorophyta) from San Salvador island, the Bahamas. (Abstract #11)
9:00 – 9:15	*President's Award Candidate* **Anna M. Crowell**, James A. Nienow & A. Bruce Cahoon· The complete chloroplast and mitochondrial genome sequences for an Appalachian isolate of the freshwater diatom, *Nitzschia palea*. (Abstract #6)

9:15 – 9:30	*President's Award Candidate* **Djihane Damoo** & Dion Durnford. Long-term survival of *Chlamydomonas reinhardtii* during conditional senescence. (Abstract #7)
9:30 – 9:45	*President's Award Candidate* **Katherine S. A. Cripps** & Gary W. Saunders**.** Unravelling *Rhodomela* spp. in Canadian waters: revisions in a cryptic red algal genus of the Ceramiales (Florideophyceae). (Abstract #5)
9:45 – 10:00	*Wilce Award Candidate* **Dominique S. Derminio** & Gregory L. Boyer Light intensity effects on *Microcystis aeruginosa* pigments, cell migration, and toxin levels. (Abstract #8)
10:00 – 10:15	*Wilce Award Candidate* **Trevor T. Bringloe** and Gary W. Saunders. Trans-Arctic speciation of Florideophyceae (Rhodophyta) since the opening of the Bering Strait, with consideration of the "species pump" hypothesis. (Abstract #2)
10:15 – 10:30	*Wilce Award Candidate* **Christopher Paight** & Christopher E. Lane**.** There and back again: a parasites tale. (Abstract #20)
10:30 – 10:45	*Wilce Award Candidate* **Daniel I. Wolf** & Morgan L. Vis. Multi-marker metabarcoding assessment of biodiversity within stream biofilm communities along an acid mine drainage recovery gradient. (Abstract #26)
10:45 – 11:00	***Coffee Break**, Moulton Lounge*
11:00 – 12:00	*Broaden Your Impact* Keynote Address **Dr. Sunshine Menezes**: Don't be a one trick (*Navicula matta)poni…*: Creative approaches for engaging public audiences in science. Metcalf institute for Marine & Environmental Reporting University of Rhode Island
12:00 – 1:30 PM	Lunch, *Alumni Lounge* Executive Committee Meeting, *Student Dining Room, Bartels Hall* Session II Speakers load presentations on computer, *Alumni Lounge*

SESSION II ***Student Presentations,* Moderator – Morgan Vis**

1:30 – 1:45 *Wilce Award Candidate*
Amber O. Brown, Amanda Foss, **Alyssa D. Garvey**, Quincy A. Gibson, Chelsea D. Villanueva & Dale A. Casamatta. *Komarekiella delphikthonos* sp. nov. (Cyanobacteria): an epidermal cyanobacterium implicated in an estuarine bottlenose dolphin (*Tursiops truncatus*) fatality. (Abstract #13)

1:45 – 2:00 *Wilce Award Candidate*
Jillian M. Freese & Christopher E. Lane. Putting *Asterocolax* in its place. (Abstract #12)

2:00 – 2:15 *Wilce Award Candidate*
Robin S. Sleith & Kenneth G. Karol. Assembling the nuclear genome of an invasive charophyte. (Abstract #24)

2:15 – 2:30 *Wilce Award Candidate*
Brandon O'Brien, Christopher Neefus, & Benjamin Brandt. The spatial module – new tools and applications in the macroalgae herbarium portal. (Abstract #19)

2:30 – 2:45 *Wilce Award Candidate*
Pattarasiri Rangsrikitphoti & Dion G. Durnford. Transcriptome changes following short-term light stress in *Bigelowiella natans*. (Abstract #21)

2:45 – 3:00 *Wilce Award Candidate*
Arley F. Muth & Ken H. Dunton. Arctic crustose coralline algae ecological function and abiotic factors controlling their distribution. (Abstract #18)

3:00 – 3:15 *Wilce Award Candidate*
Cody Brooks & Gary W. Saunders. The kelp conveyor hypothesis: exploring long-distance genetic connectivity of red algae in the northeast Pacific. (Abstract #3)

3:15 – 3:30 *Wilce Award Candidate*
Zacharias J. Smith and Gregory Boyer. Paralytic shellfish toxins in New York state freshwater. (Abstract #25)

3:30 – 3:45 ***Coffee Break**, Moulton Lounge*

3:45 – 4:45 *Panel Discussion*: Pitch you plan to *Broaden Your Impact*

Josie Iselin, Sunshine Menezes & Bruce Barber

Are you ready to share your love of algae with the world, but not sure how to do it most effectively? Do you have an outreach activity in mind, but want to get professional input on how to reach your target audience? Are you inspired to collaborate on algal art but don't know where to start? This session can help! Our panelists offer a range of public engagement perspectives, and will help you refine your ideas to clarify the target audience, objective, and the partners you need to make it a success. Come prepared to share (or "pitch") your idea and the panelists will offer their input. We encourage constructive comments from all participants! The more pitches, the richer this session will be. You will leave with many new ideas for sharing your phycological passions with the world.

4:45 – 5:00 ***Break***

5:00 – 6:30 ***Session III: Milan Keser Poster Session & Mixer****, Dodds Hall*

Sponsored by:

Dominion Energy®

7:00 – 10:00 *Social Hour & Banquet, Awards, Silent & Live Auction, Alumni Lounge*

Sunday, April 15th, 2018

7:30 – 8:15 AM Coffee & Pastries, *Classroom 111/112*, Westside Hall
Speaker Presentation File Upload, *Classroom 111/112*
Balogh Books, Westside Hall Lounge

8:15 – 8:30 Opening Remarks

8:30 – 9:15 *Broaden Your Impact* Keynote Address

Bruce Barber: Podcasting 101: Using audio storytelling to communicate and teach

SESSION IV ***Contributed Papers,*** **Moderator – Susan Brawley**

9:15 – 9:30 **Ira A. Levine** & Tiffany Cannis. Algae Foundation – Algal-based educational initiatives through the Algae Technology Educational Consortium (ATEC) and the Algae Academy**.** (Abstract #17)

9:30 – 9:45	**Peter A. Siver**. *Mallomonas intermedia* and *M. pseudocoronata*: neoendemics, recent migrants, or paleoendemics? (Abstract #23)
9:45 – 10:00	**Andreas Holzinger**, Anderas Albert, Jenny Uhl, Martin Rippin, Burkhard Becker, Martina Pichrtová[4]. Arctic and Antarctic *Zygnema* sp. (Zygnematophyceae) under UV and desiccation stress: a metabolomic and transcriptomic approach. (Abstract #15)
10:00 – 10:15	**Bruce Cahoon**[1], Ashley G. Huffman[1], Megan M. Krager[2], Roseanna M. Crowel. A short-term temporal meta-barcoding survey of planktonic protists in Appalachia - Natural Tunnel State Park, Virginia, USA. (Abstract #4)
10:15 – 10:30	Amanda Keilty[1], **James Fischer**, George Knoecklein & Constance Trolle. Saving lakes one app and website at a time. (Abstract #10)
10:30 – 10:45	***Coffee Break***
SESSION V	***Contributed Papers,* Moderator – Karolina Fučíková**
10:45 – 11:00	**Ursula S.R. Roese**, Andrea L. Call, Katharina H.C. Roese & Kristin M. Burkholder. Marine marcoalgal extracts and their effect against gram positive and gram negative human pathogens. (Abstract #22)
11:00 – 11:15	Christina Bonsell & **Kenneth H. Dunton**. Long-term trends in benthic irradiance and kelp production reveal implications of warming for arctic inner shelves. (Abstract #9)
11:15 – 11:30	**Lindsay Green-Gavrielidis**, Carol Thornber, Dave Ullman, Chris Kincaid, Austin Humphries. Optimizing site selection for kelp-oyster cultivation systems in Rhode Island. (Abstract #14)
11:30 – 11:45	**Simona Augyte**, C. Yarish, S. Lindell, E. Fischell, D. Bailey, J-L. Jannink, B. Smith and G. Wikfors. New tools for selectively improving strains of sugar kelp *Saccharina latissima* for food and fuel. (Abstract #1)
11:45 – 12:00	***Coffee Break***
12:00 -1:00 PM	NEAS Annual Business Meeting, *Classroom 111/112,* Westside Hall
1:00 PM	Lunch: Marketplace Dining, Bartels Hall (you will need the lunch ticket provided in your registration packet)

BIOGRAPHIES

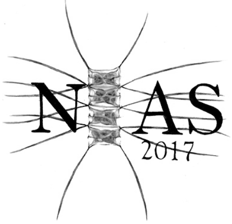
Sunshine Menezes is executive director of Metcalf Institute at the University of Rhode Island and Clinical Associate Professor of Environmental Communication in the URI Department of Natural Resources Science. Her professional experience and research interests span nanoplankton taxonomy, estuarine ecology, and oceanography; science communication and engagement; environmental policy, and advancing multidisciplinary graduate education that promotes societal participation in science. Menezes earned a B.S. in zoology from Michigan State University and a Ph.D. in oceanography from the URI Graduate School of Oceanography. She currently serves on a national Broadening Participation Task Force. She was a Rhode Island Foundation Fellow and served on the selection committee for the American Geophysical Union's Walter Sullivan Award for Excellence in Science Journalism.

Josie Iselin is a fine art photographer using her scanner to capture portraits of organisms from our near-shore ocean universe. She has designed seven books of her work, including An Ocean Garden: The Secret Life of Seaweed, as well as a line of scarves and shower curtains. She is continuing to research the life of seaweeds. Her work is on view at www.josieiselin.com

Bruce Barber has been involved in radio for 40 years, starting in college, and spending 17 years as the "Barber" half of "Smith and Barber The Morning Show" on WPLR in New Haven. That program ran for 17 years, and became one of the most popular morning radio shows in the state. Bruce joined Connecticut Public Radio as an independent producer in 2007, a role that continues to this day. He is also the host and creator of "The Real Life Survival Guide", a series of radio shows and podcasts that aired on WNPR from 2008 to 2014.

Bruce became the general manager of WNHU, the University of New Haven's 1700 watt FM radio station, in 2016, and teaches courses in podcasting and radio production.

Nicholas Bezio, an illustrator and marine biologist who designed the 2018 (and 2017) meeting logo. Bezio specializes in colored pencil illustrations and wildlife photography and creates works of art that accurately reflect the behavior, ecology and biodiversity of some of Earth's most beautiful yet strange organisms. Bezio's illustrations resonate with an old world feel, that evokes the excitement of discovery that early field biologists must have felt when they explored the "new world" for the first time. Bezio, unsurprisingly, derives inspiration from the likes of Ernst Haeckel, a well known Marine Scientist and Illustrator, famous for his stunning drawings featured in ***Kunstformen der Natur*** (known in English as ***Art Forms in Nature***). To see more of Bezio's stunning drawings and photographs, visit him on-line at http://www.nickbezio.com/.



Undergraduate Posters (President's Award)

[28] TERMINATOR OR BIOREMEDIATOR: CONTRASTING EFFECTS OF *ULVA LACTUCA* IN COASTAL AREAS**. Haley Barravecchia, Sarita Chiu** & Paulette Peckol.

[29] EFFECTS OF BOAT FUEL ON WATER CHEMISTRY OF LAKE ERIE. **Cole Beale** & Sarah Whorley.

[30] RESOLVING THE RED ALGAL DIVERSITY OF RHODE ISLAND THROUGH DNA BARCODING. **Alicia Beauvais** & Brian Wysor.

[31] MACROALGAE AS BIOINDICATORS FOR MERCURY CONTAMINATION IN THE LONG ISLAND SOUND. **Cassandra Bhageloo**, Vincent Breslin, Sean Grace.

[33] ANTIMICROBIAL ACTIVITY OF RED AND BROWN ALGAE AGAINST MRSA AND OTHER GRAM POSITIVE BACTERIA. **Andrea L. Call**, Katharina H.C. Roese, Kristin M. Burkholder, Ursula S.R. Roese,

[36] POTENTIAL RISK OF -METHYLAMINO-L-ALANINE IN EASTERN LAKE ERIE AND EFFECTS OF NEUROTOXIN IN *DANIO RERIO*. **Maria C. DeLuna** & Robert Gunther.

[41] A NEW SPECIES FROM BERMUDA SPLIT FROM THE PANTROPICAL *DIGENEA SIMPLEX* COMPLEX (RHODOMELACEAE, CERAMIALES). **Bilal F. Hamzeh**, Craig W. Schneider, Christopher E. Lane & Gary W. Saunders.

[43] THE PARADOX OF *DE NOVO* PURINE SYNTHESIS WITHIN PARASITIC PHYLUM APICOMPLEXA. **Liz Hunter**, Chris Paight, & Christopher E. Lane.

[46] WATER CHEMISTRY, ALGAL ENZYME ACTIVITY AND FATTY ACID CONCENTRATION AS INDICATORS OF WATER QUALITY OF ERIE COUNTY STREAMS. **Mopati Kuswani** & Sarah Whorley.

[51] SURVEY OF FRESHWATER RED ALGAE FROM THE BATRACHOSPERMALES (RHODOPHYTA) IN SOUTH CAROLINA**. Alexis M. Redmond**[1], Emily K. Hollingsworth[2] & Morgan L. Vis.

[54] ANTIMICROBIAL EFFECTS OF MACROALGAL EXTRACTS AGAINST GRAM NEGATIVE HUMAN PATHOGENS INCLUDING *KLEBSIELLA PNEUMONIAE* AND *SALMONELLA* TYPHIMURIUM. **Katharina H.C. Roese**, Andrea L. Call, Kristin M. Burkholder, Ursula S.R. Roese.

[57] A NOVEL CRYPTIC SPECIES OF GREEN ALGAE FROM THE CALIFORNIA DESERT. **Melissa Taylor**, Nicole Pietrasiak & Karolina Fučíková.

Graduate Student Posters (Trainor Award)

[34] THE INVASIVE RED ALGA *GRATELOUPIA TURUTURU* (HALYMENIALES, RHODOPHYTA) REACHES MID-COAST MAINE: ARE CURRENT BIOSECURITY MEASURES ENOUGH? **Kyle Capistrant-Fossa**[1] and Susan H. Brawley

[35] UNRAVELING THE RELATIVE GEOGRAPHICAL DISTRIBUTION OF KELP GAMETOPHYTES AND SPOROPHYTES IN THE NORTHWEST ATLANTIC AND CANADIAN ARCTIC. **Marie Dankworth** and Gary W. Saunders.

[38] USING ANCIENT DNA TO STUDY TRENDS IN PALAEOPLANKTONIC ASSEMBLAGES SINCE THE LAST GLACIAL MAXIMUM IN BAFFIN BAY, CANADA. **Joshua R. Evans**, Audrey Limoges, Adrian Reyes-Prieto & Gary W. Saunders.

[50] GENE EXPRESSION PROFILES OF SODIUM EXPORT MECHANISMS IN *CHARA LONGIFOLIA* (C. B. ROB.) AND *CHARA AUSTRALIS* (R. BR.). **Shaunna Phipps**, Tomoaki Nishiyama & Mary A Bisson

[53] DIVERSIFYING NEW ENGLAND SEA VEGETABLE AQUACULTURE: MODIFYING KELP NURSERY AND GROW OUT TECHNOLOGIES FOR NORI PRODUCTION. **Jaclyn Robidoux** & Chris Neefus.

[55] HARMFUL ALGAL BLOOMS IN NEW YORK'S FINGER LAKES – A HARBINGER OF CHANGE TO COME? **Kristen N. Slodysko** & Gregory Boyer.

[58] STRUCTURAL COMPARISON OF DESERT AND AQUATIC SPECIES OF *TETRADESMUS* (CHLOROPHYCEAE, CHLOROPHYTA) THROUGH THE CYCLE OF DESICCATION AND REHYDRATION. **Elizaveta Terlova**, Louise A. Lewis, Xuanhao Sun, Maritza Abril.

Contributed Posters

[27] INVESTIGATING THE PHYSIOLOGICAL FUNCTION OF GFA IN *PHAEODACTYLUM TRICORNUTUM*. **Katherine Battey** & Deborah Robertson.

[32] CHARACTERIZATION OF SAR CLADE COMMUNITY COMPOSITION IN INDONESIAN MARINE ENVIRONMENTS. **Erin Borbee**, Austin Humphries, Hawis Madduppa, & Christopher Lane.

[37] CADMIUM SEQUESTRATION IN THE GREEN ALGAE *CHARA AUSTRALIS.* **Kaitlynn Donahue** & Mary Bisson.

[39] *DISPORA SPECIOSA*, THE FIRST COCCOID MEMBER OF MICROSPORACEAE. **Karolina Fučíková**[1] & Lenka Štenclová.

[40] CHLOROPLAST GENOMES OF THREE CLOSELY RELATED *HALAMPHORA* SPP. (BACILLARIOPHYCEAE): A CASE OF CONSERVED GENE CONTENT AND EXTENSIVE GENOME REARRANGEMENT. **Sarah E. Hamsher**, Kyle G. Keepers, Cloe S. Pogoda, Joshua G. Stepanek, Nolan C. Kane, & J. Patrick Kociolek.

[42] STOMATOCYST PRODUCTION AND ENVIRONMENTAL INDUCEMENT IN *OCHROMONAS PINGUIS*, A MIXOTROPHIC CHRYSOPHYTE. **Dale A. Holen**.

[44] MERCURY SORPTION IN CHONDRUS CRISPUS (STACKHOUSE 1797) IN LONG ISLAND SOUND COASTAL HARBORS. **Lela Jackson**, Vincent Breslin, Sean Grace.

[45] CHARACTERIZATION OF A NEW SPECIES IN THE GENUS *DIDYMOSPHENIA* AND OF *CYMBELLA JANISCHII* (BACILLARIOPHYTA) FROM CONNECTICUT, USA. **Diba Khan-Bureau**, Eduardo A. Morales, Luc Ector, Michael S. Beauchene, & Louise Lewis.

[47] ALGAE TORCH: A COST-EFFECTIVE TOOL FOR IDENTIFYING THREATENING ALGAL BLOOMS. **Wyatt Leinoff** & Gregory Boyer.

[48] A SUMMARY OF NEW SILICA-SCALED CHRYSOPHYTES SPECIES DESCRIBED FROM A MIDDLE EOCENE MAAR LAKE. **Anne-Marie Lizarralde** and Peter A. Siver.

[49] A SURVEY OF MICROBIAL EUKARYOTES FROM THE SAR CLADE THROUGHOUT ICELAND. **Daniela Lopes Paim Pinto**, Hilary McManus, Christopher E. Lane.

[52] FORMALDEHYDE DEHYDROGENASE AS A SELECTABLE MARKER FOR TRANSFORMATION IN MARINE DIATOMS. Christina Campagna[1] & **Deborah L. Robertson.**

[56] EXPLORING THE FRESHWATER RED ALGAL DIVERSITY OF AFRICA: PAST AND PRESENT. **Amanda L. Szinte**, Jonathan C. Taylor, Adesalu T. Abosede & Morgan L. Vis.

[59] SEQUENCING A NOVEL EUSTIGMATOPHYCEAE INDENTIFIES A POTENTIAL SECONDARY ENDOSYMBIOITIC EVENT. **Kristina X Terpis**, Laura Eme, J Craig Bailey, Christopher E Lane.

[60] REVIEW OF RECENT TAXONOMIC CHANGES IN FRESHWATER RED ALGAE (RHODOPHYTA). **Morgan L. Vis** & Orlando Necchi Jr.

ABSTRACTS

Oral presentation abstracts **(in alphabetical order by presenting author).** PA = President's Award Candidate, WA = Wilce Award Candidate.

[1] NEW TOOLS FOR SELECTIVELY IMPROVING STRAINS OF SUGAR KELP *SACCHARINA LATISSIMA* FOR FOOD AND FUEL. **Simona Augyte**[1], Charlie. Yarish[1], S. Lindell[2], E. Fischell[2], D. Bailey[2], J-L. Jannink[3], B. Smith[4] and Gary Wikfors[5]. [1]Department of Ecology & Evolutionary Biology, University of Connecticut, Stamford, CT. [2]Biology and Applied Ocean Physics and Engineering Departments, Woods Hole Oceanographic Institution, Woods Hole, MA. [3]Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY.

As a part of ARPA-E's MARINER program, a team of scientists and entrepreneurs is pursuing a selective breeding program to improve the productivity and composition of sugar kelp, *Saccharina latissima,* which could serve as feedstock for biofuels. Our project goal is to select *S. latissima* genetically suited to offshore farm environments and possess qualities of increased dry matter yield per unit area (≥ 10% per generation) and improved composition for use as a bioenergy feedstock. We will develop several complementary tools to reach this objective. To facilitate high-throughput creation of family crosses, the NOAA Milford Lab and UCONN are developing cell sorting methods to efficiently isolate and clone gametophytes. USDA/Cornell and HudsonAlpha will employ PacBio and Illumina sequencing to create a deep-sequenced reference genome and establish a variant catalog for our founding populations and families. WHOI, UCONN and GreenWave will oversee field trials of 144 families (from 12 different 'strains') planted in triplicate plots on two farm sites (nearshore and offshore) over two growing seasons. The resulting phenotypic data will be associated with genetic markers (GWAS) and primary productivity and composition traits of variants. A goal is to develop methods to predict offspring performance based upon genotype and breeding values of parents as a short cut around extensive and expensive field testing. A separate ARPA-E project will test the potential labor-saving use of WHOI's robotic autonomous underwater vehicles and sensors for conducting phenotypic measurements of family test plots. These will be compared to conventional hands-on field measurements.

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[2] (WA) TRANS-ARCTIC SPECIATION OF FLORIDEOPHYCEAE (RHODOPHYTA) SINCE THE OPENING OF THE BERING STRAIT, WITH CONSIDERATION OF THE "SPECIES PUMP" HYPOTHESIS. Trevor T. Bringloe and Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB, Canada.

The opening of the Bering Strait initiated significant biotic interchange that is postulated to have played a major role in phylogeographic patterns of northern marine flora and fauna. In addition, the "species pump" hypothesis asserts that glaciation events promoted speciation due to repeated isolation of populations over the past 2.6 million years. Here, speciation events in red marine macroalgae (Florideophyceae) believed to have been precipitated by the opening of the Bering Strait were assessed using time-calibrated phylogenies, and the applicability of the “species pump” hypothesis to trans-Arctic lineages was considered. Sequence data for trans-Arctic genera of marine macroalgae were amalgamated and supplemented with sampling from the Northwest Atlantic, Northern Alaska, Norway, and Nome, Alaska (2014-2017). Bayesian and Maximum-Likelihood phylogenies were built using the 5’ end of the cytochrome *c* oxidase subunit I gene (COI-5P), the full length nuclear internal transcribed spacer region (ITS), and the ribulose-1 5-biphosphate carboxylase large subunit gene (*rbc*L), and nodes were timed using calibrated COI-5P and *rbc*L molecular clocks. The final dataset represented 181 species, broadly representing 14 trans-Arctic lineages. Pacific to Atlantic speciation events were inferred in 12 cases, whereas the opposite scenario (Atlantic to Pacific) was inferred in two; half of these events appeared to occur during the Pleistocene. Our results are in agreement with previous studies, in that trans-Arctic speciation events post-dated the opening of the Bering Strait with a clear Pacific to Atlantic bias. Evidence for the “species pump” hypothesis (as applied to trans-Arctic interchange) was lacking given trans-Arctic speciation events did not appear to occur primarily during the Pleistocene. Secondary contact during interglacial periods and a slow rate of evolution in marine macroalgae are hypothesized to have impeded speciation in diverging trans-Arctic populations.

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[3] (WA) THE KELP CONVEYOR HYPOTHESIS: EXPLORING LONG-DISTANCE GENETIC CONNECTIVITY OF RED ALGAE IN THE NORTHEAST PACIFIC. **Cody Brooks** & Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

Roughly 10% of the seaweed flora in Haida Gwaii (an archipelago in northern British Columbia) is also found in California, but not in nearby southern British Columbia presenting an unexpected disjunct distribution pattern. The dispersal system responsible for this unexpected pattern is unknown. The kelp conveyor hypothesis posits that winter storms in California dislodge massive quantities of kelp which subsequently raft on the Winter Davidson current – a northbound current dominant from November to February. These kelp rafts are expected to transport non-buoyant algal species from California to Haida Gwaii, thus causing the observed disjunct distribution. If the hypothesis is valid, this pattern initially observed at the species level should also be reflected at the population level in species with continuous distributions along the west coast of North America. Further, as the kelp conveyor is expected to have greater impact on subtidal species, we selected the predominantly low intertidal to subtidal species *Cryptopleura ruprechtiana* and the predominantly mid intertidal *Mastocarpus intermedius* for this study. Samples were collected from California, Haida Gwaii and southern British Columbia and sequenced using the mitochondrial cytochrome c oxidase subunit I (COI-5P) and the nuclear internal transcribed spacer (ITS). Although our results are preliminary, patterns of haplotype diversity and genetic differentiation indicate direct gene flow from California to Haida Gwaii in *C. ruprechtiana,* an observation consistent with the kelp conveyor hypothesis. However, populations of *M. intermedius* in California appear more genetically distant to their northerly cousins, which the kelp conveyor predicts for a mid intertidal species. The kelp conveyor hypothesis has potential implications for long-distance impacts on the flora of British Columbia. Although kelp rafting has been reported elsewhere, this study marks the first test of this particular pattern at the population level.

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[4] A SHORT-TERM TEMPORAL META-BARCODING SURVEY OF PLANKTONIC PROTISTS IN APPALACHIA - NATURAL TUNNEL STATE PARK, VIRGINIA, USA. A. **Bruce Cahoon**[1], Ashley G. Huffman[1], Megan M. Krager[2] & Roseanna M. Crowell[1]. [1]Department of Natural Sciences, University of Virginia's College at Wise, Wise, VA. [2] Natural Tunnel State Park, Duffield, VA.

The purpose of this study was to survey freshwater planktonic protists in an under-sampled region of Appalachia, and address three questions: 'How diverse is the eukaryotic microbiome?', 'Is that microbiome temporally dynamic?', and 'What abiotic factors affect changes?'. Water samples were collected from the Natural Tunnel State Park in Scott County, Virginia (USA) over fourteen weeks and barcodes from 23S and 18S rRNA regions were sequenced, identifying 3663 OTUs putatively representing 19 phyla, 213 families 332 genera. The greatest diversity was found in P:Chlorophyta and P:Intramacronucleata and the greatest abundance in P:Bacillariophyta and P:Cryptophyta. The five sites had distinctive protist profiles defined by the photoautotrophs. Temporal analyses demonstrated these profiles changed dramatically during the study period and each area's microbiome was distinct for short periods of time. The proportion of abundant versus rare protists remained steady despite very little overlap of taxa between time points. We posit there are limited numbers of microbial niches in the systems we surveyed and the rare microbial biome quickly fills vacated niches. The rapid changes in protist populations are likely due to micro-climate or -environmental effects but there was no single contributing factor. Instead there appears to be interplay between collection date, phosphate concentration, ammonia concentration, and conductivity.

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[5] (PA) UNRAVELLING *RHODOMELA* SPP. IN CANADIAN WATERS: REVISIONS IN A CRYPTIC RED ALGAL GENUS OF THE CERAMIALES (FLORIDEOPHYCEAE). **Katherine S. A. Cripps** & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, Canada.

It has long been known that there is a need for taxonomic revision in the red algal genus *Rhodomela*, which has species widely distributed in colder waters of the Northern Hemisphere. Species in this genus have overlapping morphologies, resulting in ambiguous assignment of specimens to morphospecies and potentially masking overlooked species diversity. Specimens of *Rhodomela* were collected in the NW and NE Atlantic, Bering Strait and western Bering Sea in the intertidal and subtidal via SCUBA or dredge and assessed using three barcode markers – COI-5P, *rbc*L, and ITS. These sequence data were variously used to complete barcode gap, as well as phylogenetic, analyses. Morphological and anatomical characteristics were also observed. Five genetic groups were determined from our samples in the study area; four of which matched previously described species, viz. *R. confervoides*, *R. lycopodioides*, *R. virgata* and *R. sibirica*, while the fifth genetic group formed a cryptic complex with *R. virgata* (referred to as *R. sp._1virgata*). Results for the Canadian Arctic and NW Atlantic were particularly surprising given that only *R. confervoides* and *R. lycopodioides* were recorded in these waters, while four of five genetic groups were present in this area, but excluding the expected *R. confervoides*. An updated perspective on *Rhodomela* spp. in the Arctic and Atlantic Canadian waters is provided.

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[6] (PA) THE COMPLETE CHLOROPLAST AND MITOCHONDRIAL GENOME SEQUENCES FOR AN APPALACHIAN ISOLATE OF THE FRESHWATER DIATOM, *NITZSCHIA PALEA*.

Anna M. Crowell[1], James A. Nienow[2] & A. Bruce Cahoon[1]. [1]Department of Natural Sciences, University of Virginia's College at Wise, Wise, VA. [2]Department of Biology, Valdosta State University, Valdosta, GA.

Nitzschia palea is a common freshwater diatom used as a bioindicator due to its tolerance of polluted waterways. It is also suspected to be the ancestral diatom of the tertiary endosymbiont within some strains of the "dinotom" dinoflagellate *Durinskia baltica*. Despite these interesting aspects of *N. palea*, its organellar genomes are not available in public databases. A putative strain of *N. palea* was collected from a pond on the University of Virginia's College at Wise campus and cultured. Three genetic markers were initially sequenced - nuclear 18S rDNA and the chloroplast markers 23S rDNA and *rbcL*. The initial 18S nuclear marker matched *N. palea* but the chloroplast markers 23S and *rbcL* most closely matched archived sequences for *D. baltica*. Morphological characteristics were also determined using phase-contrast, differential interference, and scanning electron microscopy. The cells were identified as *N. palea* and named, variety Wise, VA. Next, total DNA from *N. palea* was deep sequenced using Illumina MiSeq technology and the chloroplast and mitochondrial genomes were assembled using a combination of template and de novo based assembly strategies. The chloroplast genome of *N. palea* is 119,447 bp with a quadripartite structure, 135 protein coding, 28 tRNA, and 3 rRNA genes. The mitochondrial genome is 37,754 bp with a single repeat region as found in other diatom chondriomes, 37 protein coding, 23 tRNA, and 2 rRNA genes. The chloroplast genomes of *N. palea* and *D. baltica* have identical gene content and order and a 94.8% sequence similarity with most differences occuring in intergenic regions. The *N. palea* mitochondrial genome and *D. baltica's* endosymbiont mitochondrial genome also have identical gene content and order with a sequence similarity of 90.7%. These data provide the sequences of two organelles for a widespread diatom and has shown that all of the organelle genes have been conserved in the *N. palea* and *D. baltica* endosymbiosis.

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[7] (PA) LONG-TERM SURVIVAL OF *CHLAMYDOMONAS REINHARDTII* DURING CONDITIONAL SENESCENCE. **Djihane Damoo** & Dion Durnford. Department of Biology, University of New Brunswick, Fredericton, New Brunswick, Canada.

Microalgae, such as *Chlamydomonas reinhardtii,* undergo conditional senescence when grown in batch culture due to nutrient limitation. Once in the stationary phase, the cells must still adapt to changes in light intensity to extend their lifespan, and the photo-protective strategies they use to survive long-term nutrient deprivation are not clear. Here we explore plastid and photo-physiological adaptations in *Chlamydomonas reinhardtii* during a long-term ageing experiment by methodically sampling them over a period of 4.5 months. We observed that over this time period there were drastic declines in chlorophyll and RuBisCO content, suggesting the gradual degradation of the chloroplasts. Cell viability, however, was stable for weeks, then dropped to a minimum of 15%. At this late stage, there was only 3% of the maximum chlorophyll per cell remaining. Despite the ongoing changes in the plastid, the main antenna protein associated with Photosystem II (LHCII), remained high, well into the ageing process. In addition, the light-stress related protein (LHCSR) was upregulated and remained abundant for two months before then declining. The presence of LHCSR roughly correlated with increases in energy-dependent light dissipation mechanisms, which would reduce photo-oxidative damage during senescence. A late decline in LHCSR abundance, however, correlated with high levels of dark fluorescence (Fo) indicating a transition to a high fluorescence state. This suggests a shift in the photo-protective mechanism of *Chlamydomonas reinhardtii*, from an energy-dependent process to one relying on bulk antenna fluorescence. These stepwise changes seemed to be used to extend lifespan during conditional senescence. Therefore, we anticipate that this research will help further understand the various molecular acclimations carried out by *Chlamydomonas* to maximize their survival under abiotic stress.

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[8] (WA) LIGHT INTENSITY EFFECTS ON *MICROCYSTIS AERUGINOSA* PIGMENTS, CELL MIGRATION, AND TOXIN LEVELS. **Dominique S. Derminio** & Gregory L. Boyer. The State University of New York, College of Environmental Science and Forestry, Syracuse, NY.

Cyanobacterial harmful algal blooms (cHABS) are a common occurrence in many lakes across New York State. Cyanobacteria gather light energy for growth within photosystem II using a phycobilisome. Phycobilisomes contain two major pigment-proteins complexes in their light-gathering antenna complex: phycocyanin (PC) and phycoerythrin (PE). To understand how this antenna changes with light intensity, an 18-hour experiment was conducted on a natural toxic cHABs in Lake Neatahwanta (Fulton, NY, USA). Light intensity, cyanobacteria biomass as both cell number and pigment fluorescence, and toxicity were measured at 2-hr intervals at four depths between the hours of 4:00 am and 10:00 pm. Toxicity per liter did not significantly change with time of day or depth. In contrast, pigments (chl-*a* and PC) did vary with time of day and depth. *Microcystis* cell numbers were significantly different between depths ($p = 0.02$), but not time of day.

There was a significant difference in PC to PE ratio based on fluorescence measurements over the course of the day. This study will improve the fundamental understanding of how *Microcystis* pigment composition responds to an ever-changing light field and has important implications for the use of fluorescent techniques in monitoring cHABs.

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[9] LONG-TERM TRENDS IN BENTHIC IRRADIANCE AND KELP PRODUCTION REVEAL IMPLICATIONS OF WARMING FOR ARCTIC INNER SHELVES. Christina Bonsell & **Kenneth H. Dunton**. Marine Science Institute, The University of Texas at Austin, Port Aransas, Texas.

Previous studies have predicted that long-term decreases in sea-ice extent will lead to enhanced production by benthic polar macrophytes, with potential to change ecosystem structure. Here, we synthesize a multidecadal dataset of annual growth by the Arctic endemic kelp *Laminaria solidungula* and corresponding measurements of *in situ* benthic irradiance from Stefansson Sound in the central Beaufort Sea. We incorporate long-term data on sea ice concentration (National Sea Ice Data Center) and wind (National Weather Service) to assess how ice extent and summer wind dynamics affect the benthic light environment and annual kelp production. We find evidence of significant changes in sea ice extent in Stefansson Sound, with an extension in the ice-free season by approximately 17 days since 1979. Although kelp elongation varies significantly between sites and years (3.8 to 49.8 cm yr^{-1}), there is no evidence for increased production with either earlier ice break-up or a longer summer ice-free period. This is explained by very low light transmittance to the benthos during the summer season (light attenuation values ranging from 0.5 to 0.8 m^{-1}), resulting in minimal potential for kelp production on most days. Additionally, on month-long timescales in the ice-free summer, benthic light levels and wind speed are negatively related. The frequent, wind-driven resuspension of sediments following ice break-up significantly reduce light to the sea bed, nullifying the benefits of an increased ice-free season on annual kelp growth. Instead, benthic light and primary production may depend substantially on the 1-3 week period surrounding ice break-up when intermediate sea ice concentrations reduce wind-driven sediment resuspension. These results suggest that both benthic and water column primary production along the inner shelf of Arctic marginal seas may decrease, not increase, with reductions in sea ice extent.

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[10] SAVING LAKES ONE APP AND WEBSITE AT A TIME**.** Amanda Keilty[1], **James Fischer**, George Knoecklein & Constance Trolle. [1]Johnson State College Bethlehem, CT 06751. [2]White Memorial Conservation Center. [3]Northeast Aquatic Research, [4]Bantam Lake Protective Association.

Bantam Lake experiences cyanobacteria blooms annually, but the bloom of 2016 was unusually intense and sustained. It ultimately resulted in beach closures and restricted lake usage when seasonal use was at its highest. As a result, incidence/crisis communication to stakeholders became the primary job for the Bantam Lake Protective Association. The BLPA decided that a proactive approach was necessary in 2017. They contracted Northeast Aquatic Research for weekly assessments of cyanobacteria activity (cell counts/ml) and other lake measurements to effectively manage the blooms. This data was also useful when informing stakeholders about the state of the lake. We developed *Bantam Lake Cyanos* as a communication portal that provides up-to-date forecasts of cyanobacteria activity and other lake measurements via a website and smartphone app. The website also informs visitors of the health risks associated with blooms and the daily decisions they could make to reduce nutrient run-off, which aids in the bloom growth and formation. App users shared images of blooms, thereby turning them into citizen scientists and alerting lake managers of changes to the lake. We will review usage statistics for these communication portals that indicates their relevance to stakeholders.

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[11] (PA) MOLECULAR IDENTIFICATION AND DISTRIBUTION OF *HALIMEDA* SPP. (CHLOROPHYTA) FROM SAN SALVADOR ISLAND, THE BAHAMAS. **Sabrina Foote** & Amy Carlile. Department of Biology and Environmental Science, University of New Haven, West Haven, CT.

Halimeda spp. are ecologically important components of benthic tropical communities because of their role as prominent primary producers and carbonate sediment factories. Within the genus *Halimeda* there are several examples of cryptic species, making molecular analysis necessary for species identification. This study uses molecular methods to characterize the identity and distribution of *Halimeda* species found on San Salvador Island, the Bahamas. Samples were collected in shallow near-shore waters from nine sites on the north, south, and west sides of the island. The plastid encoded *rps*19-*rps*3 and the nuclear ribosomal ITS1-5.8S-ITS2 region were sequenced to identify the species. Microscopic morphological characters, such as the diameter of peripheral utricles, were measured and reconciled with the species identifications from molecular data. Of the 7 species we predicted based on previous observations of the island flora, *H. discoidea* and *H. tuna* were not molecularly identified; however, *H. scabra*, which was initially misidentified based on morphological observations in the field, was found in abundance. This and previous studies show that it is necessary to examine both molecular and morphological data when identifying *Halimeda.*

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[12] (WA) PUTTING *ASTEROCOLAX* IN ITS PLACE. **Jillian M. Freese** & Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI, USA.

While parasites are common throughout the tree of life, the extremely close relationship between parasitic red algae and their hosts makes them particularly distinct. These parasites are morphologically diminished, have reduced or entirely lack pigmentation, and are host specific. Limited to the Florideophyceae, red algal parasites are found in eight orders with the greatest diversity found in the Ceramiales. Within the Ceramiales, a third of the parasites in the Delesseriaceae are described in the genus *Asterocolax* (Feldmann & G. Feldmann). Since the Feldmann's initial description, several *Asterocolax* have been described infecting a number of new hosts, but few have been recognized as new species. Despite their extremely similar external appearance, each *Asterocolax* species likely evolved from its host. Two new Delesseriaceaen parasites have been found from Friday Harbor, San Juan Island, WA and Boulder Point, Barrow, AK. A phylogenetic analysis of the internal transcribed spacer region distributes *Asterocolax* throughout the tree, with the majority of parasites falling as sister species to their host. The initial description of algal species based on morphological characteristics led to the creation of parasitic genera, but molecular phylogenetics demonstrates that the *Asterocolax,* and probably many other red algal parasites, belong in the genera of their hosts. Here, we rename the *Asterocolax* parasites to reflect their phylogeny, and add two additional parasites to this complex and interesting clade.

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[13] (WA) *KOMAREKIELLA DELPHIKTHONOS* SP. NOV. (CYANOBACTERIA): AN EPIDERMAL CYANOBACTERIUM IMPLICATED IN AN ESTUARINE BOTTLENOSE DOLPHIN (*TURSIOPS TRUNCATUS*) FATALITY.

Amber O. Brown[1], Amanda Foss[2], **Alyssa D. Garvey[1]**, Quincy A. Gibson[1], Chelsea D. Villanueva[1] & Dale A. Casamatta[1]. [1] University of North Florida, Department of Biology, Jacksonville, FL. [2]Greenwater Laboratories/CyanoLab, Palatka, FL.

Cyanobacteria are a diverse set of photosynthetic, prokaryotic organisms that are integral to most aquatic ecosystems with many species having the ability to produce toxic secondary metabolites, known as cyanotoxins. Many of these cyanotoxins are associated with harmful algal blooms (HABs), which can have deleterious impacts on aquatic animals and ecosystems. The St. Johns River (SJR, Jacksonville, FL, USA) is characterized by recurrent HABs and diverse toxin-producing cyanobacterial taxa, while also providing a critical habitat for a distinct community of bottlenose dolphins (*Tursiops truncatus*). On January 15, 2015, an adult male dolphin, known as “MKNA”, stranded in an oligohaline habitat with an epidermal algal mat present on the dorsal fin, flanks, peduncle, and fluke. Investigation of this mat revealed the presence of bacteria, fungi, and cyanobacteria. While gross necropsy was unable to determine cause of the death, subsequent toxin analysis revealed low levels of microcystins/nodularins (MCs/NODs) in MKNA’s hepatic tissue. Cultures of the epidermal mat produced a Nostocalean isolate that was closely aligned (98%) with the recently erected genus, *Komarekiella*. Additional toxin analyses were run on both the original epidermal mat sample and on samples grown in culture. ELISA analyses revealed MCs/NODs presence from the original sample and was confirmed via the MMPB technique. A total evidence approach of molecular, genetic, and ecological examination determined this isolate to have many unique characters, constituting the erection of a new species within the *Komarekiella* genus, *Komarekiella delphikthonos.* This discovery warrants an area of further investigation as toxic, epiphytic cyanobacteria may be a source of health decline and mortality for animals living within the SJR.

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[14] OPTIMIZING SITE SELECTION FOR KELP-OYSTER CULTIVATION SYSTEMS IN RHODE ISLAND.

Lindsay Green-Gavrielidis[1], Carol Thornber[1], Dave Ullman[2], Chris Kincaid[2], Austin Humphries[2,3]. [1]Department of Natural Resources Science, University of Rhode Island, Kingston, RI. [2]Graduate School of Oceanography, University of Rhode Island, Narragansett, RI. [3]Department of Fisheries, Animal, and Veterinary Sciences, University of Rhode Island, Kingston, RI.

There is a growing interest among shellfish farmers to transition from monoculture to polyculture or integrated multi-trophic aquaculture (IMTA) systems that incorporate kelp into their existing farms. IMTA systems consist of the co-culture of multiple species from different trophic levels and attempt to reduce environmental impacts through water quality improvement. Industry interest is driving an expansion of kelp-shellfish IMTAs, however little information is available to help farmers determine where these systems will be successful. The primary goal of this on-going research project is to develop a spatially explicit model that combines the biological requirements for kelp and oyster growth with the hydrodynamics of Narragansett Bay (NB). In order to determine conditions for optimal kelp growth, we established six kelp-oyster IMTAs in collaboration with industry partners across a biophysical and geochemical gradient; three sites were located in shallow coastal salt ponds and three in the deeper waters of NB. Reproductive sugar kelp (*Saccharina latissima*) was wild harvested, spawned, and cultured in a kelp nursery. Two 60m longlines of kelp seed string were deployed at each site; the first longline was deployed in early November 2017 and the second was deployed 3-5 weeks later to test for optimal planting time. By mid-February 2018, the average length of blades from the first and second planting ranged from 0.47 to 0.66 m and 0.15 to 0.39 m, respectively. Kelp length was similar at sites in coastal salt ponds and NB. This talk will discuss kelp production at our sites and the conceptual framework that we are using to develop a spatially explicit model to optimize kelp-oyster IMTA site selection.

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[15] ARCTIC AND ANTARCTIC *ZYGNEMA* SP. (ZYGNEMATOPHYCEAE) UNDER UV AND DESICCATION STRESS: A METABOLOMIC AND TRANSCRIPTOMIC APPROACH

Andreas Holzinger[1], Anderas Albert[2], Jenny Uhl[2], Martin Rippin[3], Burkhard Becker[3], Martina Pichrtová[4]. [1]Department of Botany, University of Innsbruck, Austria, [2]Research Unit Environmental Simulation, Helmholtz Centrum Munich (GmbH), Germany; [3]University of Cologne, Botanical Institute, Biocenter, Cologne, Germany; [4]Department of Botany, Charles University, Czech Republic.

Conjugating green algae (Zygnematophyceae) are considered to be closest algal relatives to land plants (Embryophyta) and therefore their common ancestor is supposed to have adaptations that enabled colonization of land. Today, several members of this group still grow in harsh aeroterrestrial environments. In Polar or high Alpine regions, some filamentous Zygnematophyceae often dominate and typically produce relatively large amounts of biomass. They however have to withstand UV radiation and desiccation in their natural environments. Zygenmatophyceae can form modified vegetative cells so-

called pre-akinetes over the growing season or by increased culture age (6-7 months), which are very resistant. These are permanent stages, rich in storage compound and lipids. Fatty acid composition shows a significant change upon pre-akinete formation. Metabolomics of young vegetative cells (1 month) and pre-akinetes show a clear shift of metabolites during this transition, e.g. osmotically active substances increase. In sun-simulation experiments with moderately increased UV-A and UV-B radiation, a high tolerance was found in pre-akinetes. On the metabolite level, the different strains (temperate *Zygnema* S, arctic *Zygnema* B and Anarctic *Zygenma* C) as well as vegetative vs. pre-akinete stage were clearly distinguishable. For the UV-tolerance, enhanced levels of phenolic compounds were induced particularly in young vegetative cells. *Zygnema* S was also exposed to 86% relative air humidity until the effective quantum yield ceased. When desiccation effects were investigated by transcriptomics, an up-regulation of protection mechanisms like ROS scavenging, DNA-repair, chaperons and aquaporins was found. This regulation was more pronounced in young vegetative cells from liquid cultures than in 7-month old cultures.

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[16] (PA) MEASUREMENT OF *PSEUDO-NITZSCHIA*'S (BACILLARIOPHYCEAE) PHYSIOLOGICAL ADAPTATIONS IN BETWEEN BLOOMS**.** **Kyla Kelly**[1], Amy Carlile[1], Gary Wikfors[2]. [1] Department of Biology and Environmental Science, University of New Haven, West Haven, CT. [2]National Oceanographic and Atmospheric Administration (NOAA) Northeast Fisheries Science Center, Milford, CT.

Pseudo-nitzschia has been known to produce the toxin domoic acid, which can cause amnesic shellfish poisoning in humans. Bloom events and domoic acid production are becoming increasingly common and severe. It has been hypothesized that seed populations of *Pseudo-nitzschia* reside in the aphotic zone and bloom when upwelling brings cells and nutrients to the surface. How this genus is able to survive for long periods of time without sunlight or a resting cyst stage currently is not known. Cultures of *Pseudo-nitzschia pungens* were incubated at 4℃ 0:24 light:dark for 10 weeks. Weekly subcultures were examined for changes in physiology by measuring intracellular lipid content, chlorophyll a, cell size and complexity, mortality, metabolic activity, photosynthetic efficiency, and oxygen. To determine how quickly cultures could recover, new medium was inoculated weekly to grow cells from each culture at 18℃ 12:12 light:dark, and optical density was measured. Initial results show that cell abundance, photosynthetic efficiency, and oxygen declined with increasing time spent in the dark. After an initial decline, intracellular lipid content increased for three weeks before slowly declining again. Phytoplankton often produce lipids when they are stressed, but lipids also are used as a backup energy store when nutrients are limited. Metabolic activity remained relatively constant, except for a sharp decline during week four, coinciding with a mass die off of cells. Metabolism subsequently returned to previous levels of activity. Cells have not been able to recover when grown in the light. It is likely that this species *Pseudo-nitzschia* is able to survive unfavorable conditions by adjusting physiology to conserve resources but has limited ability to recover from such conditions.

[17] ALGAE FOUNDATION – ALGAL-BASED EDUCATIONAL INITIATIVES THROUGH THE EFFORTS OF ITS ALGAE TECHNOLOGY EDUCATIONAL CONSORTIUM (ATEC) AND THE ALGAE ACADEMY**.** **Ira A. Levine**[1] & Tiffany Cannis[2]. [1]Algae Foundation and University of Southern Maine, Portland, ME. [2]Algae Foundation and Global Algae Innovations, Inc.

The Algae Foundation is a non-profit organization dedicated to all forms of algal-based education, and the mission to promote the "Power of Algae" to transform human society and the environment upon which it depends. Currently the Foundation is in it's the third of a four year ATEC Initiative to develop an educational curriculum for two community college degrees, one in Algal Biology and Cultivation, and another in Algal Biotechnology. The Algae Foundation's K-12 STEM initiative, The Algae Academy, is gaining national attention through its rollout of its algal-based curriculum kits.

The Algae Foundation's four-year DOE award to develop algal-based bioeconomy workforce preparation programs. The ATEC initiatives are providing training programs, adopted by community colleges across the nation. Secondly, the development of an algal-based retraining program entitled, Algae Cultivation Extension Short-courses (ACES) will support existing aquaculturists in expanding their skill sets and assisting with the development of multitrophic aquaculture enterprises. Lastly, the Algae Academy initiated its STEM initiative with 300 students in San Diego, California, USA area (2016) and expanded to two additional states, Michigan and Ohio, reaching nearly 5000 students during the Spring of 2017. This current year, the Algae Academy's goal is to expand to an additional three states (Maine, New Mexico, and Texas) reaching ~ 20000 students.

Accomplishments include: Initial graduating class of Santa Fe Community College's algal cultivation students scheduled for May 2018; initiation of the ATEC algal biotechnology degree program at Austin Community College (September 2018). Formal adoption of the ATEC curriculum has been established with five community colleges with ongoing discussions with an additional 9 more schools.

Introduction to Algae Massive Open Online Course (Algal MOOC) was released to the general public on February 15, 2018, co-produced with the University of California, San Diego and organized on the Coursera network platform. The Algal MOOC is free for all participants https://www.coursera.org/learn/algae

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[18] (WA) ARCTIC CRUSTOSE CORALLINE ALGAE ECOLOGICAL FUNCTION AND ABIOTIC FACTORS CONTROLLING THEIR DISTRIBUTION. **Arley F. Muth** & Ken H. Dunton. Marine Science Institute, University of Texas, Port Aransas, TX.

Crustose coralline algae (CCA) are ecologically important worldwide, however, few studies have focused on the significance of CCAs in the Arctic. On the Alaska Beaufort Sea coast, CCAs are common in Stefansson Sound, an area of glacially deposited boulders and cobbles that support a rich benthic community, including the Arctic endemic kelp *Laminaria solidungula.* This work explored how patterns of CCA cover decrease with proximity to the Sagavanirktok River mouth in Stefansson Sound. To better quantify the relationship between CCAs and other species, cobbles were collected from sites with varying CCA coverage and analyzed for algal biomass. Photo quadrats were used to determine kelp densities. When CCA was present, red algal biomass was reduced and kelp densities were three times greater than areas without CCA. Mesocosm experiments focused on the effects of salinity on the photosynthetic efficiency, pigment composition, and dissolution of CCA. Results indicated that low salinities alone affected CCA physiology, and novel, continuous pH data from the Boulder Patch suggests that salinity is likely the factor driving CCA distribution in Stefansson Sound, not pH. Future studies will continue to explore seawater chemistry changes and the effects of these changes on CCA presence within Stefansson Sound.

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[19] (WA) THE SPATIAL MODULE – NEW TOOLS AND APPLICATIONS IN THE MACROALGAE HERBARIUM PORTAL. **Brandon O'Brien[1]**, Christopher Neefus[1] & Benjamin Brandt[2]. [1]University of New Hampshire, Department of Biological Sciences**.** [2]Northern Arizona University, Merriam-Powell Center for Environmental Research and Department of Biological Sciences.

The Macroalgae Herbarium Portal (http://macroalgae.org/portal/index.php) is an online database of digitized and georeferenced macroalgae records compiled from 49 US herbaria. Here we introduce the Spatial Module, a new addition to the Herbarium Portal (http://macroalgae.org/portal/spatial/index.php). The Spatial Module provides a web-based platform for users to search, sort, and analyze macroalgae occurrence records within an intuitive map interface. Using these tools, users can import and edit vector and raster layer files, export layers and occurrence records, and visualize occurrences both spatially and temporally. A brief demonstration will highlight the use of these tools, and provide an example of the potential applications of the Spatial Module. Finally, we will discuss upcoming upgrades and future directions for the Macroalgae Herbarium Portal.

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[20] (WA) THERE AND BACK AGAIN: A PARASITES TALE. **Christopher Paight** & Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI.

Parasitism has been referred to as an "evolutionary dead end", because the transition to parasitism is unidirectional. Once an organism becomes an obligate parasite, it is likely to remain an obligate parasite due to the loss of metabolic pathways. *Nephromyces* is a genus in the parasitic phylum Apicomplexa, but has an apparent mutualistic relationship with *Molgula* tunicates. Support for a mutualistic relationship is based largely on a nearly 100% host infection rate with no known clearance of *Nephromyces*. Because transition away from obligate parasite is so rare, little is known about the evolutionary steps involved in such a transition - particularly in lineages with such a long history of obligate parasitism as Apicomplexa. In order to examine this unusual evolutionary transition, we sequenced transcriptomes from *Nephromyces* and its parasitic sister taxon, *Cardiosporidium ciona*, which is an excellent model for what *Nephromyces* might have looked like as a parasite. Both *C. ciona* and *Nephromyces* have tunicate hosts and bacterial endosymbionts, but each maintains a different lifestyle. A comparison of

Nephromyces, C. ciona, and their endosymbionts will be presented with a focus on carbon and nitrogen dynamics from uric acid to glucose, vitamins and amino acids.

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[21] (WA) TRANSCRIPTOME CHANGES FOLLOWING SHORT-TERM LIGHT STRESS IN *BIGELOWIELLA NATANS*. **Pattarasiri Rangsrikitphoti** & Dion G. Durnford. Department of Biology, University of New Brunswick, Fredericton, New Brunswick, Canada.

Chlorarachniophytes are marine amoeboflagellates within the Rhizaria (SAR supergroup) whose plastid was acquired secondarily via a green algal endosymbiont. For a photosynthetic endosymbiont to evolve into a plastid, the transcriptional regulatory network for responding to abiotic stresses, like changes in light intensity, would have to be integrated. This presumably requires both transfer of light-responsive genes from the endosymbiont to the host and modification of host gene expression to appropriately respond to photo-oxidative or light-limitation stress. However, the light response mechanism has not been studied in chlorarachniophytes. We conducted an RNA-seq experiment to identify differentially-expressed genes in the model chlorarachniophyte, *Bigelowiella natans*, following four hours of high (HL) or very-low (VL) light, compared to a control low-light condition. In response to HL, there were increased expression of genes involved in Calvin-Benson cycle, primary metabolism, protein synthesis, and reactive-oxygen scavenging, all in an attempt to optimize photosynthesis, increase energy sinks, and minimize photo-oxidative stress. In contrast, a transfer to VL resulted in a reduced expression of genes involved in carbon fixation and the increase expression of genes to balance redox state in the mitochondria. Our data also suggest that the nucleomorph had little transcriptional response to light stress. Only a single, differentially expressed gene was identified in response to HL and none in VL, indicating key genes for light responsiveness were transferred into the host nucleus during plastid evolution. While many of the genes that changed expression in response to light intensity were derived from photosynthetic lineages, there were a large number that were likely from the host, based on top BLAST-hit identification. Here we propose that the host and endosymbiont responded to a common signal, making the regulatory integration of the endosymbiont genes with the host regulatory framework simpler in an evolutionary context.

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[22] MARINE MARCOALGAL EXTRACTS AND THEIR EFFECT AGAINST GRAM POSITIVE AND GRAM NEGATIVE HUMAN PATHOGENS. **Ursula S.R. Roese**, Andrea L. Call, Katharina H.C. Roese & Kristin M. Burkholder, Department of Biology, University of New England, Biddeford, ME.

Secondary metabolites in macroalgae have ecological functions in their marine environment, but they biomedical applications against human pathogens are still underexplored. Three macroalgal species, brown alga *Fucus vesiculosus*, and red algae species *Chondrus crispus* and *Ahnfeltia plicata* were collected from the intertidal zone of the Gulf of Maine and their identity confirmed by DNA barcoding. Algae were extracted with solvents of different polarity including methanol, dichloromethane and pentane. The antimicrobial activity of all extracts was investigated against an array of WHO priority pathogens. These microbes included four gram positive pathogens (methicillin-sensitive *Staphylococcus aureus* strain Newman (MSSA), methicillin-resistant *Staphylococcus aureus* (MRSA) strain USA300, *Bacillus cereus*, and *Listeria monocytogenes*) as well as five gram negative pathogens (*Pseudomonas aeruginosa*, *Proteus mirabilis*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, and *Escherichia coli*). Antimicrobial activity was tested in a disc diffusion assay followed by a Minimum Inhibitory Concentration (MIC) assay. All three algal species tested showed antimicrobial activity against several human pathogens. Extracts of the red alga *Ahneltia plicata* showed the highest potential, followed by *Chondrus crispus* and *Fucus vesiculosus*. Of the three solvents tested, extracts with the most polar solvent, methanol, showed the highest antimicrobial activity. Pentane, the least polar solvent, was the least effective at extracting the active compound. Of the nine human pathogens tested, six were inhibited by algae extracts. The six pathogens include two gram positive microbes, methicillin-sensitive *Staphylococcus aureus* strain Newman (MSSA) and methicillin-resistant *Staphylococcus aureus* (MRSA) strain USA300, as well as four gram negative pathogens, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Salmonella typhimurium*, and *Klebsiella pneumoniae*. Interestingly both, gram positive and gram negative human pathogens were affected. Gram-positive pathogens are often more susceptible to antimicrobial compounds, compared to gram-negative pathogens due to difference in cell wall structure.

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[23] *MALLOMONAS INTERMEDIA* AND *M. PSEUDOCORONATA*: NEOENDEMICS, RECENT MIGRANTS, OR PALEOENDEMICS? **Peter A. Siver**. Botany Department, Connecticut College, New London, CT.

The Synurophyceae is a well-supported clade of ecologically successful heterokont algae that are found almost exclusively in freshwater ecosystems. The group is characterized by formation of a highly organized cell covering consisting of precisely overlapping siliceous scales. Upon death of the organism, the scales can become incorporated into the sediment record and eventually fossilize. Many synurophytes are only known from specific geographic regions of the world, and are repeatedly listed as “endemics.” *Mallomonas intermedia* has a unique combination of characters and is often referred to as a flagship “European endemic.” Indeed, this species is a common element of phytoplankton communities across the continent, but has never been reported elsewhere….until now. Recently, *M. intermedia* was discovered thriving in a remote desert locality in western North America, and more interestingly in a 52 Ma fossil deposit also from western NA. These findings raise obvious questions regarding endemism status and suggest this species is perhaps more appropriately a paleoendemic and not a neoendemic. In similar fashion, *M. pseudocoronata* is a North American endemic, recorded from hundreds of localities across the United States and Canada. A decade ago, this species was uncovered growing in Arctic Russia in a region that was, interestingly, not covered with ice during the last glaciation. A few years later, *M. pseudocoronata* was reported forming blooms in a suite of lakes in southern Sweden that had been previously monitored for decades and never observed. Is this species a recent migrant to Sweden, or has it always been present? Additional findings that now "blur" the endemic status of other synurophyes (e.g. *M. multiunca* and *M. neoampla*) will be discussed.

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[24] (WA) ASSEMBLING THE NUCLEAR GENOME OF AN INVASIVE CHAROPHYTE. **Robin S. Sleith**[1,2] & Kenneth G. Karol[2]. [1]The Graduate Center, City University of New York, New York, NY, U.S.A. [2]Cullman Program for Molecular Systematics, New York Botanical Garden, Bronx, NY, U.S.A.

Understanding the ecological and evolutionary mechanisms by which a species becomes invasive is of central importance to theoreticians and conservationists alike. Invasions provide a natural experiment for investigating rapid evolution and the basis of adaptive variation. Aquatic invasive species have been identified as one of the leading causes of biodiversity loss and ecosystem decline in freshwater systems. We are sequencing and assembling the genome of *Nitellopsis obtusa* (Characeae) (Desv. in Loisel.) J. Groves, an aquatic invasive species, to allow fine scale analysis of allele frequency shifts in adaptive loci in response to novel environmental conditions in the invaded range. *Nitellopsis obtusa* is native to Europe and Asia where it is considered rare and endangered. The first collection of *N. obtusa* in North America was in the Saint Lawrence River in 1974, where it was hypothesized to be introduced by ballast water from trans-oceanic shipping. In 1983 it was recorded in the St. Clair-Detroit River system in Michigan and has spread rapidly throughout Michigan's inland lakes, northern Indiana, western New York and in isolated areas of Minnesota, Pennsylvania, Vermont and Wisconsin. We use a combination of short read (Illumina) and long read (PacBio) evidence to assemble a genome estimated to be 2-3 gigabases. A range of assemblers (ABySS, Canu, SOAPdenovo) were assessed to determine the best assembly algorithm. MAKER was used to annotate contigs using evidence-based annotations from *Arabidopsis*, *Amborella*, *Physcomitrella*, and *Klebsormidium*. Genome assembly and annotation completeness was analyzed using the BUSCO pipeline. The phylogenetic placement of *N. obtusa* in the green algal group closely related to land plants will have important implications for understanding the adaptations to life on dry land. Furthermore, investigation of non-model organisms has been identified as a valuable source of genomic and evolutionary information that enable powerful comparative genomic analyses.

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[25] (WA) PARALYTIC SHELLFISH TOXINS IN NEW YORK STATE FRESHWATER. **Zacharias J. Smith** and Gregory Boyer. State University of New York College of Environmental Science and Forestry, Syracuse, NY.

Most research in the United States on freshwater cyanobacteria toxins has focused on the occurrence of microcystins. However, the rich diversity in cyanobacteria flora may suppose a presence of other cyanobacterial toxins. Paralytic Shellfish Toxins (PSTs) are known to be produced by cyanobacteria genera commonly found in New York Lakes. In the Northeast United States, reports of PST production by cyanobacteria have appeared in the literature, but little is known about the frequency of appearance, levels of toxin present in surface water, or the analogs that are produced. Freshwater samples collected between 2016 and 2017 from a wide variety of lakes across New York were analyzed for PSTs by HPLC with post-column oxidation and fluorescent detection. PST presence was confirmed using Abraxis PST ELISA assays. A description of the monitoring program, analytical techniques, and assessment of surface water toxicity will be presented.

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[26] (WA) MULTI-MARKER METABARCODING ASSESSMENT OF BIODIVERSITY WITHIN STREAM BIOFILM COMMUNITIES ALONG AN ACID MINE DRAINAGE RECOVERY GRADIENT.

Daniel I. Wolf & Morgan L. Vis. Environmental and Plant Biology, Ohio University, Athens, OH, U.S.A.

In southeastern Ohio, historical coal mining has exposed streams to acid mine drainage. Active remediation of these streams has proven to be successful for some streams, while others have not recovered based on macroinvertebrate assessment. In this study, biofilms were collected from three improving not recovered streams, three recovered streams, and two unimpaired streams. The biodiversity was characterized by metabarcoding using four barcode markers and high-throughput amplicon sequencing. Two universal markers, 16S for prokaryotes and 18S for eukaryotes, were sequenced along with the algal chloroplast specific marker (UPA) and a diatom chloroplast specific marker (*rbc*L). For each marker, the ordination of Bray-Curtis Index calculated from the total operational taxonomic units (OTUs) present in each stream showed the unimpaired and recovered streams clustered, while improving not recovered streams were more distant. Focusing on the algal OTUs only, the Shannon index for the *rbc*L and UPA markers showed significantly lower alpha diversity in improving not recovered streams compared to unimpaired streams, but the recovered streams were not significantly different from the other two stream types. Further examination of the UPA marker revealed a decrease in relative abundance of diatoms and increase of cyanobacteria in improving not recovered streams compared to recovered and unimpaired streams. The same 10 algal phyla were identified with the 18S and UPA marker, but the UPA included Cyanobacteria as well. A total of 21 diatom genera were identified from the *rbc*L marker data and these were investigated for taxa that have been reported to be indicators of high water quality. *Cymbella*, *Encyonema*, and *Cocconeis* were observed in higher relative abundance in recovered and unimpaired streams than in improving not recovered streams. Overall, results from this study support previous findings using other methods to assess stream impairment from AMD.

Poster presentation abstracts **(in alphabetical order by presenting author)** PA = President's Award Candidate, TA=Trainor Award Candidate.

[27] INVESTIGATING THE PHYSIOLOGICAL FUNCTION OF GFA IN *PHAEODACTYLUM TRICORNUTUM*. **Katherine Battey** & Deborah Robertson. Biochemistry and Molecular Biology, Clark University, Worcester, MA.

Formaldehyde dehydrogenase (FALDH) is a dual catalytic enzyme that is responsible for 1) the oxidation of formaldehyde to glutathione and formate and 2) the nitrosation of proteins, which has been hypothesized to play a role in stress response and signaling. In diatoms, the number of genes encoding FALDH varies and a positive relationship between the number of copies of FALDH and the ability to metabolize formaldehyde has been shown. In *Phaeodactylum tricornutum* there is only a single copy of FALDH and unlike other diatoms*, P. tricornutum* has a gene encoding the Glutathione-Formaldehyde Activating protein (GFA), the function of which is not understood in diatoms. To better understand the physiological role of GFA, expression of GFA and FALDH was monitored following the addition of exogenous formaldehyde and during a diurnal light cycle. GFA transcript levels were increased in the presence of formaldehyde, suggesting a role in formaldehyde metabolism. Future experiments will examine the expression of GFA and FALDH during a diurnal light cycle to better understand the role of these enzymes in modulating stress responses and protein nitrosation.

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[28] (PA) TERMINATOR OR BIOREMEDIATOR: CONTRASTING EFFECTS OF *ULVA LACTUCA* IN COASTAL AREAS**. Haley Barravecchia, Sarita Chiu** & Paulette Peckol. Biological Sciences, Smith College, Northampton, MA.

Ulva lactuca is an abundant seaweed in rocky intertidal and shallow subtidal areas, often co-occurring with other common macroalgae, such as *Fucus vesiculosus* and *Chondrus crispus*. While *Ulva* spp. release an allelochemical substance, likely acrylic acid, that results in high mortality of invertebrates and microalgae, this species also accumulates pollutants such as heavy metals. Thus, *Ulva* spp. may serve a role of bioremediation in polluted, coastal areas. We investigated these dual roles of *U. lactuca* in laboratory experiments aimed at characterizing toxic and bioremediation effects. Both *F. vesiculosus* and *C. crispus* had significantly lower growth rates when held in the presence of *U. lactuca* compared with single-species treatments. Notably, *Chondrus* fronds bleached white and individuals died after several days' contact with *Ulva*. We simulated high, mid, and low intertidal tidepools by varying flushing rates. Mixed-species treatments *(Fucus* and *Ulva* or *Chondrus* and *Ulva*) showed a clear flushing effect, with fronds held in high and mid tidepool conditions demonstrating much lower growth rates compared with the single-species treatment. Growth of *Fucus* and *Chondrus* receiving frequent flushing (simulated low intertidal pools) showed less variation between single- and mixed-species treatments, though the difference remained significant for *C. crispus*. In contrast, *U. lactuca* growth was similar when held in single- or mixed-species treatments across the flushing gradient. These results suggest that under conditions of high biomass, *U. lactuca* may strongly affect macroalgal distribution and abundance patterns in coastal areas, particularly in tidepool assemblages. However, we measured copper uptake and accumulation by *U. lactuca* across a concentration gradient, indicating that this species may bioremediate coastal pollution. In a natural setting, bioremediation is likely more successful where this species is prolific, such as under eutrophic conditions. These contrasting effects of *U. lactuca* highlight the complex role of this species in coastal systems.

[29] (PA) EFFECTS OF BOAT FUEL ON WATER CHEMISTRY OF LAKE ERIE. **Cole Beale** & Sarah Whorley. Department of Natural Sciences, Daemen College, Amherst, NY.

Western New York provides many opportunities for public access to Lake Erie. In the summer months the lake sees an increase in usage for leisure purposes. With 17 boat launches available for public use in Erie Country, there are many opportunities for large amounts of the population to use the lake. Areas of higher boat traffic are exposed to unnatural conditions caused by exposure to boat fuel. Boat fuel contains heavy metals, specifically lead, that can create harmful conditions in the lake. Common metal ions in the water column were all below detection levels, however lake water was uniformly high in Na+. Phytoplankton taxonomy was dominated by *Fragillaria crotonensis*, however several deep water samples have higher concentrations of *Microcystis* than samples from near shore. Phytoplankton essential fatty acid and lead concentrations will indicate further ecosystem patterns with regard to recreational boating patterns on eastern Lake Erie.

[30] (PA) RESOLVING THE RED ALGAL DIVERSITY OF RHODE ISLAND THROUGH DNA BARCODING. **Alicia Beauvais**[1] & Brian Wysor. Department of Biology, Marine Biology & Environmental Science, Roger Williams University, Bristol, RI.

Comprehensive species inventories are required to monitor for changes in community structure resulting from global climate change and biological invasions. For marine macroalgae, phenotypic plasticity, morphological convergence, and species hybridization complicate specimen identification, such that molecular tools are required for elucidating species richness. As part of a larger project to establish a comprehensive species inventory for marine macroalgae in Rhode Island, we characterized the morphological and molecular diversity of three genera (*Polysiphonia, Melanothamnus,* and *Vertebrata*) of the red algal family Rhodomelaceae, which has a history of challenging identification and problematic taxonomy. Based on morphological and molecular work, nine species have been identified in Rhode Island, including two introduced species. Given prevailing currents and trends of increasing sea surface temperature, some 16 additional species that are known from southern U.S. coastlines, and 11 species that are known to be introduced around the world, might be expected to disperse and establish populations in Rhode Island waters in the future. This work establishes a firm molecular basis for monitoring

Rhode Island algal diversity, which is especially important given the disproportionate incidence of species introductions from the Rhodomelaceae.

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[31] (PA) MACROALGAE AS BIOINDICATORS FOR MERCURY CONTAMINATION IN THE LONG ISLAND SOUND. **Cassandra Bhageloo**[1], Vincent Breslin[2], Sean Grace[3]. [1]Chemistry Department, Southern Connecticut State University, New Haven, CT; [2]Environment, Geography and Marine Sciences Department, Southern Connecticut State University, New Haven, CT; [3]Biology Department, Southern Connecticut State University, New Haven, CT.

The objective of this study was to determine the effectiveness of macroalgae as bioindicators for mercury contamination in Long Island Sound. Characteristics that make macroalgae good bioindicators for metal contamination include wide distribution and abundance, ease of collection and identification, year round availability, and tolerance of a wide variety of temperatures and salinities. This study focused on determining the mercury content of six species of macroalgae including green (*Ulva lactuca, Codium fragile*), brown (*Fucus vesiculosus, Fucus distichus*) and red (*Chondrus crispus*, *Grateloupia turutura*) algae sampled from seven locations (Stamford to Westbrook) in fall 2017 along the Connecticut shoreline. Freeze-dried algae tissue samples (0.100-0.250 g) were analyzed directly for mercury by thermal decomposition amalgamation and atomic absorption spectrophotometry using a Milestone DMA-80 direct mercury analyzer. Good agreement was achieved for measured and certified mercury concentrations (18.6 µg/kg) from European Reference Material (ERM) CD200 Bladderwrack (*Fucus vesiculosus*). Results showed that macroalgal tissue mercury concentrations in Long Island Sound varied by species. *Codium fragile* tissue mercury contents were lowest and ranged from 3.5 µg/kg in Norwalk to 8.1 µg/kg in Milford. Highest measured mercury concentrations were measured in *Fucus vesiculosus* with concentrations ranging from 28.4 µg/kg in New Haven to 42.1 µg/kg in Norwalk. In general, mercury concentrations were lowest in green algae species, intermediate in red algae species and highest in brown algae species.

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[32] CHARACTERIZATION OF SAR CLADE COMMUNITY COMPOSITION IN INDONESIAN MARINE ENVIRONMENTS. **Erin Borbee**[1], Austin Humphries[2], Hawis Madduppa[3], & Christopher Lane[1]. [1]Department of Biological Sciences, University of Rhode Island, Kingston, RI. [2]Department of Fisheries and Animal Science, University of Rhode Island, Kingston, RI. [3]Department of Marine Science & Technology, Faculty of Fisheries & Marine Sciences, Bogor Agricultural University, Bogor, Jawa Barat, Indonesia.

Stramenopiles, Alveolates, and Rhizaria make up a major branch in the eukaryotic tree of life. The wide diversity in both morphology and ecological function within the SAR clade makes it an interesting focus for biodiversity research but SAR diversity is poorly understood, particularly among microbial members. This project is aimed toward expanding the molecular data available on the SAR clade to help better understand the true diversity of the group, while also trying to identify areas in which SAR biodiversity is high. We have collected water samples from various marine environments around Indonesia, with a particular focus on samples from reefs with different levels of protections from fishing pressure (i.e. open access, fully protected zones). Using high-throughput sequencing of the V9 region of 18S rRNA gene, we have begun to characterize the eukaryotic communities at the different sampling sites. Ongoing work is focused on identifying major groups and patterns in SAR abundance and diversity of these regions in the context of fisheries protection status to give us a better understanding of the ecosystem-level effects of management.

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[33] (PA) ANTIMICROBIAL ACTIVITY OF RED AND BROWN ALGAE AGAINST MRSA AND OTHER GRAM POSITIVE BACTERIA. **Andrea L. Call**, Katharina H.C. Roese, Kristin M. Burkholder, Ursula S.R. Roese, Department of Biology, University of New England, Biddeford, ME.

Three macroalgae species on the rocky intertidal coast of Maine, *Ahnfeltia plicata*, *Chondrus crispus*, and *Fucus vesiculosus,* were explored as a source of bioactive compounds. This research focuses on the potential use of these compounds against four gram positive microbes, deemed by the Worlds Health Organization as priority pathogens in regards to the need for antibiotic development. These four microbes include methicillin-resistant *Staphylococcus aureus* (MRSA) strain USA300, methicillin-sensitive *Staphylococcus aureus* strain Newman (MSSA), *Bacilllus cereus*, and *Listeria monocytogenes.* Extracts were prepared from all three algae species using solvents of varying polarity including methanol, dichloromethane, and pentane. Antimicrobial properties were then evaluated in a disk assay. Of the three solvents, methanolic extracts were the most active, which was seen through greater inhibition of the target microbes. *Ahnfeltia plicata* showed the most activity against the pathogens, with *Chondrus crispus* being the second most active and *Fucus vesiculosus* the least. Of the four pathogens tested against, the extracts only showed activity against methicillin-resistant *Staphylococcus aureus* (MRSA) strain USA300 and methicillin-sensitive *Staphylococcus aureus* strain Newman (MSSA). In comparison to the commercial antibiotic controls, some of the algae extracts showed greater antimicrobial capacity, with regards to the inhibition of microbial growth.

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[34] (TA) THE INVASIVE RED ALGA *GRATELOUPIA TURUTURU* (HALYMENIALES, RHODOPHYTA) REACHES MID-COAST MAINE: ARE CURRENT BIOSECURITY MEASURES ENOUGH? **Kyle Capistrant-Fossa**[1] and Susan H. Brawley. School of Marine Sciences, University of Maine, Orono, ME.

The invasive red alga *Grateloupia turuturu* was discovered in the effluent from the Darling Marine Center's (DMC) seawater lab in Walpole, ME. This represents over 200 km of expansion in its range along the New England shore. The site of the invasion was monitored monthly from September 22, 2017 - February 14, 2018. The only position along the DMC shore (~280 m) where *G. turuturu* was found was the original site of discovery. Multiple life history stages were found: tetrasporophytes (September), carposporophyte (October), and vegetative (November/February). Large blades in February had some damaged green areas where blades were partially exposed to cold air temperatures, but small blades underneath the seawater were not damaged. Current regulation by the Maine Department of Marine Resources requires disinfection through chlorination by 50 ppm free chlorine for 2h for shellfish broodstock waste. This treatment was tested on the red alga *Porphyra umbilicalis* because there was not enough test material of *G. turuturu* available. The *Porphyra* developed small green patches following treatment, but the damage did not spread during recovery. Additionally, the free chlorine concentration of the seawater had dropped to less than 10 ppm at the end of the 2h period. This evidence suggests that the government biosecurity regulations may not be effective and need review.

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[35] (TA) UNRAVELING THE RELATIVE GEOGRAPHICAL DISTRIBUTION OF KELP GAMETOPHYTES AND SPOROPHYTES IN THE NORTHWEST ATLANTIC AND CANADIAN ARCTIC. **Marie Dankworth** and Gary W. Saunders. Centre For Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

Intensive research has been conducted in recent decades on species of the Laminariales, but the focus has been largely on the macroscopic sporophyte generation. In the Bay of Fundy (northwest Atlantic) sea surface temperature has risen 1.0 °C per decade on average since the early 1980’s, particularly during spring and autumn. Northward range shifts have already been reported for intertidal species and pelagic fish communities in this region. We are interested in how this change is impacting both life history stages of kelp species. The objectives of our study are: (1) to assess the presence of the microscopic stage of *Saccharina nigripes* relative to the macroscopic stage in the Bay of Fundy. This local ecological survey will provide new insights on kelp community composition in the study area and shed light on the presence of “banks of microscopic stages.” (2) We will explore the distribution of *Alaria esculenta* and *Agarum clathratum* over time along the New England coast relative to contemporary gametophyte distributions. (3) We will explore cryptic diversity of the brown algal seaweed flora in the Canadian Arctic with a focus on microscopic stages and species. To address these research questions, we will use: (1 and 2) PCR amplification of the nuclear internal transcribed spacer (ITS) region with species-specific primers to detect gametophytes (from randomly sampled rock scrapes) and sporophytes (from small pieces of randomly sampled thalli) from several locations in the Bay of Fundy (1) and along the New England coast (2); and, (3) develop metabarcoding methodologies to determine the distribution of kelp gametophytes and other microscopic brown algae in the Canadian Arctic from a variety of field sources (e.g. rock scrapes).

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[36] (PA) POTENTIAL RISK OF -METHYLAMINO-L-ALANINE IN EASTERN LAKE ERIE AND EFFECTS OF NEUROTOXIN IN *DANIO RERIO*. **Maria C. DeLuna** & Robert Gunther. Daemen College, Amherst, NY.

Cyanobacteria, also known as blue-green algae (BGA), may produce neurotoxins that are destructive to nervous tissue (Cox et al., 2003). Beta-Methylamino-L-alanine (BMAA) is a neurotoxic, non-proteinogenic, amino acid released from cyanobacteria, which has been linked to neurodegenerative diseases such as Alzheimer disease (AD) and Amyotrophic Lateral Sclerosis (ALS) (Murch et al., 2004). The purpose of this study was to identify genera of cyanobacteria from water samples of Lake Erie and show bioaccumulation of BMAA in *Danio rerio* (zebrafish) from the algae identified in Eastern Lake Erie. Water samples collected from Lake Erie were analyzed and two kinds of BGA were identified known as *Chroococcus* and microcystins. Next, *Danio rerio* were co-cultured with *Chroococcus* for 5 weeks. Zebrafish samples were homogenized and then zebrafish, algae, and water samples were analyzed using a competitive ELISA. The data shows high concentration of BMAA across the samples. Unexpected high levels of BMAA in these samples warrants further investigation.

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[37] CADMIUM SEQUESTRATION IN THE GREEN ALGAE *CHARA AUSTRALIS*. **Kaitlynn Donahue** & Mary Bisson. Department of Biology, University of Buffalo, Buffalo, NY.

Chara australis has previously been examined for its ability to sequester heavy metal cadmium (Cd) from soil as a potential method of phytoextraction. Previous findings have shown that in the presence of a Cd stress, zinc (Zn) acts to protect against Cd toxicity by an unknown mechanism. We hypothesize that Cd tolerance is related to the alga's ability to sequester Cd from the cytoplasm into the vacuole, thus decreasing stress on metabolic pathways. Preliminary experiments have been preformed to isolate the cytoplasm and vacuole of *C. australis* internode cells that were incubated in Cd. ICP-MS results have shown that Cd accumulates at higher concentrations in the large central vacuole of *C. australis* compared to the cytoplasm in the presence of Zn.

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[38] (TA) USING ANCIENT DNA TO STUDY TRENDS IN PALAEOPLANKTONIC ASSEMBLAGES SINCE THE LAST GLACIAL MAXIMUM IN BAFFIN BAY, CANADA. **Joshua R. Evans[1]**, Audrey Limoges[2], Adrian Reyes-Prieto[1] & Gary W. Saunders[1]. [1]Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB, Canada; [2]Earth Sciences, University of New Brunswick, Fredericton, NB, Canada.

In recent decades, climate change has significantly altered the Arctic Ocean more than any other ocean basin. These alterations are driven by multiple environmental factors that may act alone or in concert with one another, including: increased near-surface atmospheric temperatures; multi-year sea-ice loss; and changes in the freshwater budget and dominant ocean circulation patterns. These abiotic factors directly impact planktonic assemblages that form the foundation of marine food webs, and remains of these organisms have been used as proxies for reconstruction of past environmental conditions and ocean productivity. Contemporary palynological studies of marine ecosystems have benefitted from studies of planktonic microfossils and lipid biomarkers preserved in sediments, but these proxies demonstrate limited taxonomic resolution and can only target a certain number of taxonomic groups. Ancient DNA (aDNA) is an emerging proxy that is unbiased to the many organisms that lack diagnostic physical remains, and the high resolution and diversity of taxonomic units can be used for robust surveys of palaeoenvironments. We plan to isolate environmental aDNA from sediment cores collected in Baffin Bay, Canada and use next-generation sequencing to target the V9 region of general eukaryotic and phytoplankton 18S rRNA to investigate biological community shifts and coastal open-water (polynya) formation since the onset of the Holocene (~11,600 years ago). We will highlight preliminary protocols developed for plankton aDNA research, such as essential laboratory space requirements and controls, and present trial protocols for isolation and amplification of aDNA. This approach can be combined with pre-existing and newly generated traditional proxy datasets to validate and extend our knowledge of marine plankton palaeoecology and environmental variability in the Arctic during the Holocene.

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[39] *DISPORA SPECIOSA*, THE FIRST COCCOID MEMBER OF MICROSPORACEAE.

Karolina Fučíková[1] & Lenka Štenclová[2]. [1]Assumption College, Department of Natural Sciences, Worcester, MA. [2]University of South Bohemia, Department of Botany, Na Zlaté Stoce 1, České Budějovice, Czech Republic.

The clade that currently represents the family Microsporaceae in molecular phylogenies is one of the few filament-forming groups of Chlorophyceae. Its members are the type genus *Microspora* and the more recently circumscribed genus *Parallela*, whose filaments are more loosely arranged and often multiseriate. We initially investigated the enigmatic bog-loving *Dispora speciosa* as a putative member of crucigenioid chlorophytes based on its two-dimensional colony formation. However, our plastid and nuclear ribosomal phylogenies confidently placed *Dispora* within the genus *Parallela* instead, and therefore distantly related to crucigenioids. Upon further examination of the cell morphology and ultrastructure using light, fluorescent, and electron microscopy, we found several corresponding features between *Dispora* and *Parallela*, despite *Dispora*'s apparently coccoid-colonial gross morphology. Both genera have cells with a parietal plastid positioned around a large central nucleus. The loose, multiseriate filament formation in *Parallela* can be interpreted as similar to *Dispora*'s flat colony formation in its natural state. Because we only present data from one non-type species and strain of *Dispora*, we cannot merge the entire genus with *Parallela*. We do however argue that *D. speciosa*, of which this strain is the sole available, morphologically and ecologically faithful representative, should be moved into *Parallela*, and the strain ACOI 1508 be designated as type. Our study also impacts the current view on evolution of multicellular (colonial and filamentous) forms in Chlorophyceae.

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[40] CHLOROPLAST GENOMES OF THREE CLOSELY RELATED *HALAMPHORA* SPP. (BACILLARIOPHYCEAE): A CASE OF CONSERVED GENE CONTENT AND EXTENSIVE GENOME REARRANGEMENT. **Sarah E. Hamsher**[1,2], Kyle G. Keepers[1], Cloe S. Pogoda[1], Joshua G. Stepanek[3], Nolan C. Kane[1], & J. Patrick Kociolek[1]**.** [1]Department of Ecology and Evolutionary Biology and Museum of Natural History, University of Colorado, Boulder, CO, [2]Biology Department, Temple University, Philadelphia, PA. [3]Department of Biology, St. Cloud State University, St. Cloud, MN.

Diatoms are the most diverse lineage of algae, but the diversity of their chloroplast genomes, particularly within a genus, has not been well documented. Herein, we present three *Halamphora* chloroplast genomes (*H. americana*, *H. calidilacuna,* and *H. coffeaeformis*), the first pennate diatom genus to be represented by more than one species. *Halamphora* chloroplast genomes ranged in size from ~120 to 150 kb, representing a 24% size difference within the genus. All three species shared a set of 161 features, including 129 protein-coding genes, three rRNAs, 27 tRNAs, one tmRNA, and a signal recognition particle RNA *ffs*. Differences in genome size were due to changes in the length of the inverted repeat region, intergenic regions, and the variable presence of ORFs that may encode as-yet-undescribed proteins. A comparison of these data to three previously published chloroplast genomes in the genus *Cyclotella* (Thalassiosirales) revealed that *Halamphora* has undergone extensive chloroplast genome rearrangement at the genus level. Studies such as these provide deeper insights into diatom chloroplast evolution and important genetic resources for future analyses.

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[41] (PA) A NEW SPECIES FROM BERMUDA SPLIT FROM THE PANTROPICAL *DIGENEA SIMPLEX* COMPLEX (RHODOMELACEAE, CERAMIALES). **Bilal F. Hamzeh**[1], Craig W. Schneider[1], Christopher E. Lane[2] & Gary W. Saunders[3]. [1]Department of Biology, Trinity College, Hartford, CT. [2]Department of Biological Sciences, University of Rhode Island, Kingston, RI. [3]Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

Using mitochondrial COI-5P as a barcode marker, the red algal species previously identified as *Digenea simplex* in Bermuda is found to be distinct from this species found in the Adriatic (type locality) and Mediterranean Seas, as well as other tropical locations worldwide. This finding led to a comparative study of the morphology of Bermuda specimens and *D. simplex* from the type locality, as well as other congeners. Our data show the Bermuda specimens to be morphologically, as well as genetically, distinct from *D. simplex* necessitating the description of *D. arenahauriens* sp. nov. for plants found in the islands and a single collection from the Caribbean Sea. It represents the first species partitioned from the "pantropical" *D. simplex* and we present genetic evidence of additional undescribed isolates in the species complex requiring further study.

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[42] STOMATOCYST PRODUCTION AND ENVIRONMENTAL INDUCEMENT IN *OCHROMONAS PINGUIS*, A MIXOTROPHIC CHRYSOPHYTE. **Dale A. Holen**. Pennsylvania State University, Dunmore, PA.

Under controlled laboratory conditions stomatocyst production was induced in the mixotrophic chrysophyte *Ochromonas pinguis*. During the early stages of stomatocyst development the cell enlarges significantly and secretes a gelatinous sheath that encircles the flagellate cell. The mature stomatocyst is spherical to slightly oval and ranges in size from 17.4 – 19.2 µm (length) to 15.7 – 16.9 µm (width) and consists of a smooth primary and ornamented secondary wall. The secondary wall was festooned with thick lunate ridges, some predominately elevated and plate-like in appearance. Morphologically immature but vacant stomatocysts were also observed suggesting successful excystment ensued before complete cyst development. Both uni- and bi-nucleate stomatocysts were produced. When subjected to chemical and physical perturbations stomatocyst production by *Ochromonas* ensued under all conditions except when grown in complete darkness. The rate of stomatcyst production was very low with, on average, 0.002 – 0.01% of the population undergoing encystment.

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[43] (PA) THE PARADOX OF *DE NOVO* PURINE SYNTHESIS WITHIN PARASITIC PHYLUM APICOMPLEXA. **Liz Hunter**, Chris Paight, & Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI.

Apicomplexa is a phylum synonymous with obligate parasitism, containing several species of significance for human health, including *Plasmodium*, *Toxoplasma*, and *Cryptosporidium*. Parasites rely heavily on their hosts for nutrients and basic metabolites, and as a consequence they often lose genes and pathways critical for free living organisms. One such example is the *de novo* synthesis of essential purine nucleotide inosine monophosphate, the immediate precursor for nucleotides adenine and guanine. The genus *Nephromyces* reportedly has a commensal relationship with its host, which seems unlikely given known gene losses in apicomplexa. To investigate the mechanisms behind a potential lifestyle transition, we sequenced transcriptome data from *Nephromyces* and parasitic sister taxon *Cardiosporidium*. A novel method of concentrating *Cardiosporidium* from the infected heart blood of wild populations using stained sucrose density gradients was developed to surmount the obstacles associated with sequencing this organism, which occurs in relatively low density *in vivo*. These gradients allowed for the generation of a significantly more complete RNA dataset and transcriptome of *Cardiosporidium.* Surprisingly, annotation indicates that both taxa have retained purine metabolism pathways long since lost in other apicomplexans. In combination with a genome and transcriptome previously generated from *Nephromyces*, these two data sets support the presence of a functional *de novo* purine synthesis pathway unique to this apicomplexan lineage.

[44] MERCURY SORPTION IN CHONDRUS CRISPUS (STACKHOUSE 1797) IN LONG ISLAND SOUND COASTAL HARBORS. **Lela Jackson**[1], Vincent Breslin[2] & Sean Grace[3]. [1]Chemistry, Worcester Polytechnic Institute, Worcester, MA; [2]Environment, Geography and Marine Sciences Department, Southern Connecticut State University, New Haven, CT; [3]Biology Department, Southern Connecticut State University, New Haven, CT.

Mercury is found naturally in the environment as elemental mercury (Hg) or mercury (II) sulfide (HgS). These chemical forms of mercury can be converted via anaerobic processes in sediment to monomethyl mercury (CH_3Hg) and bioaccumulate in marine food webs. Coal combustion and municipal wastewater discharges in industrial areas are major sources of mercury in coastal harbors and associated watersheds. Changes in coastal human population density, and associated industrial activity, from New York City to eastern Rhode Island is suspected to be responsible for contributing to a gradient of high to low sediment mercury contamination from west to east in Long Island Sound (LIS). Previous studies have shown that the red alga *Chondrus crispus* is capable of absorbing monomethyl mercury through its cell membranes, making the species a potential bio-indicator of mercury contamination in coastal harbors. This study examined the red alga *C. crispus* from six Connecticut harbors sampled in fall 2016 and measured the tissue mercury concentration via atomic absorption using a Milestone Direct Mercury Analyzer (DMA-80). Results of these mercury determinations were used to examine trends of mercury contamination along the northern coastline of LIS relative to the population and industrial activity surrounding each harbor. Mercury measurements using a Milestone DMA-80 accurately and precisely measured mercury in standard reference seaweed (*Fucus*; ERM-CD200; 19.2 ± 1.9 µg/kg). Results do not show a clear pattern of mercury contamination in *C. crispus* from west to east along the Connecticut coastline. Mean tissue mercury contents ranged from 10.6 µg/kg in New Haven harbor to 22.6 µg/kg in Westbrook harbor.

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[45] CHARACTERIZATION OF A NEW SPECIES IN THE GENUS *DIDYMOSPHENIA* AND OF *CYMBELLA JANISCHII* (BACILLARIOPHYTA) FROM CONNECTICUT, USA. **Diba Khan-Bureau**[1, 2], Eduardo A. Morales[3], Luc Ector[4], Michael S. Beauchene[5], & Louise Lewis[6]. [1]Natural Resources & the Environment, University of Connecticut, Storrs, CT. [2]Three Rivers Community College, Norwich, CT. [3]Laboratório da Água Universidade de Évora Parque, Évora, Portugal. [4]Luxembourg Institute of Science and Technology, Environmental Research & Innovation Department, Grand-duchy of Luxembourg. [5]Inland Fisheries Division, Department of Energy & Environmental Protection, Hartford, CT. [6]Department of Ecology & Evolutionary Biology, University of Connecticut, Storrs, CT.

Two non-native stalk-forming diatoms that were observed in the West Branch of the Farmington River, a tributary of the Connecticut River in Connecticut, are characterized morphologically and barcode marker sequences were obtained. *Cymbella janischii*, the dominant stalk-forming species during the summer of 2012, previously had not been found in the northeastern USA. Samples of *C. janischii* were examined microscopically and used to obtain four sequences of the barcode marker, the V4 region of the 18S rDNA gene. Phylogenetic analysis indicated that the four independent sequences of *C. janischii* were distinct from, but closely related to, published sequences of *C. janischii* and *C. mexicana*. A second non-native stalk-producing diatom, resembling *Didymosphenia geminata*, was examined in 2013 and first reported as *Didymosphenia* sp. The observed cells had a compressed morphology and were smaller than *D. geminata*. Sequences of the V4 region, obtained from three independent direct PCR reactions of single cells isolated from the Connecticut samples, indicated a close relationship to three published sequences of *D. geminata* from Italy, New Zealand and the USA, and to *D. siberica* and *D. dentata* from Russia. Frustules of the cells used in the PCR reactions were recovered and examined using SEM, providing a direct link between the observed morphology and sequence data. The morphology of the novel *Didymosphenia* taxon was compared with that of other *Didymosphenia* taxa, being most similar to *D. pumila*, *D. laticollis*, *D. grunowii* and smaller cells of *D. geminata*. Given the unique morphological features of this diatom, it has been named as a new species, *Didymosphenia hullii* Khan-Bureau, sp. nov.

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[46] (PA) WATER CHEMISTRY, ALGAL ENZYME ACTIVITY AND FATTY ACID CONCENTRATION AS INDICATORS OF WATER QUALITY OF ERIE COUNTY STREAMS. **Mopati Kuswani** & Sarah Whorley. Department of Natural Sciences, Daemen College, Amherst, NY.

Declines in water quality in Erie County streams are usually a result of industrial, agricultural or even residential pollution typically resulting in high nutrient levels and decreased biodiversity. This project observes how nutrient levels and seasonal changes affect the nutritional quality, enzyme function, and fatty acid concentration of algal communities in several Erie County streams. As biological indicators, algae are used in many types of water quality assessments and also make up the base of the aquatic food web. Enzyme activity of algal phosphatase as well as algal fatty acid concentration were quantified and results suggested that enzyme activity and fatty acid composition could be good indicators of the importance of algae in an aquatic ecosystem. Enzyme activity showed a gradual but significant increase with seasonal change and fatty acid levels correlated with amount of human activity. Overall stream ecosystem quality was found to be affected by human activity.

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[47] ALGAE TORCH: A COST-EFFECTIVE TOOL FOR IDENTIFYING THREATENING ALGAL BLOOMS. **Wyatt Leinoff** & Gregory Boyer. Department of Chemistry, SUNY School of Environmental Science and Forestry, Syracuse, NY.

Due to the danger of toxins that have been attributed to certain phytoplankton there has become an increasing need to analyze algae in water samples quickly and determine their hazards. Characteristic fluorescence of algae can be statistically manipulated to determine concentrations of various phytoplankton groups such as green and blue-green algae. Testing environments in which the Algae Torch is effective will help identify toxic waters in need of further testing. This new tool will allow implementation of a cost-efficient appraisal for identifying threatening algal blooms. Preliminary experiments on the Algae Torch yield comparable data to other analytical laboratory methods of fluorescent readings and cyanobacteria concentration determination to well tested field equipment. Recreational waters and water sheds alike could utilize the Algae Torch in the field to alleviate an ongoing need for expensive and time-consuming research by having an initial screening protocol utilizing the Algae Torch.

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[48] A SUMMARY OF NEW SILICA-SCALED CHRYSOPHYTES SPECIES DESCRIBED FROM A MIDDLE EOCENE MAAR LAKE. **Anne-Marie Lizarralde** and Peter A. Siver. Botany Department, Connecticut College, New London, CT.

Siliceous microfossils abound in lake sediments deposited in the Giraffe kimberlite diatreme, a Middle Eocene maar lake situated near the Arctic Circle in the Northwest Territories of Canada during the Cenozoic hot house. Overall, this extensive core contains an astonishing diversity of exquisitely preserved siliceous microfossils representing the Chrysophyceae, Synurophyceae and Bacillariophyceae, as well as sponge remains and scales from testate euglyphids and heliozoans. The purpose of this study was to summarize the diversity of silica-scaled Chrysophyceae and Synurophyceae to date. Overwhelmingly dominated by these chrysophytes, we have identified and described 17 new fossil taxa of silica-scaled Chrysophyceae and Synurophyceae. Although some taxa do not appear to have modern analogs, others can be readily traced to, or are morphologically identical with, extant species. Scale sizes, bristle, and dome variations will be discussed. Our findings prove definitively that the most common genera of scaled chrysophytes found in freshwater habitats worldwide today were well established by the middle Eocene, and that these organisms are most likely much older than 47 Ma.

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[49] A SURVEY OF MICROBIAL EUKARYOTES FROM THE SAR CLADE THROUGHOUT ICELAND. **Daniela Lopes Paim Pinto**[1], Hilary McManus[2], Christopher E. Lane[1]. [1]Department of Biological Sciences, University of Rhode Island, Kingston RI. [2]Department of Biological and Environmental Sciences, Le Moyne College, Syracuse, NY.

Although the ecological and evolutional importance of microbial eukaryotes have been widely recognized, our understanding about their diversity and distribution is rather limited to very few groups and ecosystems. Difficulties imposed by traditional cultivation approaches, the small number of scientists exploring their diversity and the broadness of these groups, make microbial eukaryotes a critical target for biodiversity research. One group of microbial eukaryotes, particularly diverse and yet understudied, is the recently proposed SAR clade (Stramenopiles, Alveolates, Rhizaria). We explored the eukaryotic microbial community composition from Iceland, focusing on microorganisms belonging to the SAR clade, using barcode-type metagenomics in a wide variety of samples from different habitats (freshwater, marine, pro-glacial and thermal lakes, glacial and soil) and locations. We generated amplicon data from the V3 and V9 hypervariable regions of the 18S rRNA gene for 27 different samples and clustered them into operational taxonomic units (OTUs). Data from V3 and V9 18S gene regions showed similar distribution patterns, per geographical region. Geography correlates better with the biodiversity of these microorganisms than type of habitat. While V3 data captured higher number of OTUs belonging to SAR, V9 data captured more diversity inside the group, especially at higher taxonomic ranks (order to genus). The community profile linked with each specific geographical region and habitat will be further discussed. The results of the present study contribute to our comprehension of SAR members' distributions across a wide range of peculiar habitats opening the way for the identification of unrecognized diversity in SAR.

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[50] (TA) GENE EXPRESSION PROFILES OF SODIUM EXPORT MECHANISMS IN *CHARA LONGIFOLIA* (C. B. ROB.) AND *CHARA AUSTRALIS* (R. BR.). **Shaunna Phipps**[1], Tomoaki Nishiyama[2] & Mary A Bisson[1]. [1]Department of Biological Sciences, University at Buffalo, Buffalo, NY. [2]Advanced Science Research Center, Kanazawa University, Japan.

Species within the genus *Chara* have a range of tolerances when exposed to or cultured in varying salinities. We examine two potential genes (SOS1 and PpENA) related to sodium export that have been previously established in embryophtes to determine their potential role in the export of Na^+ in salt-tolerant *C. longifolia* and salt-sensitive *C. australis.* Since *Chara* is more closely related to embryophytes than to other green algae, we hypothesize that similar genes are likely to be the mechanism behind sodium export in *Chara.* Illumina transcriptomes for both species assisted in identifying good candidate genes representing both a Na^+-ATPase and a Na^+/H^+ antiport in *Chara.* These genes will be examined in expression profiles of both species with acclimation to salt. Creation of time-course Illumina transcriptomes will be done using RNA from multiple time points (0hr, 6hr, 12hr, 24hr & 48hr) after salt stress for both species. The transcriptomes will provide sequence data to examine expression profiles genes involved in salt tolerance (presumably including *Chara* candidate genes representing SOS1 & PpENA). These expression profiles will give insight into the role of these sodium transport mechanisms in acclimation of salt for both *C. longifolia* and *C. australis.*

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[51] (PA) SURVEY OF FRESHWATER RED ALGAE FROM THE BATRACHOSPERMALES (RHODOPHYTA) IN SOUTH CAROLINA**. Alexis M. Redmond**[1], Emily K. Hollingsworth[2] & Morgan L. Vis[1]. [1]Department of Environmental and Plant Biology, Ohio University, Athens, OH. [2]Whitehall, MI 49461, U.S.A.

Freshwater red algae are common component of the flora in streams and rivers with high water quality. The order Batrachospermales is the most species rich and have been reported throughout North America. Thirty stream segments in South Carolina were investigated for freshwater red algal taxa from the Batrachospermales. A total of 50 specimens were collected and represented five genera and nine species as follows:

Batrachospermum gelatinosum, *B. helminthosum*, *B. macrosporum*, *B. turfosum*, *Kumanoa skujana*, *Sheathia americana*, *S. heterocortica*, *Sirodotia suecica* and *Tuomeya americana*. *Batrachospermum macrosporum* and *Tuomeya americana* were collected from the greatest number of streams and in multiple years from the same site. *Batrachospermum helminthosum* was observed in three streams and represents a new record for the state. DNA sequence data of the *rbc*L gene were available from the literature or generated in this study for eight of the nine taxa identified in the study and confirmed the morphological identification. For six of the taxa, there were data on the stream temperature, pH and conductivity. For most of the taxa, the pH and conductivity measurements were within previously reported ranges, but the water temperatures recorded in this study tended to be higher than previous reports. The diversity of Batrachospermales in South Carolina represents 57% of the generic/ infrageneric and 20% of the species diversity known in North America. Given the size of the state, this richness would appear to represent high diversity. However, diversity found in this study may still be an underestimation and more discoveries could be made by targeting more specialized habitats and taxa that are known from neighboring states, but not yet reported from South Carolina.

[52] FORMALDEHYDE DEHYDROGENASE AS A SELECTABLE MARKER FOR TRANSFORMATION IN MARINE DIATOMS. Christina Campagna[1] & **Deborah L. Robertson**[1,2]. [1]Biochemistry and Molecular Biology Program, Clark University, Worcester, MA. [2]Department of Biology, Clark University, Worcester, MA.

Formaldehyde is a carcinogen, an environmental contaminant, and a byproduct of cellular metabolism. Cells metabolize formaldehyde through the enzymatic activity of formaldehyde dehydrogenase (FALDH) and increased cellular expression of FALDH increases the rate of formaldehyde detoxification. Methods for genetic transformation of marine diatoms have advanced rapidly, however, commercially available selectable markers are expensive and may not be stable in seawater. FALDH may serve as a useful selectable marker in organisms that are not sensitive to currently available antibiotics. Using the FALDH gene found in the model organism, *Thalassiosira pseudonana*, we have generated an episomal plasmid to test whether formaldehyde resistance can be used as a selectable marker for the genetic transformation of *T. pseudonana* and *P. tricornutum*. Genetic transformation via bacterial conjugation has been successful in *P. tricornutum* and *T. pseudonana* (Karas et al. 2015). Using the pTpPuc3 plasmid as a starting point, we created an episomal plasmid containing the FALDH gene flanked by the strong LHC9 promoter and terminator sequences. The assembly was confirmed with PCR, restriction digestions, and sequencing of the expression cassette. We transformed bacterial cells containing the pTA-MOB carrier plasmid with the assembled episomal vector by electroporation. We will then transform *T. pseudonana* and *P. tricornutum* by conjugation and determine if transformed diatoms have an increased resistance to formaldehyde relative to untransformed cultures.

[53] (TA) DIVERSIFYING NEW ENGLAND SEA VEGETABLE AQUACULTURE: MODIFYING KELP NURSERY AND GROW OUT TECHNOLOGIES FOR NORI PRODUCTION. **Jaclyn Robidoux** & Chris Neefus. University of New Hampshire, Durham, NH.

The emerging New England sea vegetable aquaculture industry is currently based on the long-line production of kelp. Seeking to promote greater industry stability and sustainability, this research will contribute to diversification of aquaculture in the Gulf of Maine by adapting kelp technologies for the production of nori. Of the nori species that occur in New England, *Wildemania amplissima* (Foslie, 1891) has been chosen as the ideal candidate for long-line production due to its size, seasonality, geographic range, ammonia removal efficiency, and exceptional growth rates. Field collections of *W. amplissima* were conducted along the entire Maine coastline and samples were processed using a variety of zygotospore isolation techniques. This resulted in the establishment of free living *Conchocelis*-phase cultures from six geographically distinct locations. Modified DNA extraction techniques were used to successfully isolate and examine indicator *rbc*L genes in order to confirm the genetic correctness of both blades and free-living *Conchocelis* cultures as *W. amplissima*. Optimum environmental conditions for vegetative *Conchocelis* growth and conchospore release are being investigated by exposing conchocelis cultures to various combinations of light level, temperature and photoperiod. Further investigations will focus on developing nursery techniques for string seeding and modifications of existing kelp long-line grow-out operations. Field trials will be conducted at lease sites in Casco Bay, Maine, and the UNH Aquaculture Farm off Newcastle, New Hampshire. This research plays a key role in the development of nursery systems and species-specific culture technologies that will provide the platform for commercial nori production in the Gulf of Maine.

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[54] (PA) ANTIMICROBIAL EFFECTS OF MACROALGAL EXTRACTS AGAINST GRAM NEGATIVE HUMAN PATHOGENS INCLUDING *KLEBSIELLA PNEUMONIAE* AND *SALMONELLA* TYPHIMURIUM. **Katharina H.C. Roese**, Andrea L. Call, Kristin M. Burkholder, Ursula S.R. Roese, Department of Biology, University of New England, Biddeford, ME.

Marine macroalgae are an unexplored source of antimicrobial compounds against human pathogens. Due to these antimicrobial compounds, algae are able to survive and even thrive in a harsh environment with infectious bacteria. This research focuses on the antimicrobial properties of three macroalgae species collected in the intertidal zone on the coast of Maine: the brown alga *Fucus vesiculosus*, and red algae species *Chondrus crispus*, and *Ahnfeltia plicata*. Extracts from these three different macroalgae were tested against a variety of gram negative human pathogens. These include *Pseudomonas aeruginosa, Proteus mirabilis*, *Salmonella enterica* serovar Typhimurium (S. Typhimurium), *Klebsiella pneumoniae* and *Escherichia coli.* These pathogens were selected from the World Health Organization high priority list for Research and Development of new antibiotics. Extracts were prepared with three different solvents of varying polarity including methanol, dichloromethane, and pentane. The effects of each algal extract were measured using a disk diffusion assay. A minimum inhibitory concentration assay (MIC) was also performed for extracts that showed the greatest growth inhibition. The MIC determined the lowest concentration needed to inhibit bacterial growth. Of the three solvents tested, methanol extracts were the most effective followed by dichloromethane and pentane. The filamentous red algae *Ahnfeltia plicata* was the most effective alga in inhibiting pathogen growth. Of the four bacteria tested, *Klebsiella pneumoniae, Proteus mirabili*s *and Salmonella* Typhimurium growth was inhibited by the algal extract. Macroalgae methanol extracts inhibited these gram-negative pathogens on the WHO list for R&D, two of them even being at a priority level critical. These are very encouraging results, as overuse of antibiotics is causing them to become less effective.

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[55] (TA) HARMFUL ALGAL BLOOMS IN NEW YORK'S FINGER LAKES – A HARBINGER OF CHANGE TO COME? **Kristen N. Slodysko** & Gregory Boyer. The State University of New York, College of Environmental Science and Forestry, Syracuse, NY.

The eleven Finger Lakes are the crown jewel of central New York and serve as important resources for drinking water, recreation, and tourism. While the lakes share a similar geological origin they vary in size, depth, watershed area and type, and trophic status. Several lakes (Canandaigua, Seneca, Skaneateles, Canadice) are historically oligotrophic (TP<10) whereas other lakes (Honeoye, Otisco) are eutrophic (TP>20). In 2016, Owasco Lake suffered a severe HAB with microcystin concentrations in the lake reaching 2500 µg/L. Detectable levels of toxins were found in the City of Auburn's finished drinking water. In 2017, unusual rainfall led to the first-ever occurrence of HABs in all eleven Finger Lakes. Peak microcystin concentrations reached 200 and 400 µg/L in "oligotrophic" Skaneateles and Seneca Lake, and >800 µg/L in "eutrophic" Honeoye Lake. Nested mixed-effects models indicated algal biomass was related to N and P on a global scale. Lake specific models indicated that nutrient drivers (N vs. P) vary between the lakes. Management plans to prevent HABs in the Finger Lakes will need to be lake-specific in terms of the nutrient and action targeted. The conditions that led to the occurrence of HABs in 2017 are unlikely to be isolated events. In the future, Finger Lakes historically considered immune to HABs will need to be monitored.

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[56] EXPLORING THE FRESHWATER RED ALGAL DIVERSITY OF AFRICA: PAST AND PRESENT. **Amanda L. Szinte**[1], Jonathan C. Taylor[2], Adesalu T. Abosede[3] & Morgan L. Vis[1]. [1]Environmental and Plant Biology, Ohio University, Athens, OH. [2]School of Environmental Sciences, North-West University, Potchefstroom, South Africa. [3]Faculty of Science, University of Lagos, Akoka, Nigeria.

Historical literature, records from select herbaria and recent field collections were utilized to create a checklist of freshwater red algae from the African continent. To date, we have found records for taxa in the orders Batrachospermales, Ceramiales and Hildenbrandiales. Within the Batrachospermales, species belonging to the genera *Atrophycus*, *Batrachospermum*, *Kumanoa*, *Nothocladus*, *Sirodotia* and *Tuomeya* have been reported. For the Ceramiales and Hildenbrandiales, *Bostrychia*, *Caloglossa* and *Hildenbrandia* have been noted. Among the taxa are species that were first described from African locations including *Batrachospermum breutelii*, *Nothocladus afroaustralis* and *Hildenbrandia angolensis*. The first two species have only been reported from a few locations whereas *Hildenbrandia angolensis* has been reported from numerous locations on other continents. The reports of freshwater red algae have been from seven countries, but the majority of records are from South Africa. Sequence data for a handful of specimens have confirmed species of *Atrophycus*, *Kumanoa* and *Sirodotia* on the continent. Multiple species of both *Kumanoa* and *Sirodotia* are indicated by the sequence data. *Atrophycus ater* is a cosmopolitan species based on similar sequence data from numerous continents. Using morphology from recent collections, we have identified *Batrachospermum macrosporum* and *Sirodotia* sp. and are in the process of naming more specimens. Our preliminary results suggest that there are quite a few species from multiple genera in the Batrachospermales present in this flora and further sampling efforts would undoubtedly uncover more species.

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[57] (PA) A NOVEL CRYPTIC SPECIES OF GREEN ALGAE FROM THE CALIFORNIA DESERT. **Melissa Taylor**[1], Nicole Pietrasiak[2] & Karolina Fučíková[1]. [1]Assumption College, Department of Natural Sciences, Worcester, MA. [2]New Mexico State University, Department of Plant and Environmental Sciences, Las Cruces, NM.

Green algae are a diverse group of plant life, yet are still vastly understudied compared to land plants. For many years, these algae were characterized through their morphology and life cycles. It has since become apparent that a better understanding of their evolutionary and phylogenetic history can be obtained through phylogenetic and genomic analyses. A desert strain of green algae, referred to as WJT24VFNP31, was isolated from Joshua Tree National Park (JTNP) in southern California as part of a larger biodiversity survey. The alga's organellar genomes were sequenced, annotated and used for phylogenetic analysis. A morphological analysis of the algae was conducted to determine its phenotypic characteristics such as size, number of chloroplasts, flagellation, and number of nuclei. Although morphologically this strain is consistent with the coccoid genera *Bracteacoccus* and *Pseudomuriella*, phylogenomic analyses demonstrate that it is not closely related to any other known green algal species. As a result, we propose that WJT24VFNP31 be placed into its own new species and genus in the class Chlorophyceae. By studying cryptic green algae, such as WJT24VFNP31, a better understanding of the biodiversity of JTNP and green algae in general can be obtained.

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[58] (TA) STRUCTURAL COMPARISON OF DESERT AND AQUATIC SPECIES OF *TETRADESMUS* (CHLOROPHYCEAE, CHLOROPHYTA) THROUGH THE CYCLE OF DESICCATION AND REHYDRATION. **Elizaveta Terlova**[1], Louise A. Lewis[1], Xuanhao Sun[2], Maritza Abril[2]. [1]Ecology and Evolutionary Biology, University of Connecticut, [2]Bioscience Electron Microscopy Laboratory, University of Connecticut.

Algae, mosses, and vascular plants include desiccation tolerant species capable of surviving extreme loss of cytoplasmic water. Chlorophyte green algae have evolved to occupy land multiple times, which may have led to diverse adaptations to arid habitats — distinct from those in land plants and Charophyta. Prior studies of desiccation tolerant Charophyta cells during drying showed intact membranes with severe cell shrinkage (plasmolysis), a condition that the tolerant species survive. Using LM with vital staining and TEM we investigated the cell structure upon desiccation and rehydration of two congeneric species of Chlorophyta, one from freshwater habitats and the other isolated from desert soil crusts. Cells from the liquid medium served as a hydrated control. For TEM, algal cells were desiccated in an air chamber containing silica gel for 24 h (treatment 1), after which the cells were rehydrated for 1 h in growth medium (treatment 2). The control and two treatment samples were chemically fixed and examined using TEM. Vital fluorescent dye also was used to examine the integrity of the membranes under a desiccation and rehydration cycle simulated with 4000M sorbitol. Under TEM, no noticeable cytoplasmic shrinkage was observed for either species under dehydration, with intact thylakoid membranes and other membranes. Upon rehydration, cells of the aquatic species seemed to have a denser cytoplasm compared to the other treatments. Cells examined using a vital fluorescent stain indicated that membranes of both species experience a degree of damage upon desiccation. But only the desert species indicated membrane integrity upon rehydration. The absence of severe cytoplasmic shrinkage in both species is in contrast to Charophyta species and may be due to the lack of the large central vacuole in the examined algae.

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[59] SEQUENCING A NOVEL EUSTIGMATOPHYCEAE INDENTIFIES A POTENTIAL SECONDARY ENDOSYMBIOITIC EVENT. **Kristina X Terpis**[1], Laura Eme[2], J Craig Bailey[3], Christopher E Lane[1]. [1]Biological Sciences, University of Rhode Island, Kingston, RI. [2]Cell and Molecular Biology, Uppsala University, Biomedical Centre, Uppsala, Sweden. [3]Biology, University of North Carolina-Wilmington, Center for Marine Science, Wilmington, NC.

Stramenopiles (heterokonts) form a monophyletic clade consisting of macroscopic multicellular algae and microscopic unicellular organisms (protists). Heterokonts are classified into 17 different classes, of which 10 are photosynthetic. They are found in a wide range of habitats (marine, freshwater, and terrestrial) and exhibit different trophic modes (autotrophic, heterotrophic, mixotrophic). As part of a larger effort to construct a robust phylogeny for stramenopiles, transcriptomes were generated to interrogate relationships of photosynthetic stramenopiles (ochrophytes). As part of our initial data screening, we examined copies of the plastid-encoded *rbc*L and the nuclear SSU rDNA from previously undescribed species. During this process, the data from a culture morphologically identified as a strain of Eustigmatophyceae expectedly contained plastid genes that grouped within the Eustigmatophyceae. However, some nuclear genes from the same strain appeared to group within the Chrysophyceae. We further used a robust approach to examine the phylogenetic position of 159 conserved eukaryotic genes extracted from the transcriptome data of this culture, which revealed an unusual pattern. The vast majority of genes are phylogenetically affiliated with Eustigmatophyceae, but 24 ribosomal proteins exist in multiple copies in the transcriptome. In all cases one copy is of expected eustigmatophyte origin, but a second copy appears to have a chrysophyte origin. Implications and possible explanations for this curious pattern will be discussed.

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[60] REVIEW OF RECENT TAXONOMIC CHANGES IN FRESHWATER RED ALGAE (RHODOPHYTA). **Morgan L. Vis**[1] & Orlando Necchi Jr[2]. [1]Environmental and Plant Biology, Ohio University, Athens, OH. [2]Zoology and Botany Department, São Paulo State University, São José do Rio Preto, São Paulo, Brazil.

Since the advent of molecular systematics studies of freshwater red algae, numerous insights have necessitated taxonomic changes. Within the freshwater order Batrachospermales, rectifying the paraphyly of *Batrachospermum* has been a focus. New genera have been proposed in the last few years to accommodate sections of the genus as well as clades of taxa that previously had no sectional designation. These ‘Batrachospermum-like’ genera include *Atrophycus*, *Lympha*, *Nocturama*, *Sheathia*, *Virescentia*, and *Volatus*. The genus *Nothocladus* has been expanded to include most species previously placed in *Batrachospermum* from Australasia. In the near future, it is likely that six more genera will be proposed for current ‘*Batrachospermum’* species completing the task of rendering *Batrachospermum* monophyletic. Although this genus has been shrinking due to the description of these new genera, four new species have been added to *Batrachospermum* sensu stricto. Recent studies of the Thoreales have expanded the diversity in *Thorea* with at least nine species recognized from DNA sequence data and potentially 17 species based on the literature. Outside of these strictly freshwater orders, there have been two notable recent discoveries in the Corallinales and the Acrochaetiales. *Pneophyllum cetineasis* is a new crustose coralline species discovered growing in a freshwater habitat even though the other species of the genus are marine. Within the Acrochaetiales, a new family and genus has been described to accommodate a red algal endophyte, *Ottia meiospora*, of *Nothocladus* species in Australasia. The systematics of the freshwater red algae have been dynamic in recent years and this trend will continue in the near future. However, we have a new book project underway to synthesize these new developments and provide a comprehensive treatment of this charismatic group of organisms.

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