



73rd Annual Meeting of the **Phycological Society of America**

Algae and Climate Change



June 23-27, 2019

Fort Lauderdale, Florida

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The **Phycological Society of America** (PSA) was founded in 1946 to promote research and teaching in all fields of Phycology. The society publishes the *Journal of Phycology* and the *Phycological Newsletter*. Annual meetings are held, often jointly with other national or international societies of mutual member interest. PSA awards include the **Bold Award** for the best student paper at the annual meeting, the **Lewin Award** for the best student poster at the annual meeting, the **Provasoli Award** for outstanding papers published in the *Journal of Phycology*, The PSA Award of Excellence (given to an eminent phycologist to recognize career excellence), the **Lang Fellowship** for early career researchers, and the **Prescott Award** for the best Phycology book published within the previous two years. The society provides financial aid to graduate student members through **Croasdale Fellowships** for enrollment in phycology courses, **Hoshaw Travel Awards** for travel to the annual meeting and **Grants-In-Aid** for supporting research. To join PSA, contact the membership director or visit the website: www.psaalgae.org



LOCAL ORGANIZERS FOR THE 2019 PSA ANNUAL MEETING:

H. Dail Laughinghouse IV, University of Florida/IFAS

David Berthold, University of Florida/IFAS

Evelyn Gaiser, Florida International University

Ligia Collado-Vides, Florida International University

PSA Program Director

Amy Carlile, University of New Haven

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Michael H. Graham, Moss Landing Marine Laboratories, Moss Landing, CA, USA

Communications Director

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Student Member Representative

Arley Muth, University of Texas Marine Science Institute, Port Aransas, TX, USA

Chair, Board of Trustees

Morgan L. Vis, Department of Environmental and Plant Biology, Ohio University, Athens, OH, USA



MEETING ACKNOWLEDGEMENTS

We would like to acknowledge the following parties and people whose excellent assistance greatly facilitated this meeting:

- Chris MacTaggart for creating our 2019 annual meeting logo!



- Kirsten Müller, Dail Laughinghouse, David Berthold, and Vera R. Werner for providing beautiful program images and illustrations.



- University of Florida IFAS



- SePRO



- USA Scientific



The wonderful volunteers that helped shape our meeting:

- Max Barbosa
- Emily Becks
- Ariel Elazar
- Vladimír Fristák
- Danielle Hatt
- Forrest Lefler
- Viviana Mazzei
- Kristy Sullivan



Presidential Message

Welcome to the 73rd Annual Meeting of the Phycological Society of America in Sunny Fort Lauderdale, Florida. We have an exciting program for you with an emphasis on Climate Change and Harmful Algal blooms. I would like to thank the local organizing committee, Dail Laughinghouse, David Berthold, Evelyn Gaiser and Ligia Collado-Vides and our Program Director, Amy Carlile, for putting together a meeting with interesting excursions that highlight Florida's natural environment and a program that emphasizes key issues in Phycology today. Thank you also to Chris MacTaggart for the beautiful drawing for the meeting logo. The PSA Executive Committee has also implemented, for the first time, a code of conduct for our meetings. Please take a look at this on page (xii) and it is also available on our website (<https://www.psaalgae.org/psa-code-of-conduct>).



Please feel free to connect me and any of the executive committee during the meeting. If you have any questions, concerns or suggestions, you are welcome to email me at kmmuller@uwaterloo.ca.

Have a wonderful and productive meeting and stay cool!

Kirsten Müller

2019 PSA President



Organizing Committee Welcome Message

Welcome Phycophiles! It is our pleasure to welcome you to Fort Lauderdale (Hollywood), FL for the 73rd Annual Meeting of the Phycological Society of America from June 23 to June 27, 2019 in Hollywood Beach. We are proud to present a diverse panel of subjects on micro- and macroalgae in a changing climate. During this time, we hope you also take advantage and explore South Florida through activities, people, food, and nature. There is a lot to be discovered not only in our rich poster presentations and oral talks, but also in the beautiful culture and nature that surrounds us here in South Florida.



We hope that you have a fruitful and enjoyable meeting,

Dail Laughinghouse, David Berthold, Evelyn Gaiser, Ligia Collado-Vides

Journal of Phycology

AN INTERNATIONAL JOURNAL OF ALGAL RESEARCH



A PUBLICATION OF THE
PHYCOLOGICAL SOCIETY
OF AMERICA

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- The golden paradox – a new heterokont lineage with chloroplasts surrounded by two membranes
- *Odorella benthonica* gen. & sp. nov. (Pleurocapsales, Cyanobacteria): an odor and prolific toxin producer isolated from a California aqueduct
- Collections from the mesophytic zone off Bermuda reveal three species of Kallymeniaceae (Gigartinales, Rhodophyta) in genera with transoceanic distributions



<http://bit.ly/journalofphy>



WILEY



General Fort Lauderdale & Hotel Information

Meeting Venue

The 73rd Psychological Society of America annual meeting is held at the magnificent beachside Hollywood Beach Marriott. Fort Lauderdale is in the greater Miami-Fort Lauderdale-West Palm Beach metropolitan area with a population of over 6 million. The conference venue is in Hollywood Beach, which is ~6 miles (10 km) from the Ft. Lauderdale-Hollywood International Airport (FLL) and ~27 miles (44 km) from Miami International Airport (MIA).



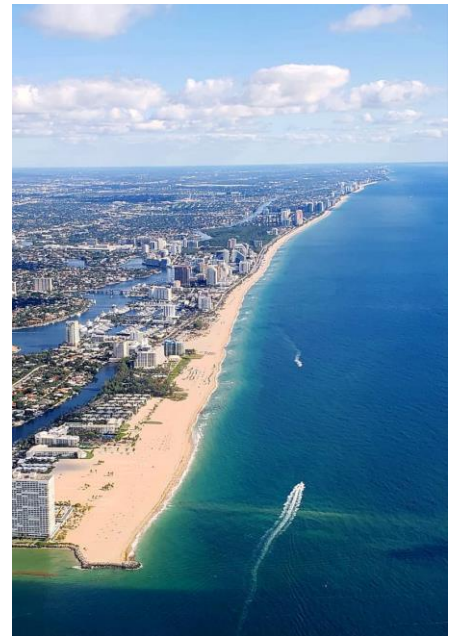
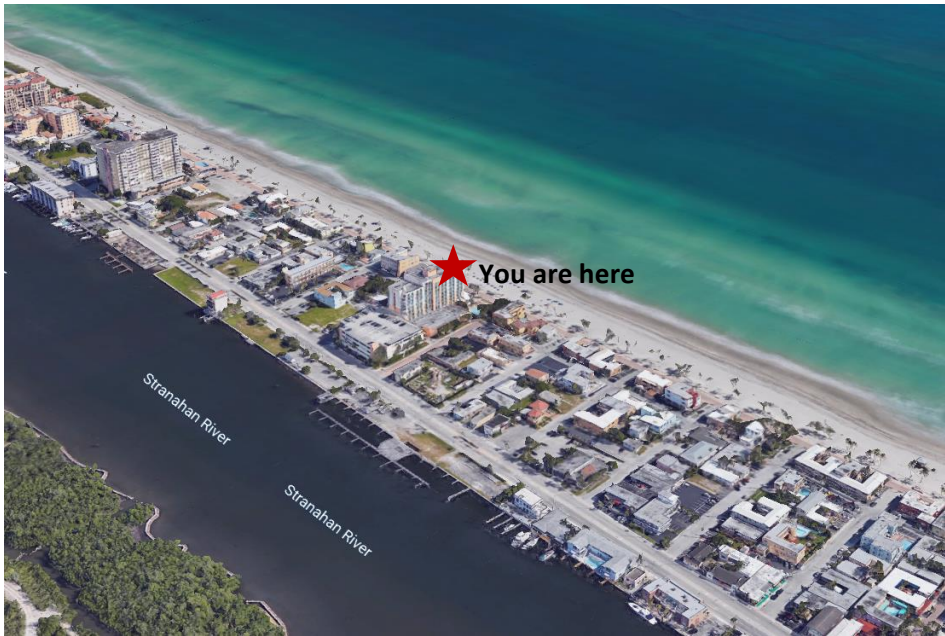
2501 North Ocean Drive, Hollywood, Florida 33019

+1-954-924-2202

FLOOR PLAN



Map and Glance of Hollywood Beach Marriott and Hollywood Beach



Hotel Information

We have a special group rate (\$149.00 per night + taxes) at the Hollywood Beach Marriott. Online reservation can be made online or by calling the reservations team at +1 855-314-1984 and mention that you are with the Psychological Society of America Annual Meeting. When reserving online, an amenity fee will be added, but that will be removed at the property when you pay. The reservation cut-off date with this price is June 3rd, 2019. There are some rooms available for up to 3 days prior and after the conference for those that want to enjoy more days in the sun.

Getting Around: Parking/ Car Rentals/ Bus Station/ Train Station

In addition to regular taxis, Lyft, or Uber, Hollywood/Ft. Lauderdale offers many other options to facilitate sight-seeing and exploration. You can catch the Sun Trolley to downtown Fort Lauderdale (9:30-18:30) or you can check out a bicycle with AvMed Rides powered by **Broward B-cycle**. Motorized scooters are also an efficient way to cruise around on the boardwalk. Car rentals can be found nearby or you can arrange to travel by bus through the **Broward County Transit** or by train using the **Amtrak** or **Tri Rail**. There is on-site parking available at the hotel.

For much more information, please refer to the city brochures provided in your welcome kit.



PSA Meeting Code of Conduct

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

Expected Behavior

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

Unacceptable Behavior

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

Consequences

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

Reporting Unacceptable Behavior

- If you are the subject of unacceptable behavior or have witnessed any such behavior, please immediately notify a member of the PSA leadership.
- Notification should be done by contacting PSA leadership on-site or e-mailing your concern to one or more of the following representatives for 2019: Kirsten Müller, PSA President (kmmuller@uwaterloo.ca), Amy Carlile, Program Director (acarlile@newhaven.edu), Dail Laughinghouse, 2019 Local Organizer (hlaughinghouse@ufl.edu).
- Anyone experiencing or witnessing behavior that constitutes an immediate or serious threat to public safety at a PSA meeting is advised to either tell a security guard or locate a venue phone and ask for security.

PROGRAM

We are hosting an exciting program with excellent keynote and plenary lectures centered on *Algae* and *Climate Change*.

Presidential Symposium: Climate change and our fragile polar ecosystems



The plenary lecture will be given by **Susan R. Eaton**. This symposium includes seminars by **Dr. Warwick Vincent** (Université Laval) on cyanobacteria and the Pole to Pole Paradox; **Dr. Hilary McManus** (Le Moyne College) on women in STEM, Antarctica and how diversity in leadership can inform climate change policy; and **Maggie Amsler** (University of Alabama) on her experiences in 27 trips to Antarctica.

Applied Symposium: From micro to macro: nuisance algae and their management

This symposium will include presentations on micro- and macro- harmful and nuisance algae from



freshwater to marine environments. The lectures will cover algal biology and ecology, bloom dynamics, toxin production and fate, and algal management.

Plenary Speaker: **Dr. Clarissa Anderson** (Scripps Institution of Oceanography, UC San Diego)

Speakers: **Dr. Ligia Collado-Vides** (Florida International University), **Dr. West Bishop** (SePRO Corporation), **Dr. Barry Rosen** (US Geological Survey), and **Dr. Patrick Kangas** (University of Maryland)

Student-Organized Symposium: What goes on, on the inside? Connecting algal physiology, their distribution and climate change



This symposium includes presentations on algal physiology and their response to increased temperatures and ocean acidification in temperate and tropical systems, as well as using freshwater diatoms to assess long term changes to aquatic communities.

Speakers: **Dr. Catriona Hurd** (University of Tasmania), **Dr. Maggie Johnson** (Smithsonian Institution), and **Dr. Evelyn Gaiser** (Florida International University)

PSA 2019 Annual Meeting Schedule of Events

Saturday, June 22nd

- 06:30-14:30** **Excursion to Key Largo** (meet in Hollywood Beach Marriott lobby)
- 07:30-14:00** **Excursion to Everglades** (meet in Hollywood Beach Marriott lobby)
- 08:30-11:30** **AlgaeBase Meeting** (Sunset Key Boardroom, PH level)
- 13:30-16:30** **Board of Trustees Meeting** (Sunset Key Boardroom, PH level)

Sunday, June 23rd

- 08:30-16:30** **Executive Committee Meeting** (Sunset Key Boardroom, PH level)
- 13:00-16:00** **Remote Sensing Workshop** (Atlantic Room)
- 16:00-18:00** **Registration** (Pre-Function Area)
- 18:00-20:00** **Opening Mixer** (Grand Ballroom Salon B)

Monday, June 24th



07:00-08:30 **Registration** (Pre-Function Area)

08:00-12:00 **Poster set-up** (Grand Ballroom Salon B)

08:30-08:45 **Opening Remarks** (Grand Ballroom Salon A)

Kirsten Müller (PSA President), Dail Laughinghouse (Lead Local Organizer), Amy Carlile (PSA Program Director)

08:45-09:45 **Morning Plenary Lecture** (Grand Ballroom Salon A) (*Moderator: Kirsten Müller*)



08:45 BRINGING THE OCEAN TO EYE LEVEL: EMPOWERING THE NEXT GENERATION OF WOMEN LEADERS IN THE ARCTIC
Susan Eaton, Sedna Epic Expedition, Calgary, AB Canada.
susaneaton@shaw.ca

09:45-10:15 **COFFEE BREAK** (Pre-Function Area)

10:15-12:00 **PSA Presidential Symposium: Climate change and our fragile polar ecosystems** (Grand Ballroom Salon A) (*Moderator: Kirsten Müller*)



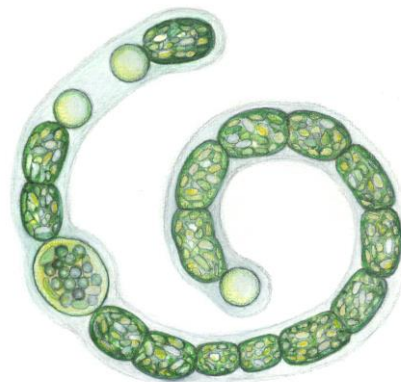
10:15 ARCTIC CYANOBACTERIA AND THE POLAR PARADOX
Warwick Vincent, Université Laval, Quebec City, QC Canada.
warwick.vincent@bio.ulaval.ca



10:50 HOMEWARD BOUND: LEADERSHIP, SCIENCE AND ANTARCTICA
Hilary McManus, Le Moyne College, Syracuse, NY United States.
mcmnuha@lemoyne.edu



11:25 ANTARCTICA'S CRYSTALLINE WEB OF LIFE: ITS BEAUTY AND ITS PERILS
Maggie Amsler, University of Alabama at Birmingham, Birmingham, AL United States.
mamsler@uab.edu



12:00-13:30 **LUNCH** (Pre-Function Area)

12:00-16:30 **Poster set-up** (Grand Ballroom Salon B)

13:30-14:45 **Contributed Session: Global Change** (Grand Ballroom Salon A) (Moderator: Hilary McManus)

13:30 SEAGRASS LOSS AND MACROALGAE INCREASE IN NORTH BISCAYNE BAY ASSOCIATED WITH LONG-TERM WATER QUALITY DECLINE

Collado-Vides, L., Florida International University, United States, colladol@fiu.edu

Varona, G., Miami-Dade Division of Environmental Resources Management, Miami, FL, USA, United States, Galia.Varona@miamidade.gov

Abdelrahman, O., Miami-Dade Division of Environmental Resources Management, Miami, FL, USA, United States, Omar.Abdelrahman@miamidade.gov

Avila, C., Miami-Dade Division of Environmental Resources Management, Miami, FL, USA, United States, cavila@sfwmd.gov

13:45 THE FUTURE OF CALCIFYING RED ALGAE IN THE LEVANTINE BASIN: NON-NATIVE VS NATIVE AND HAPLOID VS. DIPLOID RESPONSES TO CLIMATE CHANGE

Schoenrock, K. M., National University of Galway, Ireland, kathryn.schoenrock@nuigalway.ie

Rilov, G., Israel Oceanography and Limnological Research, Israel, rilovg@ocean.org.il

Hadfield, S. A., University of Alabama at Birmingham, United States, sakh@uab.edu

14:00 IRISH GREEN TIDES IN A CLIMATE CHANGE CONTEXT

Bermejo, R., Earth and Ocean Sciences, National University of Ireland, Galway, Ireland, ricardo.bermejo@uca.es

Galindo-Ponce, M., Earth and Ocean Sciences, National University of Ireland, Galway, Ireland, Maria.Galindo.Ponce@hotmail.com

Linderhoff, C., Earth and Ocean Sciences, National University of Ireland, Galway, Ireland, Charlene97@live.nl

Morrison, L., Earth and Ocean Sciences, National University of Ireland, Galway, Ireland, liam.morrison@nuigalway.ie

14:15 ANCIENT WATERBODIES UNDER GREENHOUSE CONDITIONS: THE POTENTIAL IMPACT OF CLIMATE WARMING ON THE FRESHWATER ALGAL FLORA OF ARCTIC LAKES

Siver, P. A., Connecticut College, United States, pasiv@conncoll.edu

14:30 DISTRIBUTION OF SNOW ALGAE COMMUNITIES IN THE PACIFIC NORTHWEST

Kodner, R. B., Western Washington University, United States, robin.kodner@wwu.edu

Mallon, R., Western Washington University, United States, rachael.mallon@gmail.com

McLaughlin, R., University of British Columbia, Canada, mclaughlinr2@gmail.com

Rouche, N., Western Washington University, United States, rouechn@wwu.edu

13:30-14:45 **Contributed Session: Genomics** (Atlantic Room) (Moderator: Stacey Krueger-Hadfield)

13:30 THE ORGANELLE GENOMES OF *NITZSCHIA PALEA* DEMONSTRATE HIGH SEQUENCE SIMILARITY TO THOSE OF *DURINSKIA BALTICA*.

Crowell, R. M., The University of Virginia's College at Wise, United States, rc907218@ohio.edu

Nienow, J. A., Valdosta State University, United States, jnienow@valdosta.edu
Cahoon, A. B., The University of Virginia's College at Wise, United States, abc6c@uvawise.edu

13:45 GENOMIC VARIATION ACROSS STRAINS OF THE TOXIC BLOOM-FORMING HAPTOPHYTE *PRYMNESIUM PARVUM* REVEALS POSSIBLE TOXICITY DETERMINANTS

[Pendleton, A., Purdue University, United States, pendlea@purdue.edu](mailto:pendlea@purdue.edu)
[Auber, R., Purdue University, United States, rauber@purdue.edu](mailto:rauber@purdue.edu)
[Southard, G., Texas Parks and Wildlife Department, United States](mailto:wwd17@psu.edu)
[Driscoll, W., Penn State Harrisburg, United States, wwd17@psu.edu](mailto:jwisecav@purdue.edu)
[Wisecaver, J., Purdue University, United States, jwisecav@purdue.edu](mailto:jwisecav@purdue.edu)

14:00 HIGHLY CONTIGOUS DE NOVO GENOME ASSEMBLY OF THE HAPTOPHYE *PRYMNESIUM PARVUM* USING OXFORD NANOPORE SEQUENCING

[Auber, R. P., Purdue University, United States, rauber@purdue.edu](mailto:rauber@purdue.edu)
[Pendleton, A. L., Purdue University, United States, pendlea@purdue.edu](mailto:pendlea@purdue.edu)
[Driscoll, W. W., PennState, Harrisburg, United States, wwd17@psu.edu](mailto:wwd17@psu.edu)
[Wisecaver, J. H., Purdue University, United States, jwisecav@purdue.edu](mailto:jwisecav@purdue.edu)

14:15 PROMISING PROSPECTS OF NANOPORE SEQUENCING FOR ALGAL HOLOGEN AND STRUCTURAL VARIATION DISCOVERY

[Sauvage, T., Smithsonian Marine Station, United States, sauvaget@si.edu](mailto:sauvaget@si.edu)
[Schmidt, W. E., Biology Department, University of Louisiana at Lafayette, United States, william.schmidt.algae@gmail.com](mailto:william.schmidt.algae@gmail.com)
[Yoon, H. S., Department of Biological Sciences, Sungkyunkwan University, South Korea, hwansu@gmail.com](mailto:hwansu@gmail.com)
[Paul, V., Smithsonian Marine Station, United States, paul@si.edu](mailto:paul@si.edu)
[Fredericq, S., Biology Department, University of Louisiana at Lafayette, United States, slf9209@louisiana.edu](mailto:slf9209@louisiana.edu)

14:30 GENOMIC REGIONS ASSOCIATED WITH THE PRODUCTION OF DIFFERENT CLASSES OF SMALL NON-CODING RNAs IN *GRACILARIOPSIS ANDERSONII*.

[Lopes Paim Pinto, D., University of Rhode Island, United States, dpaim@uri.edu](mailto:dpaim@uri.edu)
[Blouin, N., INBRE Bioinformatics Core, University of Wyoming, United States, nblouin@uwyo.edu](mailto:nblouin@uwyo.edu)
[Lane, C. E., University of Rhode Island, United States, clane@uri.edu](mailto:clane@uri.edu)



14:45-15:15 COFFEE BREAK (Pre-Function Area)

15:15-16:30 Lightning Talks (Grand Ballroom Salon A) (Moderator: Ligia Collado-Vides)

Lightning talks are quick as lightning: 3 minutes each, no extra time for questions

ALTERATIONS TO THE MICRO-GEO-ENVIRONMENT AND ITS IMPACT ON ALGAL EXOSKELETONS: A PERSPECTIVE IN COCCOLITHOPHORES

[Pokrzywinski, K., US Army Engineer Research and Development Center, United States, kaytee.l.pokrzywinski@erdc.dren.mil](mailto:kaytee.l.pokrzywinski@erdc.dren.mil)

AN INTERNATIONAL DATABASE OF OOSPORE IMAGES

[Casanova, M. T., The Natural History Museum, London, United Kingdom, m.casanova@nhm.ac.uk](mailto:m.casanova@nhm.ac.uk)

CONSUMPTION OF PROLIFERATING CYANOBACTERIAL MATS ON A CARIBBEAN CORAL REEF

McCoy, S. J., Florida State University, United States, mccoy@bio.fsu.edu

CORAL-ALGAL COMPETITION AND OVERGROWTH DYNAMICS OF A RAPIDLY EMERGING RED ALGA (*RAMICRUSTA* SP.) IN ST. THOMAS, US VIRGIN ISLANDS

Hollister, K. J., University of the Virgin Islands, U.S. Virgin Islands, karlihollister@gmail.com

DIFFERENT HOSTS, DIFFERENT LIFESTYLES: PHOTOSYNTHESIS IN THE EPIZOIC DIATOM GENUS *TURSIOCOLA*

Ashworth, M. P., University of Texas, Austin, United States, mashworth@utexas.edu

DO NOT IGNORE THE NAGOYA PROTOCOL

Delwiche, C. F., University of Maryland, United States, delwiche@umd.edu

HONOR BY ASSOCIATION, LEVERAGING CO-EXPRESSION NETWORKS FOR GENE DISCOVERY IN SPECIALIZED METABOLIC PATHWAYS

Wisecaver, J., Purdue University, United States, jwisecav@purdue.edu

KELP HAIRCUTS: DO THEY INCREASE HARVEST-ABLE BIOMASS AND/OR DESIRABLE NUTRITIONAL COMPOUNDS IN FARMED *SACCHARINA LATISSIMA*?

Grebe, G., University of Maine / University of New England, United States, gretchen.grebe@maine.edu

LIGHT REDUCTION INSIDE KELP FORESTS CAN CONSTRAINT THEIR INVASION BY THE EXOTIC SEAWEED *UNDARIA PINNATIFIDA*

Sandoval-Gil, J. M., University of Baja California, Mexico, jmsandovalgil@gmail.com

MANGROVE ASSOCIATED RED ALGAL GENUS RECORDED FROM THE SUNDARBANS (THE WORLD LARGEST MANGROVE) FOREST, BANGLADESH

Islam, M. A., Hiroshima University, Japan, fisharif34@gmail.com

MIXOTROPHS: AN UNEXPECTED GUEST AT THE TEA PARTY

Sullivan, K. L., Florida International University, United States, ksull027@fiu.edu

NEARSHORE GROUNDWATER DEPENDENT ECOSYSTEMS AND THEIR ECOLOGICAL, CULTURAL, AND SOCIO-ECONOMIC VALUES IN KONA, HAWAI'I

Gibson, V. L., University of Hawai'i at Manoa

PERFORMANCE OF 3D MANUFACTURED SUBSTRATA IN THE ALGAL TURF SCRUBBER APPROACH

Blersch, D. M., Auburn University, United States, dmb0040@auburn.edu

PIONEERING A CITIZEN SCIENCE APPROACH TO MONITOR LANDINGS OF PELAGIC *SARGASSUM*

Iporac, L. A., Florida International University, United States, lipor001@fiu.edu

SYMBIOTIC DINOFLAGELLATE LINEAGE CAUSES HOST DEATH

Turnham, K. E., Penn State University, United States, ket7@psu.edu

THE LIVING SNOW PROJECT: COMMUNITY SUPPORTED PHYCOLOGY RESEARCH

Kodner, R. B., Western Washington University, United States, robin.kodner@wwu.edu

THE UNUSUAL METABOLIC OPERATION OF *EUGLENA*

Inwongwan, S., Department of Plant Sciences, University of Oxford, United Kingdom, sahutchai.inwongwan@new.ox.ac.uk

USING SATELLITE IMAGERY TO RECONSTRUCT BIOLOGICAL INVASIONS: THE CASE OF THE CLONAKILTY ESTUARY

Bermejo, R., Earth and Ocean Sciences, National University of Ireland, Galway, H91 TK33, Ireland., ricardo.bermejo@uca.es

VIRAL EDNA SURVEYS FROM AQUATIC HABITATS SHOW A DIVERSE CLASS OF SELFISH GENETIC ELEMENTS HAVE INVADDED THE GENOMES OF ALGAE INFECTING PHYCODNAVIRUSES.

Zanis, M. J., Seattle University, United States, zanism@seattleu.edu

WATERBORNE CHEMICAL CUES FROM MACROALGAE FOR CORAL LARVAE

Paul, V. J., Smithsonian Marine Station, United States, paul@si.edu

NOVEL BIODIVERSITY OF MARINE, TERRESTRIAL, AND FRESHWATER ALGAE ISOLATED THROUGHOUT SOUTH FLORIDA

Berthold, D. E., University of Florida IFAS, United States, dberthold@ufl.edu

16:30-18:30 **PSA Poster Session and Refreshments (Grand Ballroom Salon B)**

(#Eligible for PSA Student Lewin Award)

P1

IMPACTS OF MACROALGAL-ASSOCIATED GASTROPODS ON EPIPHYTIC MICROALGAE ON THE ECOLOGICALLY IMPORTANT ANTARCTIC BROWN ALGA *HIMANTOTHALLUS GRANDIFOLIUS*

Amsler, C. D., University of Alabama at Birmingham, United States, amsler@uab.edu

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Curtis, M. D., University of Alabama at Birmingham, United States, curtismi@uab.edu

McClintock, J. B., curtismi@uab.edu, United States, mcclinto@uab.edu

Baker, B. J., University of South Florida, United States, bjbaker@usf.edu

P2

A PRELIMINARY FLORA OF THE BENTHIC, CORAL-ASSOCIATED DIATOMS OF GRAY'S REEF NATIONAL MARINE SANCTUARY, GEORGIA, USA

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P3

SYSTEMATIC IDENTIFICATION AND ECOLOGY OF *CHARA* (CHARALES) IN STORMWATER TREATMENT AREAS OF SOUTH FLORIDA: A PRELIMINARY STUDY

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P4

EFFECTS OF GLYPHOSATE (RODEO) ON THE GROWTH OF *MICROCYSTIS AERUGINOSA* (CYANOBACTERIA)

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P5

PHYSIOLOGICAL DIFFERENTIATION AMONG GREEN ALGAL TURF SPECIES ON SOFT SEDIMENTS IN MANGROVE FORESTS IN TAMPA BAY, FL.: A CASE OF LIGHT NICHE PARTITIONING?

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#P6

THREE NEW GENERA OF MARINE CYANOBACTERIA FROM THE COAST OF SOUTH FLORIDA

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P7

PERFORMANCE OF 3D MANUFACTURED SUBSTRATA IN THE ALGAL TURF SCRUBBER APPROACH

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P8

COMPOSITION AND DOMINANCE OF BEACH CAST SEAWEEDS ON THE SOUTHEAST AND NORTHEAST COAST OF BRAZIL

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P9

A POLYPHASIC ASSESSMENT OF PHYLLOSHERE ASSOCIATED CYANOBACTERIA COLLECTED FROM NORTHEAST JACKSONVILLE, FLORIDA (USA).

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P10

PHYMATOLITHON CONCAVUM SP. NOV. (HAPALIDIACEAE, RHODOPHYTA) FROM THE NORTHEAST ATLANTIC OCEAN

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P11

MORPHOLOGICAL AND MOLECULAR ANALYSES UNCOVER A NEW SPECIES OF DIGenea (RHODOMELACEAE, RHODOPHYTA) FROM TROPICAL WESTERN ATLANTIC

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P12

THE NAGOYA PROTOCOL: WHAT IT IS AND WHY PHYCOLOGISTS SHOULD CARE

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P13

CAN PHOSLOCK® BE USED TO BIND AND SEDIMENT MICROCYSTIN-LR IN AQUATIC SYSTEMS?

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P14

DOES THE PRESENCE OF EYESPOTS INFLUENCE PLASTID-ASSOCIATED GALACTOLIPID COMPOSITION IN DINOFLAGELLATES?

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P15

MELANOTHAMNUS MANITICOLUS SP. NOV., AN EPIZOIC SPECIES EVOLVED FOR LIFE ON THE WEST INDIAN MANATEE

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P16

OVERVIEW OF LAURENCIA COMPLEX (CERAMIALES, RHODOPHYTA) DIVERSITY IN CUBA ASSESSED THROUGH MOLECULAR MARKERS

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P17

DIFFERENTIAL GENE EXPRESSION IN GREEN ALGAL COMPETITION

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P18

HARMFUL MACROALGAL BLOOMS: SOCIAL IMPACTS OF THE SARGASSUM INFLUX IN THE CARIBBEAN

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EFFECTS OF LIGHT, NUTRIENTS AND PREY ON INGESTION AND GROWTH OF A NEWLY IDENTIFIED MIXOTROPHIC ALGA, CHRYSOLEPIDOMONAS DENDROLEPIDOTA (CHRYSOPHYCEAE)

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COMPARING LONG-TERM STANDING STOCK AND TISSUE C:N:P RATIOS BETWEEN HALIMEDA AND PENICILLUS (CHLOROPHYTA) ACROSS A TROPHIC GRADIENT WITHIN FLORIDA BAY, USA.

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THE COSTS ASSOCIATED WITH BEING ABLE TO EAT THE BRUSSELS SPROUTS OF THE OCEAN

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#P22

CORAL-ALGAL COMPETITION AND OVERGROWTH DYNAMICS OF A RAPIDLY EMERGING RED ALGA (*RAMICRUSTA* SP.) IN ST. THOMAS, US VIRGIN ISLANDS

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P23

CYANOBACTERIAL BIOACTIVE METABOLITES – IS THERE A BETTER SYSTEM FOR CLASSIFICATION

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P24

CONTRIBUTION OF CHLOROPLASTS TO HETEROTROPHIC METABOLISM IN *EUGLENA GRACILIS*

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P25

A CITIZEN SCIENCE APPROACH TO MONITOR PELAGIC SARGASSUM LANDINGS IN SOUTH FLORIDA


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ASSESSING INVERTEBRATE HABITAT PREFERENCE IN A SHALLOW TROPICAL COASTAL BAY



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P27

CHARACTERIZATION OF ALGAL SEDIMENTATION, ADHESION, AND MORPHOLOGICAL TYPES SUCCESSION IN DIFFERENT SUBSTRATES

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INVESTIGATING THE EFFECT OF SURFACE ENERGY ON ATTACHED CULTIVATION OF ALGAE

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EISENIA ARBOREA: USING BARCODING TECHNIQUES TO GAIN INSIGHTS INTO DEEP WATER KELP SPECIATION PATTERNS

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P30

A STUDY IN OCHRE: GENETIC DIVERSITY OF LAMINARIA HYPERBOREA FORESTS ALONG THE IRISH COASTLINE

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#P31

HIGH-THROUGHPUT SEQUENCING OF CYANOBACTERIAL COMMUNITIES IN BOREAL PLAIN LAKES

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NOVEL SPECIES OF NEOLYNGBYA FROM BENTHIC CYANOBACTERIAL MATS OF COASTAL SOUTH FLORIDA.

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THE EFFECTS OF ALGAECIDES AND HERBICIDES ON A *MICROCYSTIS* WINTER BLOOM IN LAKE OKEECHOBEE, FLORIDA (USA)

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MICROALGAL EXTRACTS REDUCE CELL VIABILITY AND IMPROVE ANTIBIOTIC SENSITIVITY IN MICROBIAL BIOFILMS

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LIGHT-CONTROLLED PH UPREGULATION IN TROPICAL MACROALGAE: A PROPOSED MECHANISM TO SUSTAIN CALCIFICATION UNDER OCEAN ACIDIFICATION

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ENSO EFFECTS NEW PRODUCTION AND EUKARYOTIC PHYTOPLANKTON IN THE GALAPAGOS ARCHIPELAGO

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P37

MONITORING PROGRAM FOR PELAGIC *SARGASSUM* LANDINGS IN SOUTH FLORIDA

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DIVERSITY OF NEMALIALES (RHODOPHYTA) SPECIES FROM MESOPHOTIC ENVIRONMENTS IN THE HAWAIIAN ISLANDS

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ALTERATIONS TO THE MICRO-GEO-ENVIRONMENT AND ITS IMPACT ON ALGAL EXOSKELETONS: A PERSPECTIVE IN COCCOLITHOPHORES

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UNRAVELLING SPATIAL PATTERNS OF ALGAL ARRANGEMENT IN GIANT CLAMS

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P41

REVISION OF THE GENUS *SIRODOTIA* (BATRACHOSPERMALES, RHODOPHYTA).

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NEW SPECIES OF *GALENE* AND *HOWELLA* GEN. NOV. (HALYMENIACEAE, RHODOPHYTA) FROM THE MESOPHOTIC ZONE OFF BERMUDA

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THE DIVERSITY AND RESILIENCE OF KELP ECOSYSTEMS IN IRELAND

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FOUR NEW TO SCIENCE FILAMENTOUS CYANOBACTERIA ISOLATED FROM LAGUNA MADRE, TEXAS BASED ON TOTAL EVIDENCE APPROACH INCLUDING BIOCHEMISTRY

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P45

SEASONAL VERTICAL DISTRIBUTION OF PHYTOPLANKTON IN A SUBTROPICAL DYSTROPHIC LAKE

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EXPLORING THE FRESHWATER RHODOPHYTA DIVERSITY OF AFRICA

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RE-EVALUATION OF THE *SHEATHIA ARCUATA* SPECIES COMPLEX (BATRACHOSPERMALES, RHODOPHYTA)

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A COMPARISON OF PERIPHYTON DIVERSITY USING ILLUMINA SEQUENCING

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MORPHOLOGICAL AND MOLECULAR ASSESSMENT OF *HALIMEDA* (BRYOPSIDALES, CHLOROPHYTA) IN CARRIE BOW CAY, BELIZE

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HONOR BY ASSOCIATION, LEVERAGING CO-EXPRESSION NETWORKS FOR GENE DISCOVERY IN SPECIALIZED METABOLIC PATHWAYS

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INSIGHTS INTO ST JOHN ISLAND'S (USVI) RICH BENTHIC MACROALGAL FLORA (CHLOROPHYTA, PHAEOPHYTA, RHODOPHYTA) AND TRENDS IN CARIBBEAN BIODIVERSITY

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DIPLURA KOREANA SP. NOV. (ISHIGEALES, PHAEOPHYCEAE) FROM KOREA

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P53

VIRAL EDNA SURVEYS FROM AQUATIC HABITATS SHOW A DIVERSE CLASS OF SELFISH GENETIC ELEMENTS HAVE INVADDED THE GENOMES OF ALGAE INFECTING PHYCODNAVIRUSES.

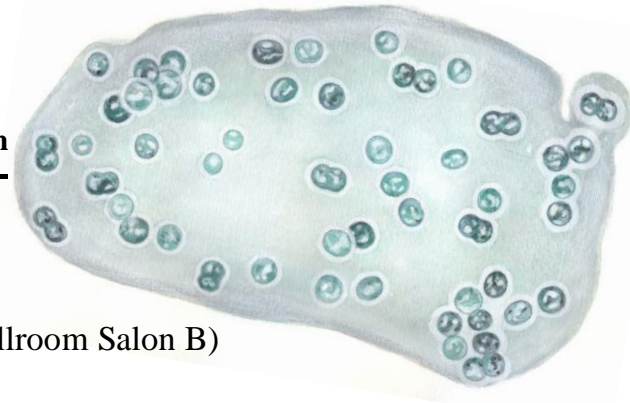
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Tuesday, June 25th



07:00-08:30 **Registration** (Pre-Function Area)

08:30-19:00 **Posters available for viewing** (Grand Ballroom Salon B)

08:30-09:45 **Bold Session** (Grand Ballroom Salon A) (*Moderator: Heather Spalding*)

08:30 A TWO-PRONGED APPROACH TO UNDERSTANDING *CHOREOCOLAX POLYSIPHONIAE* DEVELOPMENT AND *VERTEBRATA LANOSA* RESPONSE TO INFECTION.

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08:45 SALT INDUCED GENE EXPRESSION IN *CHARA LONGIFOLIA* C. B. ROB. AND *CHARA AUSTRALIS* R. BR.: IMPLICATIONS FOR SALT TOLERANCE MECHANISMS

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Bisson, M. A., University of Buffalo, United States, bisson@buffalo.edu

09:00 IRON AVAILABILITY DICTATES THE RESPONSE OF CORAL SYMBIONTS TO THERMAL STRESS

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Rodriguez, I. B., Academia Sinica, Taiwan

LaJeunesse, T. C., Penn State University, United States

Ho, T. Y., Academia Sinica, Taiwan

09:15 ARCTIC CRUSTOSE CORALLINE ALGAE, CARBONATE CHEMISTRY, AND THE CRITICAL ROLE OF SALINITY

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09:30 THE EFFECTS OF ENVIRONMENTAL STRESSORS ON CELL DEATH RESPONSES OF TOXIC DINOFLAGELLATE *KARENIA BREVIS* AND POTENTIAL BLOOM DECLINE PROCESSES

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09:45-10:30 **COFFEE BREAK** (Pre-Function Area)

10:30-12:00 **Bold Session** (Grand Ballroom Salon A) (*Moderator: Heather Spalding*)

10:30 ALTERATIONS IN PHOTOSYNTHETIC PERFORMANCE, METABOLIC POOLS AND LIPIDS IN *GALDIERIA SULPHURARIA* GROWN ON CORNSTOVER HYDROLYSATE

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Hanson, D., *The University of New Mexico, United States*, dthanson@unm.edu
Lammers, P., *Arizona Center for Algae Technology and Innovation, United States*, peter.lammers@asu.edu
Holguin, O., *New Mexico State University, United States*, frholgui@nmsu.edu

10:45 ASSESSMENT AND RECOMMENDATIONS FOR AN ECOSYSTEM APPROACH TO KELP AQUACULTURE

Grebe, G., *University of Maine & University of New England, United States*, gretchen.grebe@maine.edu
Byron, C. J., *University of New England, United States*, cbyron@une.edu
St. Gelais, A., *University of New England, United States*, astgelais@une.edu
Kotowicz, D. M., *Coastal Resources Center / Rhode Island Sea Grant, United States*, dkotowicz@uri.edu
Olson, T. K., *Ocean's Balance, United States*, tollefkolson@gmail.com

11:00 MULTI-MARKER METABARCODING AS A NEW APPROACH FOR MONITORING PERIPHYTIC ALGAL COMMUNITIES IN THE FLORIDA SPRINGS

Garvey, A. D., *University of North Florida, United States*, n01177173@ospreys.unf.edu
Besuden, A., *University of North Florida, United States*
Casamatta, D. A., *University of North Florida, United States*

11:15 RANKING SALISH SEA BULL KELP FORESTS ON THEIR CONNECTIVITY VALUE; A NETWORK APPROACH

Gierke, L. G., *University of Wisconsin-Milwaukee, United States*, lggierke@uwm.edu
Alberto, F. A., *University of Wisconsin-Milwaukee, United States*, albertof@uwm.edu

11:30 PHOTOSYNTHESIS, MORPHOLOGY, AND LIGHT-DEPENDENT PROTON PUMPS CONTROL TROPICAL REEF MACROALGAE RESPONSE TO OCEAN ACIDIFICATION

McNicholl, C. G., *Florida Atlantic University, United States*, cmcnicholl2015@fau.edu
Koch, M., *Florida Atlantic University, United States*, mkoch@fau.edu

11:45 OMEGA-7 PRODUCING ALKALIPHILIC DIATOM *FISTULIFERA ALCALINA* SP. NOV FROM LAKE OKEECHOBEE, FLORIDA

Berthold, D. E., *University of Florida & Florida International University, United States*, dberthold@ufl.edu
Gantar, M., *Florida International University, United States*, gantarm@fiu.edu
Frankovich, T., *Florida Bay Interagency Science Center, United States*, tfrankov@fiu.edu
Gaiser, E., *Florida International University, United States*, gaisere@fiu.edu
Laughinghouse IV, H. D., *University of Florida, United States*, hlaughinghouse@ufl.edu

12:00-13:30 LUNCH (Pre-Function Area)

Journal of Phycology Editors Meeting (Sunset Key Boardroom)

13:30-15:00 Contributed Session: Phylogeny & Systematics I (Grand Ballroom Salon A) (Moderator: Alison Sherwood)

13:30 THE SPECIES DILEMMA: A CASE STUDY WITH THE GENUS *HYPNEA* (GIGARTINALES, RHODOPHYTA) USING THE BIOLOGICAL SPECIES CONCEPT TO VERIFY DNA DIVERGENCE.

Nauer, F., *Botany Institute of Sao Paulo, Brazil*, fabionauer@gmail.com
Plastino, E. M., *Institute of Bioscience, University of Sao Paulo, Brazil*, emplasti@ib.usp.br
Fujii, M. T., *Botany Institute of Sao Paulo, Brazil*, mtfujii@ibot.sp.gov.br
Oliveira, M. C., *Institute of Bioscience, University of Sao Paulo, Brazil*, mcdolive@ib.usp.br



13:45 A MOLECULAR AND MORPHOLOGICAL REAPPRAISAL OF “RED BLADE” HAWAIIAN SEAWEEDS IN THE GENUS *KALLYMENIA* (GIGARTINALES, RHODOPHYTA)

Cabrera, F. P., University of Hawai'i, United States, feres@hawaii.edu

Sherwood, A. R., University of Hawai'i, United States, asherwoo@hawaii.edu

Huisman, J. M., Western Australian Herbarium, Australia, john.huisman@dbca.wa.gov.au

14:00 ECOLOGICAL SPECIALIZATION PROMOTES SPECIATION IN SYMBIOTIC MICROALGAE

Turnham, K. E., Penn State University, United States, ket7@psu.edu

LaJeunesse, T. C., Penn State University, United States, tcl3@psu.edu

14:15 *CORALLINA OFFICINALIS* VAR *CHILENSIS* (CORALLINALES, RHODOPHYTA) NOT A “VARIETY” AND DISCOVERED IN BOTH HEMISPHERES.

Huber, S., Department of Botany and Biodiversity Research Centre, University of British Columbia, Canada, saladsoren@gmail.com

Hughey, J., Division of Science and Mathematics, Hartnell College, United States

Miller, K. A., Herbarium, University of California at Berkeley, United States

Gabrielson, P., Herbarium, University of North Carolina, Chapel Hill, United States

Martone, P. T., Department of Botany and Biodiversity Research Centre, University of British Columbia, Canada

14:30 DIVERSITY OF THE GENUS *SHEATHIA* (BATRACHOSPERMALES, RHODOPHYTA) IN NORTHEAST INDIA AND EAST NEPAL

Necchi, O., São Paulo State University, Brazil, o.necchi@unesp.br

West, J. A., Melbourne University, Australia, jwest@unimelb.edu.au

Ganesan, E. K., Universidad de Oriente, Venezuela, ekganesan@gmail.com

Yasmin, F., Nowgong College, India, farishtayasmin@gmail.com

Rai, S. K., Tribhuvan University, Nepal, sk.khaling@gmail.com

Rossignolo, N. L., São Paulo State University, Brazil, nataliarossignolo@yahoo.com.br

14:45 MOLECULAR SYSTEMATICS OF THE SIPHONOUS GREEN ALGA *AVRAINVILLEA* (BRYOPSISDALES, CHLOROPHYTA) WITH AN EMPHASIS ON INVASIVE SPECIES IDENTIFICATION

Wade, R. M., University of Wisconsin-Milwaukee, United States, wader@uwm.edu

Sauvage, T. S., Smithsonian Marine Station, Fort Pierce, FL, United States,

tomsauv@gmail.com

Sherwood, A. R., University of Hawai'i at Manoa, United States, asherwoo@hawaii.edu

13:30-15:00 **Contributed Session: Ecology I (Atlantic Room)** (Moderator: Betty Staugler)

13:30 POTENTIAL MECHANISMS DRIVING THE GEOGRAPHIC DISTRIBUTION PATTERN OF DEFENSIVE SECONDARY METABOLITES IN THE RED SEAWEED *PLOCAMIMUM* “*CARTILAGINEUM*”

Heiser, S., University of Alabama at Birmingham, United States, heiser@uab.edu

Shilling, A., University of South Florida, United States, ashillin@mail.usf.edu

Amsler, C. D., University of Alabama at Birmingham, United States, amsler@uab.edu

Amsler, M. O., University of Alabama at Birmingham, United States, mamsler@uab.edu

McClintock, J. B., University of Alabama at Birmingham, United States, mcclinto@uab.edu

Krueger-Hadfield, S. A., University of Alabama at Birmingham, United States, sakh@uab.edu

Baker, B. J., University of South Florida, United States, bjbaker@usf.edu

13:45 WHEN FORM DOES NOT PREDICT FUNCTION: EMPIRICAL EVIDENCE VIOLATES FUNCTIONAL FORM HYPOTHESES FOR MARINE MACROALGAE.

Ryznar, E. R., University of California, Los Angeles, United States, emilyryznar@gmail.com

Fong, C. R., California State University, Northridge, United States, cat.r.fong@gmail.com

Fong, P., University of California, Los Angeles, United States, pfong@biology.ucla.edu

14:00 TISSUE WATER POTENTIAL REGULATION AND PHOTOSYNTHESIS BY *GRACILARIA SALICORNIA* IN A SUBMARINE GROUNDWATER DISCHARGE INFLUENCED SYSTEM

Gibson, V. L., University of Hawai'i at Manoa, United States

14:15 THE IMPORTANCE OF THE CHLOROPHYTE *OSTREOBIUM* SPP. DURING CORAL BLEACHING RECOVERY

Galindo-Martínez, C. T., The Pennsylvania State University, United States, czg30@psu.edu

Ávila-Magaña, V., The Pennsylvania State University, United States, vxa146@psu.edu

Medina, M., Pennsylvania State University, United States, mum55@psu.edu

Iglesias-Prieto, R., The Pennsylvania State University, United States, rzi3@psu.edu

14:30 THERMAL PLASTICITY IS INDEPENDENT OF ENVIRONMENTAL HISTORY IN THE INTERTIDAL CORALLINE ALGA *ELLISOLANDIA ELONGATA*

McCoy, S. J., Florida State University, United States, mccoy@bio.fsu.edu

Widdicombe, S., Plymouth Marine Laboratory, United Kingdom, swi@pml.ac.uk

14:45 DECIPHERING CHEMICAL SIGNALING IN ECOLOGICAL INTERACTIONS IN MARINE BENTHIC CYANOBACTERIA

Paul, V. J., Smithsonian Marine Station, United States, paul@si.edu

Gunasekera, S. P., Smithsonian Marine Station, United States, gunasekeras@si.edu

Meyer, J. L., University of Florida, United States, juliemeyer@ufl.edu

Teplitski, M., Smithsonian Marine Station, United States, maximteplitski@gmail.com

15:00-15:30 **COFFEE BREAK** (Pre-Function Area)

15:30-17:00 **Contributed Session: Phylogeny & Systematics II** (Grand Ballroom Salon A) (Moderator: Sophie McCoy)

15:30 A NEW CLASSIFICATION FOR THE GRACILARIALES (RHODOPHYTA) INCLUDING NEW SUBFAMILIES, TRIBES, SUBGENERA, AND TWO NEW GENERA, *AGAROPHYTON* AND *CRASSIPHYCUS*

Gurgel, C. F., Universidade Federal de Santa Catarina, Brazil, f.gurgel@ufsc.br

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Schmidt, W. E., The University of Louisiana at Lafayette, United States, william.schmidt.algae@gmail.com

Le, H. N., Nhatrang Institute of Technology Research and Application, lenhuhau2003@yahoo.com

Fredericq, S., The University of Louisiana at Lafayette, United States, slf9209@louisiana.edu

15:45 *MARTENSIA* (DELESSERIACEAE RHODOPHYTA) FROM SHALLOW AND MESOPHOTIC HABITATS IN THE HAWAIIAN ARCHIPELAGO: DESCRIPTION OF FOUR NEW SPECIES

Sherwood, A. R., University of Hawai'i at Manoa, United States, asherwoo@hawaii.edu

Lin, S. M., National Taiwan Ocean University, Taiwan, LINSM@ntou.edu.tw

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Spalding, H. L., College of Charleston, United States, spaldinghl@cofc.edu

Smith, C. M., University of Hawai'i at Manoa, United States, celia@hawaii.edu

Kosaki, R., NOAA Papahānaumokuākea Marine National Monument, United States, randall.kosaki@noaa.gov

16:00 TOWARDS UNDERSTANDING THE HOST AND HOLOBIOMES OF THE CARRAGEENOPHYTE RED ALGAE

Brodie, J., Natural History Museum, United Kingdom, j.brodie@nhm.ac.uk

Ward, G., Natural History Museum, United Kingdom, g.ward@nhm.ac.uk

Ross, S., Centre for the Environment, Fisheries and Aquaculture Sciences (Cefas), United Kingdom, stuart.ross@cefas.co.uk

Stentiford, G., Centre for the Environment, Fisheries and Aquaculture Sciences (Cefas), United Kingdom, grant.stentiford@cefas.co.uk

Bass, D., Centre for the Environment, Fisheries and Aquaculture Sciences (Cefas), United Kingdom, david.bass@cefas.co.uk

16:15 TAXONOMY AND BIOCHEMISTRY OF A NEW PLEUROCAPSAELEAN CYANOBACTERIUM ISOLATED FROM LAGUNA MADRE

Shalygin, S. S., Texas A&M University-Corpus Christi, United States, sergei.shalygin@tamucc.edu

Huang, I., Texas A&M University-Corpus Christi, United States, wade76924@gmail.com

Zimba, P. V., Texas A&M University-Corpus Christi, United States, paul.zimba@tamucc.edu

16:30 PRELIMINARY ASSESSMENT OF ANTARCTIC CORALLINE ALGAE (CORALLINOPHYCIDAE, RHODOPHYTA) BASED ON DNA SEQUENCING, INCLUDING SEQUENCING OF TYPE SPECIMENS

Gabrielson, P. W., University of North Carolina, Chapel Hill, United States, drseaweed@hotmail.com

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Le Gall, L., Muséum National d'Histoire Naturelle, France, linelegall@gmail.com

Pena, V., Universidade da Coruña, Spain, v.pena@udc.es

Schoenrock, K., National University of Ireland, Galway, kathryn.schoenrock@nuigalway.ie

16:45 THE POWER OF POINTS: MAXIMISING THE POTENTIAL OF CHAROPHYTE HERBARIUM DATA

Casanova, M. T., The Natural History Museum, London, United Kingdom, m.casanova@nhm.ac.uk

15:30-16:30 Contributed Session: Applied Phycology (Atlantic Ballroom) (Moderator: Kaytee Pokrzywinski)

15:30 ECOLOGICAL EFFECTS OF HARVESTING: A CASE STUDY OF HARVESTING AND POPULATION DYNAMICS OF THE CARRAGENOPHYTE *MAZZAELLA LAMINARIOIDES* IN MATANZAS, CHILE

Lopez-Vargas, G., University of Hawaii, United States, glopezv@hawaii.edu

Ticktin, T., University of Hawaii, United States, ticktin@hawaii.edu

Smith, C. M., University of Hawaii, United States, celia@hawaii.edu

15:45 UNIVERSAL PCR PRIMER SUITES FOR THE RAPID DETECTION OF ANATOXIN-A AND MICROCYSTIN-RELATED GENES IN FRESHWATER CYANOBACTERIAL COMMUNITIES

Perri, K. A., University of Texas at Austin, United States, katherineperri@utexas.edu
Manning, S. R., University of Texas at Austin, United States, schonna.manning@utexas.edu

16:00 OBSERVATIONS OF TWO RESERVOIRS IN CENTRAL TEXAS, USA DURING A DROUGHT: STATISTICAL STRATEGIES FOR DETECTING HARMFUL ALGAL BLOOMS

Gamez, T. E., Texas State University, United States, tatianaelise@live.com
Benton, L., Lower Colorado River Authority, United States, Lisa.Benton@lcra.org
Manning, S. R., University of Texas at Austin, United States, schonna.manning@utexas.edu

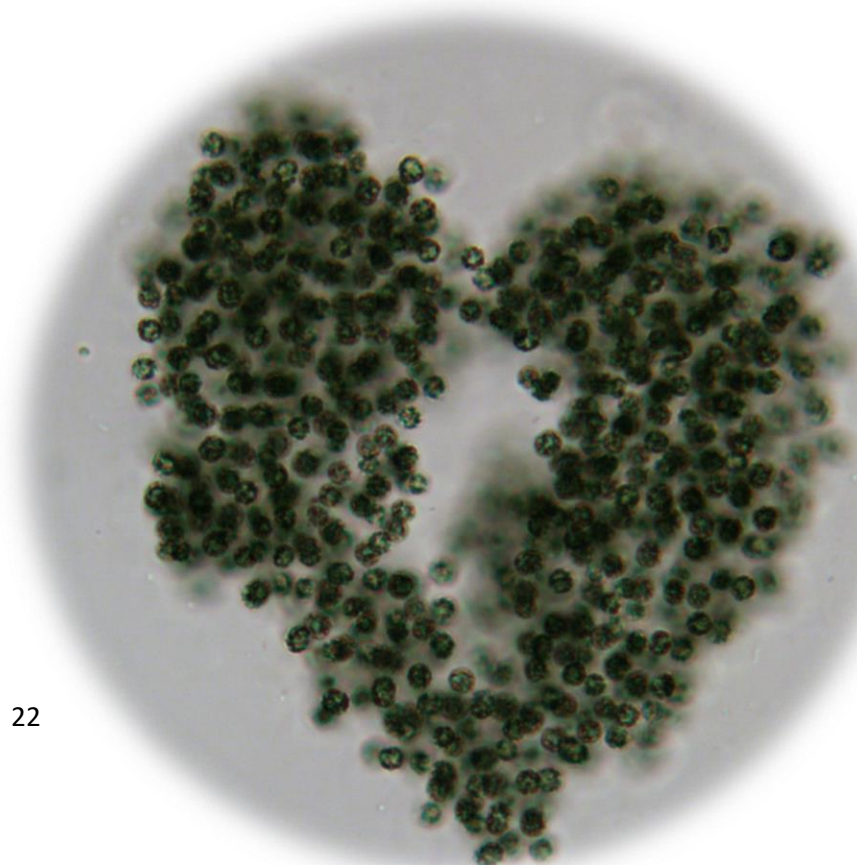
16:15 NEW TOOLS FOR SELECTIVELY IMPROVING STRAINS OF SUGAR KELP *SACCHARINA LATISSIMA* FOR FOOD AND FUEL

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Robbins, K., Cornell University, United States, krr73@cornell.edu
Schmutz, J., HudsonAlpha Institute for Biotechnology, United States, jschmutz@hudsonalpha.org *Smith, B., GreenWave, United States, bren@greenwave.org*
Wikfors, G. H., Milford Laboratory, NOAA, NMFS, NEFSC, United States, gary.wikfors@noaa.gov
Pitchford, S., Milford Laboratory, NOAA, NMFS, NEFSC, United States, steven.pitchford@noaa.gov
Robertson, L., Bell Center, Marine Biological Laboratory, United States, lroberston@mbl.edu
Kim, J. K., Incheon National University, South Korea, jang.kim@inu.ac.kr

17:00-18:00 **PSA Business Meeting** (Grand Ballroom Salon A)

18:00-20:00 **Auction, Snacks & Bar** (Grand Ballroom Salon A)

20:00 **Student Event**



Wednesday, June 26th

07:00-08:30 **Registration** (Pre-Function Area)

08:30-14:00 **Posters available for viewing** (remove by 14:00)

08:30-09:30 **Morning Plenary Lecture** (Grand Ballroom Salon A) (*Moderator: Dail Laughinghouse*)



08:30 BRINGING NEW LIFE TO HAB PREDICTION AFTER CROSSING THE VALLEY OF DEATH
Clarissa Anderson, SCCOOS, Southern California Coastal Ocean Observing System, Scripps Institution of Oceanography, La Jolla, CA United States, clrande@ucsd.edu

09:30-09:45 **COFFEE BREAK** (Pre-Function Area)

09:45-12:05 **Applied Symposium: From micro to macro: nuisance algae and their management** (Grand Ballroom Salon A) (*Moderators: Dail Laughinghouse & Schonna Manning*)



09:45 A NEW MAGNITUDE OF MACROALGAL BLOOMS; CAUSES, IMPACTS, AND CHALLENGES
Ligia Collado-Vides, Department of Biological Sciences, Florida International University, Miami, FL United States. colladol@fiu.edu



10:20 OPERATIONAL MANAGEMENT OF NOXIOUS ALGAE
West Bishop, SePRO Research and Technology Campus, Whitakers, NC United States. westb@sepro.com



10:55 THE ALGAL TURF SCRUBBER TECHNOLOGY AS “ECOLOGICAL JIJITSU”
Patrick Kangas, Department of Environmental Science and Technology, University of Maryland, College Park, MD United States. pkangas@umd.edu



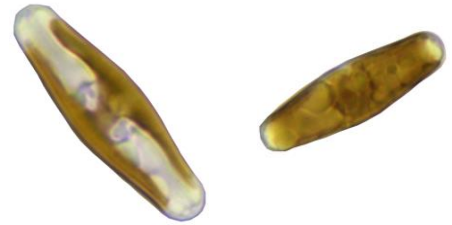
11:30 CYANOBACTERIAL ECOLOGICAL STRATEGIES AND BLOOM DYNAMICS: THE LAKE OKEECHOBEE SYSTEM
Barry Rosen, US Geological Survey, Orlando, FL United States. brosen@usgs.gov



- 12:00-18:00** **Free afternoon**
- 14:00-16:00** **Nomenclature Workshop (Atlantic Room)**
- 18:30-21:00** **PSA BANQUET (Grand Ballroom)**



Thursday, June 27



07:00-08:30

Registration (Pre-Function Area)

08:30-10:15

**Student-Organized Symposium: What goes on, on the inside?
Connecting algal physiology, their distribution and climate change**
(Grand Ballroom Salon A) (*Moderators: Arley Muth & Sabrina Heiser*)



08:30 ALGAL PHYSIOLOGY AND CLIMATE CHANGE

Catriona Hurd, Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, TAS Australia. catriona.hurd@utas.edu.au



09:05 ENVIRONMENTAL MODULATION OF TROPICAL CRUSTOSE CORALLINE RESPONSES TO OCEAN ACIDIFICATION

Maggie Johnson, Smithsonian Marine Station, Fort Pierce, FL United States. johnsonmd4@si.edu



09:40 CLIMATE CHANGE FORTUNES FROM PLANTS IN GLASS HOUSES

Evelyn Gaiser, Department of Biological Sciences & Institute of Water and Environment, Florida International University, Miami, FL United States. gaisere@fiu.edu



10:15-10:45

COFFEE BREAK (Pre-Function Area)

10:45-12:00

Contributed Session: Evolution (Grand Ballroom Salon A) (*Moderator: Frederico Gurgel*)

10:45 GENE TRANSFER ACCOMPANYING THE SECONDARY ENDOSYMBIOSIS OF EUGLENID PLASTID

Soukal, P., Charles University, BIOCEV, Czech Republic, 278120@gmail.com

Hrda, S., Charles University, BIOCEV, Czech Republic, hrdastepa@seznam.cz

Novak Vanclova, A., Charles University, BIOCEV, Czech Republic, vanclova@gmail.com

Yubuki, N., Université Paris Sud, France, yubuki@mail.ubc.ca

Lax, G., Dalhousie University, Canada, gordon.lax@dal.ca

Simpson, A., Dalhousie University, Canada, alastair.simpson@dal.ca

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Milanowski, R., University of Warsaw, Poland, milan@biol.uw.edu.pl

Hampl, V., Charles University, BIOCEV, Czech Republic, vlada@natur.cuni.cz

11:00 SUBTLE DIFFERENTIATION MAINTAINS HAPLODIPLONTIC LIFE CYCLES ... UNTIL IT DOESN'T

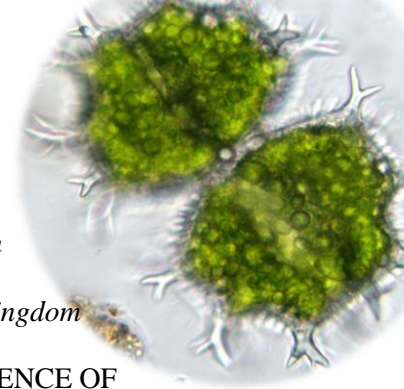
Krueger-Hadfield, S. A., University of Alabama at Birmingham, United States, sakh@uab.edu

Ryan, W. H., University of Alabama at Birmingham, United States,

Bonthond, G., GEOMAR, Germany,

DeForest, J., Ohio University, United States





Hays, C. G., *Keene State College, United States*
Adams, L., *The Marine Biological Association of the United Kingdom, United Kingdom*
Pack, K. E., *The Marine Biological Association of the United Kingdom*
Mieszkowska, N., *The Marine Biological Association of the United Kingdom, United Kingdom*

11:15 ESTIMATING THE SHIFT TO MULTICELLULARITY AND THE EMERGENCE OF SHALLOW COASTAL ECOSYSTEMS USING HETEROKONT ORGANELLAR GENOMES
Phillips, N., Arcadia University, United States, phillipsn@arcadia.edu

11:30 TRANSCRIPTOMICS AND POPULATION GENETICS REVEAL THE ROLE OF POLYPLOIDY AND LIFE HISTORY IN *MICRASTERIAS ROTATA* (DESMIDIACEAE)
Zanis, M. J., Seattle University, United States, zanism@seattleu.edu

11:45 USING AN “ALIEN INDEX”; APPROACH TO EVALUATE THE EXTENT OF HORIZONTAL GENE TRANSFER IN *DINOPHYSIS ACUMINATA*.
Gavelis, G. S., Purdue University, United States, ggavelis@purdue.edu
Wisecaver, J. H., Purdue University, United States, jwisecav@purdue.edu

10:45-12:00 **Contributed Session: Ecology II** (Atlantic Room) (Moderator: Schonna Manning)

10:45 PERIPHYTON COMMUNITIES IN THE ATCHAFALAYA FLOODPLAIN
Gallardo, K. D., Louisiana State University, United States, kstamey@lsu.edu
Errera, R. M., Great Lakes Environmental Research Laboratory, United States, reagan.errera@noaa.gov
Kaller, M. D., Louisiana State University, United States, mkalle1@lsu.edu
Kelso, W. E., Louisiana State University, United States, wkelso@lsu.edu

11:00 LOSING LARGE BROWN ALGAE: DRAMATIC SHIFTS IN MACROALGAL ASSEMBLAGES OVER 50 YEARS IN WAIKIKI, SOUTH OAHU
Spalding, H. L., College of Charleston, United States, spaldinghl@cofc.edu
Dagostino, Z. J., University of Hawai'i at Manoa, United States, zinniajd@hawaii.edu
Morrow, L., University of Hawai'i at Manoa, United States, lmorrow@hawaii.edu
Katz, R. M., University of Hawai'i at Manoa, United States, rmkatz@hawaii.edu
Strait, N., College of Charleston, United States, straits@g.cofc.edu
Philippoff, J., University of Hawai'i at Manoa, United States, philippo@hawaii.edu

11:15 LIGHT REDUCTION INSIDE KELP FORESTS CAN CONSTRAINT THEIR INVASION BY THE EXOTIC SEAWEED *UNDARIA PINNATIFIDA*
Sandoval-Gil, J. M., University of Baja California, Mexico, jmsandovalgil@gmail.com

11:30 WHY ARE THERE SUCH UNUSUALLY DENSE POPULATIONS OF *ACETABULARIA* AND *BATOPHORA* IN ANCHIALINE LAKES OF THE BAHAMAS?
Birchfield, H., University of Arkansas, Little Rock, United States, habirchfield@ualr.edu
Sheehan, K. L., Frostburg State University, United States, KLSheehan@frostburg.edu
Ashworth, M. P., University of Texas, Austin, United States, mashworth@utexas.edu
Yeager, R., University of Arkansas, Little Rock, United States, rxyeager@ualr.edu
Ford, D., University of Tennessee, Chattanooga, United States, Dawn-Ford@utc.edu
Martin, C., University of North Carolina, Chapel Hill, United States, chmartin@unc.edu
Manning, S. R., University of Texas, Austin, United States, schonna.manning@utexas.edu
Shroat-Lewis, R., University of Arkansas, Little Rock, rashroatlew@ualr.edu
Ruhl, L. S., University of Arkansas, Little Rock, United States, lsruhl@ualr.edu

Woolbright, S. A., University of Arkansas, Little Rock, United States, sawoolbright@ualr.edu

12:00-13:30 **LUNCH** (Pre-Function Area)

13:30-15:00 **Contributed Session: Harmful Algal Blooms** (Grand Ballroom Salon A)
(Moderator: Valerie Paul)

13:30 IS THERE AN ECO-FRIENDLY TREATMENT TO CONTROL CYANOBACTERIAL HARMFUL ALGAL BLOOMS?

Huang, L., Texas A&M University-Corpus Christi, Center for Coastal Studies, United States, wade76924@gmail.com

Zimba, P. V., Texas A&M University-Corpus Christi, Center for Coastal Studies, United States, paul.zimba@tamucc.edu

13:45 DIFFERENCES IN XANTHOPHYLL DE-EPOXIDASE ACTIVITY IN HIGH AND LOW TOXIC STRAINS OF *KARENIA BREVIS*

Colón, R., Florida International University, United States, rcolo030@fiu.edu

Rein, K., Florida International University, United States, reink@fiu.edu

14:00 EFFECT OF DIFFERENT MINIMUM SAMPLING AREAS ON THE ASSESSMENT OF SPATIAL VARIABILITY: A CASE STUDY IN A GREEN TIDE

O'Donnell, M., National University of Ireland, Galway, Ireland, odonnellmoya@gmail.com

14:15 COULD THE LOSS OF DMA PROVIDE A SIGNIFICANT AMOUNT OF NITROGEN (N) AND PHOSPHORUS (P) TO SUPPORT THE SUPER BLOOM IN THE INDIAN RIVER LAGOON, FLORIDA?

Hanisak, M. D., FAU Harbor Branch, United States, dhanisak@fau.edu

14:30 NUTRIENT DYNAMICS AND ECO-PHYSIOLOGY OF OPPORTUNISTIC MACROALGAL BLOOMS IN IRISH ESTUARIES AND COASTAL BAYS (SEA-MAT PROJECT)

Morrison, L., National University of Ireland Galway, Ireland, liam.morrison@nuigalway.ie

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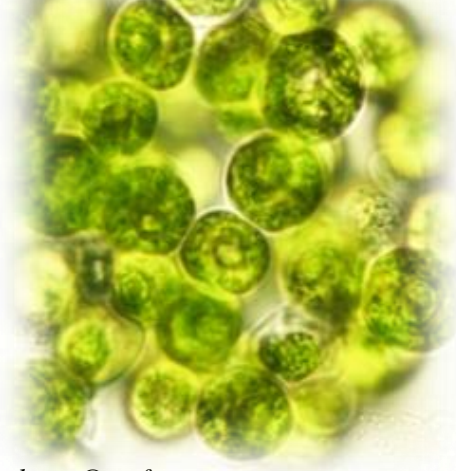
14:45 VITAMIN B12 ECOLOGY AND PHYSIOLOGY OF *KARENIA BREVIS*

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13:30-15:15 **Contributed Session: Biodiversity** (Atlantic Room) (Moderator: Amy Carlile)

13:30 MORPHOMETRIC ACCOUNT OF *CALOGLOSSA* (DELESSERIACEAE, RHODOPHYTA) INCLUDING FOUR NEW RECORDS FROM THE SUNDARBANS, BANGLADESH
Islam, M. A., Hiroshima University, Japan, fisharif34@gmail.com

13:45 DNA SEQUENCING OF TYPE SPECIMENS REVEALS TWO HOMOTYPIC SYNONYMS FOR THE CORALLINE SPECIES *HARVEYLITHON MUNITUM* (METAGONIOLITHOIDEAE, CORALLINALES)

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Hughey, J. R., Division of Mathematics, Science, and Engineering, Hartnell College, United States, jhughey@hartnell.edu
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Peña, V., Universidade da Coruña, Spain, vpena@udc.es
Gabrielson, P. W., University of North Carolina, Chapel Hill, United States, drseaweed@hotmail.com

14:00 BIOGEOGRAPHICAL PATTERNS OF INDONESIAN SAR CLADE COMMUNITIES IN RELATION TO WALLACE'S LINE

Borbee, E. M., University of Rhode Island, United States, eborbee@uri.edu
Humphries, A. T., University of Rhode Island, United States
Madduppa, H. H., Institut Pertanian Bogor, Indonesia
Lane, C. E., University of Rhode Island, United States, clane@uri.edu

14:15 A BIODIVERSITY EVALUATION OF INTERTIDAL ALGAL COMMUNITIES FROM THE ALABAMA GULF COAST VIA METABARCODING

Bombin, S., The University of Alabama, United States, sbombin@crimson.ua.edu
Wysor, B., Roger Williams University, United States, bwysor@rwu.edu
Lopez-Bautista, J., The University of Alabama, United States, jlopez@ua.edu

14:30 THE IMPORTANCE OF RHODOLITHS FOR MACROALGAL BIODIVERSITY IN GULF OF MEXICO MESOPHOTIC HABITATS

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Bradshaw, B., University of Louisiana at Lafayette, United States, Brandonbradshaw@cox.net
Schmidt, W. E., University of Louisiana at Lafayette, United States, wes4500@louisiana.edu

14:45 THE ARCTIC OCEAN BIOME AND PHYTOPLANKTON ENDEMICITY.

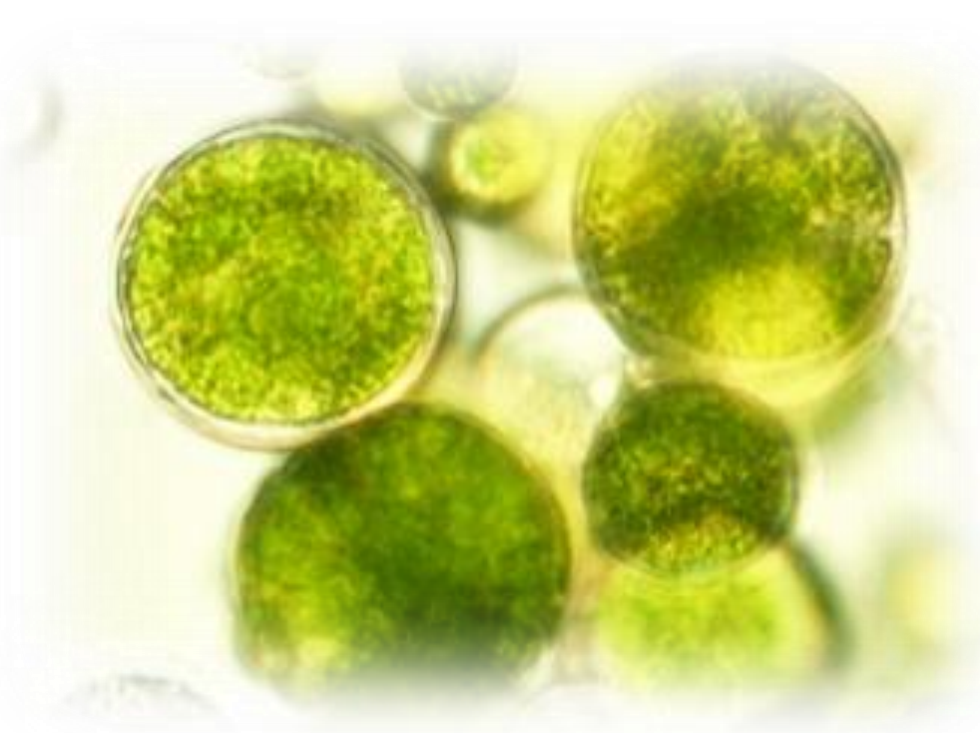
Lovejoy, C., Laval University, Canada, connie.lovejoy@bio.ulaval.ca

**15:00 GETTING INTO THE WEEDS – EYES ON SEAGRASS CITIZEN SCIENTISTS DOCUMENT
MACROALGAL DISTRIBUTION PATTERNS IN A FLORIDA ESTUARY**

Staugler, E. A., Florida Sea Grant, University of Florida IFAS Extension, United States, staugler@ufl.edu
*Smyth, A. R., Soil and Water Sciences Department, Tropical Research and Education Center, University of
Florida, United States, ashley.smyth@ufl.edu*

15:15-15:45 COFFEE BREAK (Pre-Function Area)

15:45-16:00 CLOSING REMARKS (Grand Ballroom Salon A)





**73rd Annual Meeting of the
Phycological Society of America presents:**

Algae and Climate Change

June 23-27, 2019



**PSA 2019
MEETING
ABSTRACTS**

PSA 2019 Meeting Abstracts

Plenaries

BRINGING THE OCEAN TO EYE LEVEL: EMPOWERING THE NEXT GENERATION OF WOMEN LEADERS IN THE ARCTIC

Eaton. S.R., Sedna Epic Expedition, Calgary, AB Canada, susan@sednaepic.com

The multi-year Sedna Epic Expedition is comprised of a volunteer team of women ocean explorers, scientists, photographers, videographers, artists, historians, educators and scuba divers from Canada, the USA, Mexico and New Zealand. Founded in 2014, the Sedna Epic's mandate is to scout, record and document disappearing sea ice in the Arctic. In collaboration with Inuit advisors and team members, Sedna's 60 sea women (ages 16 to 65 years) have brought the ocean to eye level for 1,000 Inuit youths, girls and Elders in Labrador, Nunavut and Greenland, using mobile touch aquariums to temporarily house sea critters and by running workshops to build underwater robots equipped with video-cameras. Taking this experiential learning concept one step further, Sedna's sea women have equipped Inuit girls and Elders with dry suits, masks, fins and snorkels, leading them on snorkel safaris to explore what lies beneath the waves in their own back yards. Team Sedna has mentored Inuit girls and young women during its dive and snorkel expeditions, introducing them to ocean careers and placing them in leadership roles during the community-based robot and aquarium programs. Through its unique ocean knowledge sharing and mobilization program, the Sedna Epic Expedition aims to inspire and empower Inuit girls and young women of the Arctic—the next generation of leaders in these matriarchal Indigenous societies—who will combat climate change and societal change in remote northern communities

BRINGING NEW LIFE TO HAB PREDICTION AFTER CROSSING THE VALLEY OF DEATH

Anderson, C. Executive Director, SCCOOS, Southern California Coastal Ocean Observing System, Scripps Institution of Oceanography, La Jolla, CA United States, clrander@ucsd.edu

Harmful algal blooms (HABs) caused by the toxic diatom *Pseudo-nitzschia* have become commonplace in coastal California, with routine shellfish advisories and annual stranding events of protected marine mammals and seabirds. Determining when and how *Pseudo-nitzschia* blooms turn toxic has become one of the perennial struggles of HAB science. Gaps in our knowledge of the biodiversity and ecophysiology of this complex genus are a significant part of the problem. The largest shellfish disaster was in 2015 with an unprecedented HAB that closed the Dungeness and rock crab fishery in California for the entire season and resulted in \$60M dollars in losses. A fundamental question affecting the mitigation of HAB events is how well the coastal oceanographic conditions that nurture these blooms explain the risk to estuarine environments where much of the commercial and recreational shellfish harvesting occurs. With the introduction of the “operational” California Harmful Algae Risk Mapping (C-HARM) system, coastal conditions conducive to blooms of *Pseudo-nitzschia* and its associated toxin, domoic acid, can be monitored in real-time. This kind of advanced warning has proven valuable to marine mammal resource managers given the tight connection between offshore toxins and animal stranding events. Useful predictions could be anything from seasonal to weather-scale forecasts depending on regional needs and modeling capabilities. Where C-HARM provides less information is in major inlets such as the San Francisco Bay-Estuary and Humboldt Bay. The latter is the site of some of the highest commercial oyster production in the nation, which is very rarely affected by toxins

even when the coastal region is experiencing a major HAB. The mystery deepens now that we have observed several seasons of periodic bursts of record high domoic acid in the waters surrounding shellfish growing sites in Humboldt Bay. Using a combination of particle tracking simulations and coincident measures of shellfish and water toxin levels, we explore the biological and physical controls that explain patterns that might underlie the mystery of Humboldt Bay. Our central aim is to improve model products for key stakeholders currently underserved by routine HAB forecasts and to identify the physical and biological factors affecting HAB risk in California estuaries. This plenary talk will delve into the various approaches taken in California and the quest to make models that are most useful to stakeholders.

Presidential Symposium. Climate Change and our Fragile Polar Ecosystems:

ARCTIC CYANOBACTERIA AND THE POLAR PARADOX

Vincent, W.F., Center for Northern Studies (CEN), Laval University, Quebec City, QC Canada

This talk is dedicated to two phycologists who contributed enormously to the understanding of cyanobacteria, and who inspired so many of us: Norma J. Lang (University of California, Davis) and Richard W. Castenholz (University of Oregon).

In 1874, Captain George Nares and his Lieutenant Pelham Aldrich were recalled urgently back to England, interrupting their command of the Challenger Expedition that was in the process of founding the new science of oceanography. Their services were needed for the more pressing duty of leading an expedition to the North Pole, the British Arctic Expedition of 1875-76, and although this goal was not achieved, the expedition returned with new knowledge of the extreme north of Canada, and a collection of botanical samples. These are now held at the Natural History Museum (NHM) of London, and they include herbarium sheets of the macroscopic cyanobacterium *Nostoc commune*. Other explorers in the polar regions, including Nordenskiöld in Svalbard and Greenland, and Scott in the Ross Sea region, brought back accounts of the widespread occurrence of *Nostoc* and other cyanobacteria in the Arctic and Antarctica. These accounts are puzzling even today, given that cyanobacteria are often considered to be warm water organisms that will increasingly dominate throughout the world as temperatures rise with global climate change. Yet cyanobacteria are often the ecosystem dominants in polar lakes, ponds and streams, with benthic species forming thick biofilms, and cyanobacteria are often the most abundant photosynthetic cells in the plankton. While picocyanobacteria can achieve extreme concentrations in polar lakes, they are conspicuously sparse or absent in the adjacent cold polar seas. This talk explores the ‘paradox of the picoplankton’ and the potential importance of top down controls on cyanobacteria in polar waters, with evidence of viral footprints across the Arctic based on molecular analysis of the historic NHM samples from the Nares expedition in the 19th century.

HOMEWARD BOUND: LEADERSHIP, SCIENCE AND ANTARCTICA.

McManus, H.A., Biological and Environmental Sciences, Le Moyne College, Syracuse, NY United States, mcmanuha@lemoyne.edu

Homeward Bound is the world’s first women-focused leadership development and science initiative that aims to build a global collaboration of 1,000 women in science over a 10-year period with Antarctica as its backdrop. The goal of the program is to increase the representation of women in STEM and in leadership roles to heighten their influence and impact in making decisions that shape the planet. The curriculum focuses on the development of leadership capabilities, strategy design and execution, and developing plans for global collaborations as science leaders working toward a sustainable future. In 2017, the second year of the Homeward Bound program, 77 female scientists from around the world were selected and worked remotely on the curriculum during 11 months prior to their departure for Antarctica. In February 2018, the participants embarked on a 21-day voyage to Antarctica, during which they continued their leadership development while participating in an immersive scientific program on

Antarctic conservation, marine and terrestrial ecosystems, and a participant-led science symposium. The program has since trained its third cohort of international women in STEM and is currently training its fourth cohort, bringing the total number of participants to 328. The next voyage to Antarctica is scheduled for November 2019.

ANTARCTICA'S CRYSTALLINE WEB OF LIFE: ITS BEAUTY AND ITS PERILS

Amsler, M., University of Alabama at Birmingham, Birmingham, AL, United States, mamsler@uab.edu

Marine communities along the Western Antarctic Peninsula are rife with relationships connecting biological and environmental partners. Woven as intricately as a spider's, but not as rapidly, this polar web formed during millions of years of isolation. Yet, post-industrial revolution global changes threaten both the tensile and elastic character of Antarctica's marine web. The Antarctic krill *Euphausia superba* ultimately owes its astronomical biomass to annual winter sea ice laden with micro-algae to protect and nourish its young of the year multitude. Spring melt of sea ice reseeds the water column for ensuing summer phytoplankton bloom vital for krill grazing. In recent decades, dips in krill biomass following a poor sea ice year are mirrored in lowered reproductive success of krill-consuming Adelie penguins. Often concomitant unseasonal rain or snow melts during egg incubation drown otherwise promise-filled nests. Warming air and sea temperatures also promote range extensions leading to 'invasives' supplanting or preying 'natives'. Decapod crabs die in waters under 0.4C but a population of deep-sea crab recently imaged on the continental slope may eventually expand upward to shallower waters. Antarctica's sublittoral, rich with macroalgal forests teeming with mutually beneficial grazers, lacks crushing predators like crabs and its inhabitants rely on chemical rather than structural defenses. The warming waters are also becoming increasingly acidic stressing calcifying organisms, including numerous invertebrate taxa and coralline algae. How resilient is this web?

Applied Symposium: From micro to macro: nuisance algae and their management

A NEW MAGNITUDE OF MACROALGAL BLOOMS: CAUSES, IMPACTS AND CHALLENGES.

Collado-Vides, L. Department of Biological Sciences, Florida International University, Miami, FL United States, colladol@fiu.edu

Algal blooms are part of our oceans and coastal ecosystems' dynamics, however in recent years reports of increase in frequency and magnitude of these blooms have caused alarm. Macroalgal blooms are also increasing and becoming harmful to ecosystems and humans. Finding causes, consequences and ability to forecast and manage these blooms are challenging scientists, managers and policy makers. Macroalgal blooms are from species of green, red and brown divisions; some are from introduced species, others are native, or from large displacements of pelagic species. Increases in nutrient availability from continental fertilizers, industrial and residential wastes, discharged at local scale and accumulated in the oceans; as well as climate change are suggested as major causes that facilitate these massive growths. While we have strong correlations, in some cases we need experimental proofs linking nutrients to some macroalgal blooms. Our studies from South Florida and the Caribbean demonstrate that losses of seagrass beds are the immediate impact of massive influxes of macroalgae on shores and beaches; and increase in frequency and magnitude of these events results in ecosystem shifts to benthic macroalgae dominated systems. In addition, lack of basic biological knowledge of blooming species needs to be addressed. The problem is dire, and needs coordinated efforts of scientists, managers and policy makers. However, macroalgal blooms are fixing carbon and incorporating nutrients, a wise use of those blooms can become an opportunity for stakeholders and for cleaning the oceans.

OPERATIONAL MANAGEMENT OF NOXIOUS ALGAE

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Many proactive measures to restore water quality may fall short in limiting harmful cyanobacterial blooms as they continue to spread and bloom in a wide diversity of ecosystems globally. Acknowledging this lack of direct correlation with blooms and uncertain outcomes and timelines for improvement, other routes of management are critical to offset risks to humans, wildlife, and in worst-case scenarios, local and regional economies. This presentation reviews a broad spectrum of management options, though will specifically look at effectiveness of some chemical controls directly to the bloom. USEPA registered products, approved for use in surface water to control cyanobacteria, are widely used and advanced formulations can provide rapid, selective and long-term efficacy when used as designed with minimal risks to non-target organisms. Operational treatments with algaecides, in concert with proactive techniques or where these were insufficient or not feasible, have shown significant control of numerous types of nuisance algae. Some examples covered include surface water reservoirs destined for human consumption, irrigation canals, swim ponds and shallow reservoirs with high recreational use. Potential for toxin release, non-target impacts, and longevity of control will be discussed and put in context with risks of unabated toxic blooms. Though proactive measures are critical, often to preserve short-term water uses and protect human health, ecological function, and economic benefits of water resources, reactive measures need to be highly considered.

THE ALGAL TURF SCRUBBER TECHNOLOGY AS "ECOLOGICAL JIJITSU"

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The algal turf scrubber™ (ATS) is an ecologically engineered technology, developed through research and development over thirty years, that removes nutrients (and other pollutants) from and adds dissolved oxygen to water through controlled growth of algae. When employed at the watershed scale the ATS has the potential to restore nutrient-enriched, low oxygen water bodies such as polluted lakes, reservoirs and bays. In the typical ATS, algae are grown attached to a screen in a shallow (10-20 cm deep), sealed basin or flowway, angled at 1 to 2 percent slope, through which water is pumped. Algae absorb pollutants as they grow, and these pollutants are removed from the water by frequent harvesting (once per week) of the algae. Based on a number of studies on polluted waters in the temperate zone, the ATS can remove on the order of 1 metric ton of nitrogen/ha/year and 0.1 metric ton of phosphorus/ha/year, it can add 5 metric tons of dissolved oxygen/ha/year and it can produce 30 metric tons of dry algal biomass/ha/year that can provide economic byproduct value. The ATS technology takes advantage of the power of microalgae to grow and to take up nutrients at a high rate in order to improve water quality. In an abstract sense the controlled algal growth of the ATS is the mirror-image of the uncontrolled algal growth of an algal bloom that impairs water quality in eutrophication. In this presentation use of the ATS as a kind of “ecological jujitsu” is explored by contrasting its structure and function with different kinds of algal blooms.

CYANOBACTERIA ECOLOGICAL STRATEGIES AND BLOOM DYNAMICS: THE LAKE OKEECHOBEE SYSTEM

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In Florida, many lakes are dominated by planktonic cyanobacteria during the warmer months. Cyanobacteria have a suite of ecological strategies, such as buoyancy regulation, luxuriant phosphorus uptake, and nitrogen fixation, that give them a competitive advantage over eukaryotic algae, particularly in warm waters. In addition to competition with the eukaryotic community, the success and subsequent dominance of one cyanobacterial species over another needs additional scrutiny to provide a better understanding of bloom dynamics. General cyanobacterial and species-specific ecological strategies, heterotrophic bacteria, nutrient concentrations, and physical factors such as water

temperature, water column stability and light availability, interact in complex ways to initiate and maintain blooms, and play a role in the demise and senescence of a bloom. At this time, no simple mechanism can be attributed to bloom formation or the predominance of a toxin-producing cyanobacterial strain. Lake Okeechobee, with an approximate area of 1891 km² footprint, has experienced cyanobacterial blooms for more than 3 decades and has been dominated by nitrogen-fixing genera (*Dolichospermum*) and non-nitrogen fixing genera (*Microcystis*), including strains that are producing cyanotoxins. A multi-agency, large-scale spatial and temporal study has been initiated to understand bloom dynamics in this system using metagenomics and a variety of physical and chemical parameters to better understand factors controlling cyanobacterial blooms in this lake.

Student Organized Symposium. What goes on, on the inside? Connecting algal physiology, their distribution and climate change:

ALGAL PHYSIOLOGY AND CLIMATE CHANGE

Hurd, C. Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, TAS Australia, catriona.hurd@utas.edu.au

Rising levels of atmospheric carbon dioxide are causing two major shifts in oceanic properties: ocean acidification (OA, also termed CO₂ enrichment) and ocean warming (OW). OA and OW each contribute to a spectrum of changes to the productivity of seaweed: whether these changes are positive, neutral or negative depends on its carbon acquisition strategy and/or temperature tolerance. OA and OW are often studied separately but in the coastal ocean, a crucial question is how the interplay of OA and OW affects the primary productivity of a physiologically diverse range of seaweeds. In this talk, I will take a physiological approach to examining how seaweed productivity might be altered in a future ocean. We have identified five mechanisms by which seaweeds acquire dissolved inorganic carbon. The vast majority of seaweeds can take up dissolved CO₂ by passive diffusion, while around 65% can additionally use bicarbonate (CCM-species) which has a higher energetic demand. One-third of seaweed species can take up CO₂ by diffusion only and do not operate a CCM (non-CCM species). I will illustrate how the energetics and mechanisms of DIC acquisition by seaweeds will define their productivity in a future high CO₂ ocean, and discuss interactions between CO₂ enrichment and rising temperature.

ENVIRONMENTAL MODULATION OF TROPICAL CRUSTOSE CORALLINE RESPONSES TO OCEAN ACIDIFICATION

Johnson, M. Smithsonian Marine Station, Fort Pierce, FL United States, johnsonmd4@si.edu

Ocean acidification (OA) is one of the most pressing environmental concerns for the persistence of marine ecosystems. Though crustose coralline algae (CCA) are considered among the most sensitive marine taxa to OA, recent research has demonstrated substantial variability in CCA responses to the changes in pH predicted with OA. Some of this variation may be linked to interspecific tolerances or sensitivities, but less is known about the contribution of co-occurring abiotic conditions. A suite of environmental factors, including temperature, nutrients, and environmental variation itself, may shape coralline responses to changes in pH. Laboratory experiments in the tropical Pacific and Caribbean demonstrate that the effects of OA on coarse CCA physiology, including calcification and photophysiology, can be modulated by simultaneous exposure to warmer temperatures or nitrogen enrichment. Further, a combination of lab and field experiments illustrate how prior exposure to highly variable pH environments can either promote acclimatization or enhance sensitivity of CCA exposed to subsequent changes in pH. These findings shed light on the importance of considering other abiotic factors and environmental history when evaluating CCA responses to changing pH. Additionally, they contribute to our understanding of the limited potential for environmental variability to promote acclimatization of CCA to OA, and improve our ability to predict how ecosystem trajectories may shift in the coming decades, within the tropics and beyond.

CLIMATE CHANGE FORTUNES FROM PLANTS IN GLASS HOUSES

Gaiser, E. Department of Biological Sciences and Institute of Water and Environment, Florida International University, Miami, FL United States, gaisere@fiu.edu.

Signals of global change abound in nature provided we take the opportunity to look for them. At the largest scale, public greenhouses cure “plant blindness” by sparking curiosity about biodiversity and inspiring observation of changes in the world around us. At the tiniest scale, microscopes provide a window into another world of “glass houses,” the diatoms, which are sending important messages about environmental change. For decades, diatoms have been employed in detecting the slightest changes in a vast array of water quality attributes, but more recently, their sensitivity to climate change variables has gained attention. In coastal wetlands, diatoms are particularly sensitive to changing salinity and nutrient availability associated with saltwater intrusion driven by sea level rise. Manipulative experiments and long-term observational studies are being combined to precisely define the ecological preferences and tolerances of hundreds of coastal diatom species in order to determine saltwater intrusion rates. In the coastal Everglades, diatom-inferred ecosystem boundaries are shifting inland at rates of several meters per year. Paleocological inferences of past salinity show the influence of decades of shifting water management practices on these rates of change. Landscape modeling approaches are now being utilized to help managers understand the implications of these changes on the rate of diatom-inferred saltwater intrusion to improve water management practices in the face of sea level rise. Public engagement is also an important element in building public literacy about science, and for encouraging local action toward global change. By engaging the public with “plants in glass houses” through a variety of forums, we are removing “plant blindfolds” even at the tiniest of scales to effect global change.

Contributed Session: Global Change

SEAGRASS LOSS AND MACROALGAE INCREASE IN NORTH BISCAYNE BAY ASSOCIATED WITH LONG-TERM WATER QUALITY DECLINE.

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Shifts from seagrass beds towards macroalgal dominated systems is becoming a frequent event in Biscayne Bay (BB), Florida. Recently an increase in macroalgal abundance has been observed in the northern areas of BB following seagrass die-off events. Sampling conducted by Miami-Dade Division of Environmental Resources Management and the United States Geological Survey prior to 2018 documented green rhizophytic macroalgae (GRA) coverage below 25% and dominance of the seagrass *Syringodium filiforme*. Between 2017-2018 GRA coverage increased at 236 sites to 37.2%, and dominant genus *Halimeda* had 25% coverage throughout 21 km² of the sampled area (24.6 km²). Water quality, affected by the discharges of the Miami River and five other canals, has declined since 2010. TP, NO₃/NO₂, Chl-a, Suspended Solids and Light Attenuation have increased. Pilot growth experiments in *Halimeda discoidea*, the dominant species in the area, show that this species can survive and grow in very low light regimes. Organic and inorganic content of *H. discoidea* estimated using the Loss by Ignition method show that the contribution of this species to the production of sand is similar to other species found in the Caribbean playing an important role in the accumulation of CaCO₃ in the soils. Calcareous rhizophytic species, help create

conditions for the colonization of seagrasses. *Halimeda discoidea* survival and growth in low-light might provide a first successional step towards a possible recovery of seagrasses in the area, as far as water quality is improved.

THE FUTURE OF CALCIFYING RED ALGAE IN THE LEVANTINE BASIN: NON-NATIVE VS NATIVE AND HAPLOID VS. DIPLOID RESPONSES TO CLIMATE CHANGE

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Krueger-Hadfield, S. A., University of Alabama at Birmingham, United States, sakh@uab.edu

The Levantine basin in the eastern Mediterranean Sea (EMS) is a naturally oligotrophic marine community has experienced multiple local species extinctions and a 3 °C increase in seawater temperature over the past 40 years. The Israeli coastline has also been colonized by a multitude of non-native species, via the Suez Canal, including a calcifying red alga *Galaxaura rugosa* found on the Syrian coastline in the late 1990s, currently dominating deeper marine habitats and found in native coralline alga *Ellisolandia elongata* macroalgal turf from 0-3 meters depth. In previous investigations native *E. elongata* responded poorly to high temperatures (>27 °C). In contrast, *G. rugosa* only becomes stressed in temperature over 33 °C which is rarely experienced in high summer meaning it may have an advantage in future oceans. Despite our basic understanding of these species response to climate change, the unique physiology of each ploidy stage has not been quantified. Here, we test the variable response of haploid and diploid life history stages to a range of temperatures reflecting pre-industrial, present day, and near-future ocean conditions in one experiment and combined increased pH and temperature conditions reflecting the same conditions in both species. The maintenance of alternative generations in life histories indicates they have unique ecophysiology, therefore we expect variable responses in haploid and diploid *G. rugosa* and *E. elongata*. Results present potential for cryptic resilience in each species.

IRISH GREEN TIDES IN A CLIMATE CHANGE CONTEXT.

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Morrison, L., Earth and Ocean Sciences, National University of Ireland, Galway, H91 TK33, Ireland, liam.morrison@nuigalway.ie

The seasonal monitoring of three green tides across Ireland revealed a multi-specific composition, containing at least eight species, and being dominated by three (*Ulva compressa*, *U. prolifera*, *U. rigida*). A temporal succession between these species was also revealed, suggesting a key role of photoperiod and temperature controlling bloom development and composition. According to the Intergovernmental Panel on Climate Change, water temperatures are predicted to increase 3.6°C by 2100 in Ireland, especially during late spring coinciding with early green tide development. Considering current and predicted temperatures, and photoperiods during bloom development, different ecophysiological experiments were developed. These experiments indicated that the growth of *U. rigida* was controlled by temperature, while *U. compressa* was determined by the photoperiod. Considering a scenario of global warming for Irish waters, an earlier development of bloom is expected in the case of *U. rigida*. This could have significant consequences for biomass balance in Irish estuaries and the maximum accumulated biomass during peak bloom.

ANCIENT WATERBODIES UNDER GREENHOUSE CONDITIONS: THE POTENTIAL IMPACT OF CLIMATE WARMING ON THE FRESHWATER ALGAL FLORA OF ARCTIC LAKES

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Craters that formed during emplacement of kimberlite pipes in the lower Canadian Arctic between the Late Cretaceous and Late Eocene often contain thick accumulations of post-eruptive stratified lacustrine sediment, representing ancient maar lake environments. These high latitude lakes existed under Greenhouse conditions and without a cryosphere. The sediment record can be extensive, providing archives of paleoenvironments spanning thousands of years. Several records, including the early Eocene Giraffe locality, contain abundant concentrations of well-preserved microfossils indicating thriving aquatic ecosystems. The Giraffe Pipe locality contains 65 meters of lake mudstones representing thousands of years of geologic history. Climate reconstructions yield wet and warm conditions, with 4x more precipitation and a mean annual temperature close to 20 °C warmer than today, and lack of winter ice. Remains of more than 200 taxa have been uncovered and used to inform not only evolutionary history of the organisms, but ontogeny of the lake. The early stages of the lake were dominated by the green alga, *Botryococcus*. However, extensive numbers of synurophytes, chrysophytes and diatoms are found throughout the waterbody, with individual species often constrained to specific strata. Taxa found today in warm environments were common, supporting the elevated temperature reconstructions. Shifts in algal composition, coupled with remains of other organisms, identify periods of stable conditions separated by sharp changes in pH, water depth and nutrient levels.

DISTRIBUTION OF SNOW ALGAE COMMUNITIES IN THE PACIFIC NORTHWEST

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Snow algae are the dominant primary producers of snowy alpine environments and are ecologically important due to their role increasing rates of snow melt by decreasing snow albedo. Although snow algae have been described on every continent, the spatiotemporal diversity of snow algae communities across alpine habitats has not been yet been addressed. The natural geography and climate of the Pacific Northwest provides diverse snowy alpine ecosystems to study the effects of latitude, elevation, and precipitation on snow algae communities. Using meta-amplicon sequencing of the 18S small subunit ribosomal gene, we describe patterns in the community structure of snow algae communities in the Pacific Northwest Cascade Mountains. Collectively, the amplicon data suggest that snow algae communities can be classified in distinct assemblages of both algal and heterotrophic communities that are distributed across the Cascades. We observe a general seasonal algal succession from early season *Chloromonas* spp. dominant communities to late season *Chlamydomonas* spp. dominant communities in both large geographic context and within a single basin. Additionally, we observe a late season increase in the relative abundance of heterotrophic taxa and an increase in overall community diversity. Our data suggests that microhabitat variability likely determine alpine snow algae community distributions and communities are not related simply by geographic proximity.

Contributed Session: Genomics

THE ORGANELLE GENOMES OF *NITZSCHIA PALEA* DEMONSTRATE HIGH SEQUENCE SIMILARITY TO THOSE OF *DURINSKIA BALTICA*.

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Nitzschia palea is a common freshwater diatom that may be the tertiary endosymbiont within the "dinotom" dinoflagellate *Durinskia baltica*. A putative strain of *N. palea* was collected from the University of Virginia's College at Wise campus and cultured. For initial identification, three markers were sequenced-nuclear 18S rDNA, the chloroplast 23S rDNA, and *rbcL*. Morphological characteristics were determined using light and scanning electron microscopy; based on these observations the cells were identified as *N. palea* and named strain "Wise." DNA from *N. palea* was deep sequenced and the organelle genomes assembled. Single gene phylogenies grouped *N. palea*-Wise within a clearly defined *N. palea* clade and showed it was most closely related to the strain "SpainA3." 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 diatoms, 37 protein-coding, 23 tRNA, and 2 rRNA genes. The chloroplast genomes of *N. palea* and *D. baltica* have identical gene content, synteny, and a 92.7% pair-wise sequence similarity. 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%. Genome-based phylogenies demonstrated that *D. baltica* is more similar to *N. palea* than any other diatom sequence currently available.

GENOMIC VARIATION ACROSS STRAINS OF THE TOXIC BLOOM-FORMING HAPTOPHYTE *PRYMNESIUM PARVUM* REVEALS POSSIBLE TOXICITY DETERMINANTS

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The golden alga, *Prymnesium parvum*, is a mixotrophic algae that capable of alternating between a photosynthesizing autotroph to an aquatic predator that utilizes toxins, called prymnesins, to kill its prey. During winter months, population blooms of *P. parvum* can lead to dangerous levels of toxins and large-scale fish kills. Many details of the toxin's metabolic pathway and the genetics of toxicity remain unclear in this species. Two strains of particular interest, 12A1 and 12B1, were isolated from the same liter of water in a Texas bloom, yet they display large phenotypic variation; 12B1 consistently displays low toxicity in lab assays, whereas its sympatric strain, 12A1, is highly toxic. Mirroring this difference, large genetic variation has been revealed through sequencing. Initial ploidy estimates with short read data predicts that all high-toxicity strains, including 12A1, are diploid whereas 12B1 appears haploid. Further, de novo genome assembly with Oxford Nanopore reads, has yielded genomes that are twice as large in toxic strains compared to the non-toxic 12B1, substantiating possible ploidy differences. Assessments of single copy orthologs indicate that 12B1 has a gene duplication rate of 1.7%, while 12A1 presents a 37% rate. These patterns are suggestive of possible whole-genome duplication or hybridization events within the lineage. We are sequencing dozens more strains that are globally and temporally varied in order to better survey genomic variation, estimate levels of population heterozygosity, and reveal genetic determinants of toxicity within *P. parvum*.

USING AN "ALIEN INDEX" APPROACH TO EVALUATE THE EXTENT OF HORIZONTAL GENE TRANSFER IN *DINOPHYSIS ACUMINATA*.

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Dinophysis is a widespread mixotrophic dinoflagellate responsible for toxic algal blooms. Like the ciliates that it feeds on, *Dinophysis* hosts kleptoplastids initially acquired from cryptophytes, and these can remain photosynthetically active for several months. Previously, it was argued that these kleptoplastids are sustained by at least four plastid-targeting proteins acquired via horizontal gene transfer (HGT), but the full contribution of HGT to metabolic processes in this organism remains unclear. Here we use phylogenomics and a novel bioinformatic tool to detect global HGT patterns in *Dinophysis acuminata*, and infer their timing, taxonomic origin, and organellar targeting. We discuss the unexpected imprint of ostensibly non-cryptophyte photogenes, whether recent ancestors were heterotrophic prior to evolving kleptoplasty, and how *Dinophysis* carries out photoregulation to protect these foreign organelles.

HIGHLY CONTIGUOUS DE NOVO GENOME ASSEMBLY OF THE HAPTOPHYTE *PRYMNESIUM PARVUM* USING OXFORD NANOPORE SEQUENCING

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Illumina short read sequencing is unmatched in terms of its high throughput capabilities and has been used to generate the majority of genome assemblies utilized today. However, short read sequencing is limited in its ability to properly assemble repetitive regions, particularly in larger eukaryotic genomes. The fact that most algal genomes are > 100Mb and highly repetitive presents a significant assembly challenge. Incorporation of ultra-long reads (> 10kb) generated by Oxford Nanopore Technologies (ONT) has the potential to improve assembly as ONT reads are long enough to span many repetitive regions. Unfortunately, ONT reads are over one hundred times more error prone than those of Illumina, which is a major limitation. To develop an optimal genome assembly strategy that utilizes the strengths of both ONT and Illumina reads, we evaluated several different algorithms for genome assembly of the toxic algae *Prymnesium parvum* (Haptophyta). Our analysis revealed stark differences in assembly metrics when comparing Illumina-only genome assemblies to hybrid assemblies that utilize both technologies. Illumina-only assemblies had N50s below 15kb and were 80% the size of hybrid assemblies. The best hybrid assembly was generated using MaSuRCA and had a contig N50 over 1.1Mb and was composed of only 255 contigs. This represents significant improvement over other public haptophyte genome assemblies. Our highly contiguous genome assembly of *P. parvum* will serve as a reference for prymnesiophyte algae and demonstrates the power of long reads to greatly improve algal genome assemblies.

PROMISING PROSPECTS OF NANOPORE SEQUENCING FOR ALGAL HOLOGENOMICS AND STRUCTURAL VARIATION DISCOVERY

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Eukaryotic algae represent low complexity metagenomes that include the host chloroplast, mitochondrial and nuclear genomes, as well as associated bacterial genomes. Together, they form a holobiont whose collective

genomes, the hologenome, may function and evolve interdependently. In 2014, faced with difficulties to assemble the chloroplast genome of the siphonous green holobiont *Caulerpa ashmeadii* with Illumina data, we entered the MinION Access Program (ONT) to test the prospects of long Nanopore reads to resolve the issue (i.e. genome fragmentation). Over the next two years, we followed the rapid improvement of the technology while troubleshooting the quality of our library preparations to produce increased read size distribution. Based on our last run in 2016 (chemistry R9), we expanded the scope of our study to document the content of *C. ashmeadii*'s hologenome with native (Nanopore-only) and hybrid (Nanopore + Illumina) tools. We document six putative endosymbiotic bacterial species, resolved organellar genomes, and assessed nuclear genome size. The abundance of some bacterial taxa exceeded that of the organelles (as number of mapped reads) and taxonomic profiles established with Nanopore reads tracked very closely those obtained for Illumina reads. Thanks to Nanopore reads, we reveal interspersed repeats and unsuspected structural variations in *C. ashmeadii*'s chloroplast genome. To our knowledge this is the first report of chloroplast genome polymorphism, i.e. chloroplast heteroplasmy, in the Ulvophyceae (Chlorophyta).

GENOMIC REGIONS ASSOCIATED WITH THE PRODUCTION OF DIFFERENT CLASSES OF SMALL NON-CODING RNAs IN *GRACILARIOPSIS ANDERSONII*.

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Genome-wide studies in eukaryotes have led to the identification of multiple classes of small non-coding RNAs (sRNAs) that influence gene expression by distinct, yet overlapping, genetic and epigenetic silencing pathways. While these mechanisms have been intensely studied in land plants and animals, gene regulatory processes in algae, especially those driven by sRNAs, remain poorly understood. Key components of the machinery for sRNA-mediated gene regulation have been reported for many algal lineages, but they also seem to have been lost entirely from several species with relatively small nuclear genomes. By employing next-generation sequencing and bioinformatics tools, we have attempted to describe the landscape of sRNA in *Gracilariopsis andersonii*. The sequencing of an sRNA library constructed from *G. andersonii* tissues produced ~55 million reads. Most of the clean sRNA reads sequenced were 19 to 20 nt in length. According to the simulated genome distribution of sRNAs, 24.39% of the *G. andersonii* genome is associated with sRNAs production and most sRNAs were distributed on either strand, with the highest count of sRNAs on the antisense strand of contig1325. Some of the classes of sRNA represented in *G. andersonii* were identified as small interfering RNAs (siRNAs), including phased siRNAs as well as microRNA candidates and others hairpin RNAs. This study provides essential insights to comprehensively understand the regulatory processes mediated by sRNAs in red algae.

Bold Award Session:

A TWO-PRONGED APPROACH TO UNDERSTANDING *CHOREOCOLAX POLYSIPHONIAE* DEVELOPMENT AND *VERTEBRATA LANOSA* RESPONSE TO INFECTION.

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Parasitic red algae are not like other parasites. Similar to other formerly photosynthetic parasites, they are reduced in size and have reduced or entirely lost pigmentation. But, the close relationship between red algal parasites and their host makes them unique among parasites. This close relationship enables direct comparisons between host and parasite to examine the effects of parasitism. *Choreocolax polysiphoniae* was one of the first red algal parasites

described, and its ecology and morphology have been well studied. However, the molecular factors involved in the development of *Choreocolax* and its host's response to infection remain unknown. Single cell transcriptomics were used to obtain *C. polysiphoniae* and its host, *Vertebrata lanosa* transcriptomes at eight time points of parasite development and uninfected tissue. Differential gene expression analysis was used to identify up and down regulated genes during parasite development and in response to infection. Gene expression profiles only represent a snapshot of cellular metabolism or activity, but changes in gene expression can dramatically influence biological processes. In *Choreocolax*, changes in gene expression corresponding to growth and its parasitic lifestyle. When compared to uninfected tissue, the infected host significantly upregulates genes involved in carbohydrate metabolism. Combining this transcriptomic data with the observed morphology more thoroughly assesses the development of *C. polysiphoniae* and the effects of infection on *V. lanosa*.

SALT INDUCED GENE EXPRESSION IN *CHARA LONGIFOLIA* C. B ROB. AND *CHARA AUSTRALIS* R. BR.: IMPLICATIONS FOR SALT TOLERANCE MECHANISMS

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Species within the genus *Chara* have different tolerance ranges when exposed to or cultured in varying salinities. We examined salt tolerant *Chara longifolia* and salt sensitive *Chara australis* for mechanisms of salt tolerance and their potential role in adaptation to salt for both species. *Chara* is more closely related to embryophytes than to other green algae; we hypothesize that genes similar to those in embryophytes are likely to be the mechanisms behind salt tolerance in *Chara*, especially genes related to Na⁺ export: Na⁺/H⁺ antiport (NHX) and a H⁺-ATPase (AHA). The presence of these candidate genes has been confirmed in *C. longifolia* and *C. australis* using previously established Illumina transcriptomes. Time-course Illumina transcriptomes were created using RNA from multiple time points (0hr, 6hr, 12hr, 24hr & 48hr) after a freshwater culture for each species was exposed to salt stress. These transcriptomes reveal differential expression that will enable us to test our hypothesis that Na⁺ export is critical to salt tolerance, as well as identify other genes that may play important roles in adaptation to salt stress. Initial analysis indicated expression of genes involved in photosynthesis and in cell wall maintenance, as well as membrane transport, show different patterns of up- and down-regulation in the two species.

IRON AVAILABILITY DICTATES THE RESPONSE OF CORAL SYMBIONTS TO THERMAL STRESS

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Trace metals are critical to the physiology of micro-algae. Mutualistic endosymbionts, Symbiodiniaceae, deliver and receive nutrients from their hosts, including reef-building stony corals. Linking the connection between macro (carbon, nitrogen, phosphorus) and micro-nutrient (trace) quotas in relation to energy cycling between host and symbiont is pertinent to understanding the holobiont's ability to withstand environmental stressors. It is hypothesized that exposure to increased iron availability (and subsequent iron sequestration/retention) may enhance the organism's ability to maintain homeostasis during stress events. To test this hypothesis, cultures of *Breviolum minutum* and *B. psygmophilum*. (formerly *Symbiodinium* clade B) cultures were exposed to a 3x3-factorial set of temperatures and iron concentrations. During exponential growth, cultures were sampled for nutrient content (trace metals and major nutrients), chlorophyll, other pigments, and photosynthetic physiology to evaluate *Breviolum* spp.

condition. Preliminary results indicate that heat stress ceases growth for both species under low iron concentrations whereas counterparts at higher iron concentrations are able to persist. Contrastingly, *B. minutum* and *B. psygmophilum* exhibit divergent changes in trace metal stoichiometry in response to changes in temperature. By combining a broad suite of physiological approaches, we have further characterized the Symbiodiniaceae iron requirement by assessing the compounding effects of iron limitation and heat stress on the stability of coral-algal symbioses.

ARCTIC CRUSTOSE CORALLINE ALGAE, CARBONATE CHEMISTRY, AND THE CRITICAL ROLE OF SALINITY

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A complete loss of crustose coralline algae (CCA) was observed with proximity to a freshwater source in Stefansson Sound, Alaska. Variations in CCA distribution lead to questions of small-scale spatial differences of seawater chemistry specifically carbonate chemistry. Autonomous SeaFET pH sensors, in conjunction with Seabird CTDs (salinity and temperature) were deployed July 2016-July 2018 inshore and offshore sites within Stefansson Sound. We found pH values were consistently lower offshore (higher salinity levels) inshore (lower salinity levels). Discrete water samples corroborated sensor results; lower salinity waters had higher pH values ($R^2=0.78$; salinity range 0-32; pH range 7.4-8.4). pH was higher (most values > 8.0) at salinities < 5 , but total alkalinity (A_T) was much lower ($R^2=0.61$, salinity range 0-32, A_T range 1800-2700 $\mu\text{Eq L}^{-1}$). Calculated aragonite saturation (Ω_{ar}) levels were similar between sites for most of the year (Ω_{ar} close to equilibrium), except during spring break up, when the inshore site had much lower saturation levels than offshore (Ω_{ar} as low as 0). Mesocosm experiments focused on the effects of salinity, A_T and associated Ω_{ar} on the photosynthetic efficiency, pigment composition, and dissolution of CCA individuals. Results indicated that low salinities and associated low A_T alone affected CCA physiology and dissolution. Stressful conditions from extreme low salinity pulses and associated Ω_{ar} levels, likely drive CCA distributions within Stefansson Sound.

THE EFFECTS OF ENVIRONMENTAL STRESSORS ON CELL DEATH RESPONSES OF TOXIC DINOFLAGELLATE *KARENIA BREVIS* AND POTENTIAL BLOOM DECLINE PROCESSES

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Historically, marine phytoplankton were presumed to replicate indefinitely. However, drastic environmental changes have been shown to induce death of algal cells, and may therefore affect development of harmful algal blooms. The Gulf of Mexico is subject to frequent toxic blooms of the dinoflagellate *Karenia brevis*, but the mechanisms of bloom termination are not well known. Here we used established cell death markers, such as reactive oxygen species (ROS), to define short-term cellular responses to different levels of osmotic, heat and cooling stress. Intensity-dependent apoptosis cell death processes were clearly observed under osmotic stress when salinities changed from 35 to 30, 25 and 20 respectively. The generation of ROS may be correlated with decreased photosynthetic efficiency by the induction of Non-Photochemical Quenching, as a way to dissipate excess energy. In contrast, the rapid heating and cooling stress within 20-30 °C did not induce cell death responses in *Karenia* cells, potentially revealing their strong thermal acclimation ability in the field. However, necrotic-like death process was found after the acute change of temperature from 30 °C to 15°C and 20°C to 35°C, suggesting the existence of different cell death modes in *Karenia*. Our research revealed detailed cell death responses on *Karenia* to environmental stressors and evaluated

potential bloom-declined indicators. Meanwhile, the presence of cell death markers in untreated populations may also highlight their house-keeping functions in cell division and aging process.

ALTERATIONS IN PHOTOSYNTHETIC PERFORMANCE, METABOLIC POOLS AND LIPIDS IN *GALDIERIA SULPHURARIA* GROWN ON CORNSTOVER HYDROLYSATE

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We describe carbon allocation and alteration in a red microalga, *Galdieria sulphuraria* using glucose- and xylose-rich corn stover hydrolysate (CSH) for mixo-, hetero- and autotrophic cultivations. During CSH supplementation we observed a significant reduction in O₂ evolution, chlorophyll and phycocyanin levels in mixo- and heterotrophic cells. Ultrastructure analysis by TEM microscopy revealed the accumulation of carbon storage molecules that was verified enzymatically as a 2fold increase in starch production during CSH supplementation. Also, we observed large chloroplasts in auto- and mixotrophic cells in contrast to smaller multi-lobed chloroplasts in heterotrophic cultures. Mass spectrometry revealed lipid class remodeling in all growth conditions whereas heterotrophic cells yielded a 1.2-fold increase in triacylglycerols over the other treatments due to culture growth stage. Additionally, thylakoid membrane lipids, SQDG in particular were down-regulated with CSH. During the 7-45day cultivation there was a 14% increase in SQDG class autotrophically while it was depleted by 10% and 30% mixo- and heterotrophically. Finally, changes were observed in fatty acid composition of total lipid pools. CSH resulted in increase in the content of C34:3 and C36:5 in MGDG and decrease in the level of these fatty acids in DGDG pool. These data together suggest that CSH increases specific growth rate, down-regulates photosynthesis and alters the relative biochemical composition of energy reserves among cultivation treatments in *Galdieria*.

ASSESSMENT AND RECOMMENDATIONS FOR AN ECOSYSTEM APPROACH TO KELP AQUACULTURE

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Kelp farming is expanding along temperate coastlines in the Americas and Europe. The economic, ecological, and social frameworks surrounding kelp farming in these new areas are in stark contrast with the conditions in progenitor kelp farming regions in China, Japan, and Korea. Thus, evaluating the potential environmental and social impacts of this growth is important to ensuring long-term sustainability of the practice. Here, a conceptual model of the human and natural relationships supporting kelp aquaculture was developed using Maine as a focal region. The principles and strategies of the Ecosystem Approach to Aquaculture (EAA), laid forth by the Food and Agriculture Organization (FAO) in 2010, were used to identify appropriate impacts of the practice and recommend areas for action, grouped by themes of: 1) ecosystem services, 2) socially just, and 3) integration. Recommendations to improve or protect the ecosystem services tangential to kelp farming include: define ecosystem and management boundaries, assess ecosystem services and environmental carrying capacity, pursue ecologically considerate

engineering, and protect the health and genetic diversity of wild kelp beds. Recommendations to ensure that kelp farming improves the well-being of all stakeholders include: increase horizontal integration, share education in Best Management Practices, and develop climate change resiliency. To ensure that kelp aquaculture is developed in the context of other sectors and goals it is also recommended that an integrated management strategy be developed for wild and farmed kelp.

MULTI-MARKER METABARCODING AS A NEW APPROACH FOR MONITORING PERIPHYTIC ALGAL COMMUNITIES IN THE FLORIDA SPRINGS

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Springs provide a unique environment from which to study biodiversity given their relatively stable habitats. Springs are also economically and culturally significant, even as these systems are presenting evidence of anthropogenic impacts. Biodiversity assessments of algal communities of Florida springs have relied on traditional morphological analyses alone, thus potentially grossly underestimating the diversity present. In this study, we employed a polyphasic approach to elucidate the algal communities from three “baseline” springs: Ichetucknee, Blue Spring, and Silver Glen. Previous studies have shown that these springs are dominated by cyanobacteria, diatoms, and green algae, thus primers were chosen accordingly (e.g., 16S, 18S, and *rbcL*). Results from microscopy and metabarcoding via the Illumina MiSeq platform revealed that morphological assessments alone underestimated biodiversity compared with molecular assessment. Further, we detected different algal communities in the three springs, which appears to be correlated with adjacent land use to each spring. For example, the Ichetucknee Springs community had greater cyanobacterial diversity, whereas the Blue Spring and Silver Glen communities were dominated by diatoms. Based on these results, we recommend that springs throughout Florida be monitored with combined morphological and molecular techniques to more comprehensively assess biodiversity with on-going and future anthropogenic alterations. More complete biodiversity assessments will facilitate preservation/restoration planning for these fragile ecosystems.

RANKING SALISH SEA BULL KELP FORESTS ON THEIR CONNECTIVITY VALUE; A NETWORK APPROACH

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Understanding population connectivity is critical to species management and maintenance of ecological function. In marine environments, population connectivity is largely controlled by ocean currents. The Northeast Pacific Bull Kelp, *Nereocystis luetkeana*, is a canopy-forming brown alga that provides critical habitat to fish and invertebrates. Concerns about population health of this ecosystem engineer species have been raised in the Salish Sea (US/Canada) and Northern California in relation to Global Change and coastal development. Genetic analysis over the species distribution revealed that the small, isolated Salish Sea populations had the lowest genetic diversity across the range. With the goal of estimating connectivity, a Hydrodynamic Transport Model (HTM) for the Salish Sea was used to simulate dispersal of spores via rafting of adult sporophytes. A network was used to estimate population connectivity with probabilities of transport as edge weights and kelp beds as nodes. Network metrics assessing betweenness centrality, diameter and path length were used to rank sites as sources and sinks of gene flow. This analysis showed that sites centrally located in the Salish Sea were important as both sources and destinations for spores. Conversely, inner Salish Sea sites were the greatest sinks of gene flow showing that geography constrains

gene flow in this system. Sites that are both effective sources and sinks of gene flow should be prioritized for conservation and restoration efforts of Bull Kelp forest ecosystems.

PHOTOSYNTHESIS, MORPHOLOGY, AND LIGHT-DEPENDENT PROTON PUMPS CONTROL TROPICAL REEF MACROALGAE RESPONSE TO OCEAN ACIDIFICATION

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While ocean acidification (OA) can negatively affect calcification in tropical reef macroalgae, the mechanisms are elusive. We examined OA effects on calcification in 9 reef macroalgae from high-light patch reefs on the Florida Reef Tract (FRT) and low-light reef ledges on Little Cayman Island (LCI). Calcification experiments were conducted at ambient (8.10) and 2100 (7.65) pH in light and dark with/without a photosystem II (PSII) inhibitor to examine role photosynthesis and light-triggered proton pumps for calcification in physiologically and morphologically-diverse species under OA. At low pH in the dark, net dissolution occurred in 89% of species with no increase in respiration. Most species exhibiting positive net calcification in the dark at ambient pH had net dissolution in the dark at low pH. In contrast, in the light, 3 FRT species had similar calcification rates at low and ambient pH. FRT species that previously showed biotic control of thalli H⁺ dynamics without PSII, also maintained 22-34% of their calcification rates independent of PSII at ambient pH. However, calcification independent of PSII was not sustained at low pH. Therefore, a combination of light-triggered proton pumps and photosynthesis promote calcification in the light, but are dependent on photosynthesis at low pH. Species with the capacity to calcify in the light under OA can compensate for low net calcification or dissolution in the dark. Thus, biotic regulation of H⁺ in the light may be key for sustained calcification in marine organisms, such as tropical reef macroalgae, under global change.

OMEGA-7 PRODUCING ALKALIPHILIC DIATOM *FISTULIFERA ALCALINA* SP. NOV FROM LAKE OKEECHOBEE, FLORIDA

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Microalgae are an exemplary source of fatty acids indispensable to human nutraceutical, pharmaceutical, and biofuel sectors. Achieving goals of producing algal-based products competitively, however, involves further improvement of microalgae technology, especially the cultivation aspect. Contamination of algal cultures is a major impediment in algal biotechnology and can be avoided by applying extremophilic algae. Our goal was to isolate alkaliphilic microalgae native to South Florida with characteristics suitable for fatty acid production. Water samples from Lake Okeechobee were subject to selection pressure using alkaline media of which resulted in the isolation of a high lipid-accumulating, alkaliphilic diatom within the genus *Fistulifera*. Lipid analysis of this diatom revealed a fatty acid profile abundant in palmitoleic acid (or omega-7), palmitic acid and eicosapentanoic acid. Based on morphological, ultrastructural, and 18S rRNA and *rbcL* gene results, we are proposing this strain as a species new to science, *Fistulifera alcalina* sp. nov. This is also the first record of *Fistulifera* in the southeastern United States (Florida, USA).

Contributed Session: Phylogeny and Systematics I

MOLECULAR SYSTEMATICS OF THE SIPHONOUS GREEN ALGA *AVRAINVILLEA* (BRYOPSIDALES, CHLOROPHYTA) WITH AN EMPHASIS ON INVASIVE SPECIES IDENTIFICATION

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Avrainvillea is commonly found throughout the tropics and recently invaded the subtropical portion of the Mediterranean Sea. Its systematic treatments to date have exclusively relied on morphology, which is problematic as many of the species descriptions' included only gross morphological features and *Avrainvillea* exhibits plasticity. *Avrainvillea* is also of particular interest because of 3 documented expansions outside its native range: "*A. amadelpha*" and *A. erecta* in the Main Hawaiian Islands (MHI) and *A. amadelpha* in the Mediterranean Sea. In this study we used Sanger sequencing of two plastid loci and high throughput genomics to reconstruct a molecular phylogeny, including 7 type specimens and 3 specimens from type localities. This phylogeny suggested morphology is not reliable for *Avrainvillea* species delimitation, as specimens previously identified by leading phycological taxonomists exhibited rampant polyphyly. Neither the Hawai'i nor Mediterranean invader are here identified as *A. amadelpha* – the Hawai'i species grouped with an *A. lacerata* isotype, while the identification of the Mediterranean species remained elusive. *A. obscura* specimens from the type locality further supported the identification of *A. erecta* in the MHI as a correct identification. Given the issues associated with morphological identification of *Avrainvillea*, further efforts to resolve its molecular phylogeny should incorporate DNA sequence data of type specimens whenever possible.

THE SPECIES DILEMMA: A CASE STUDY WITH THE GENUS *HYPNEA* (GIGARTINALES, RHODOPHYTA) USING THE BIOLOGICAL SPECIES CONCEPT TO VERIFY DNA DIVERGENCE.

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The identification of *Hypnea* Lamouroux (1813) species based only on morphological data is difficult due to the phenotypic plasticity present in this group. Studies based on DNA markers (genetic species concept) were carried out in Brazil and *H. pseudomusciformis* was recently described to accommodate three species on the Brazilian coast: *H. musciformis*, *H. nigrescens* and *H. valentiae*. However, molecular data separated *H. pseudomusciformis* in two subclades, one referring to specimens of populations in the Northeast and another referring to populations of the Southeast and South. In this study, crossing-tests were conducted between the morphological variants "musciformis" and "nigrescens" collected in São Paulo and between "musciformis" of São Paulo and Bahia, to validate the hypothesis that these variants correspond to a single species (biological species concept). In culture tests between morphological variants "musciformis" and "nigrescens", cystocarps were observed in all gametophytes. Carpospores were released, generated tetrasporophytes that became fertile and after the liberation of tetraspores. Thus, our results confirm these morphological variants as same species. In the tests between strains of São Paulo and Bahia, although cystocarps were also observed, there was no germination of carpospores and the life cycle was not completed, which could indicate the separation in two species. The crossing tests technique were essential for revealing scenarios that would go unnoticed using only morphology.

A MOLECULAR AND MORPHOLOGICAL REAPPRAISAL OF “RED BLADE” HAWAIIAN SEAWEEDS IN THE GENUS *KALLYMENIA* (GIGARTINALES, RHODOPHYTA)

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The florideophycean genus *Kallymenia* is one of several genera with a simple morphology of expanded red blades. Its paucity of distinguishable morphological characters and cosmopolitan geographic distribution prompted multiple studies to focus on molecular-assisted alpha taxonomy to unravel the species-level diversity within the genus. Previous work includes the 2010 Hawaiian Rhodophyta Biodiversity Survey, which listed several specimens of *Kallymenia*, and an in-progress assessment of Hawaiian mesophotic algal communities. As part of our effort to resolve the taxonomic placement of these red macroalgae, we will be conducting a molecular survey using multiple regions paired with a morphological assessment for an integrative taxonomic approach. Over 100 specimens of florideophyte red algae, preliminarily identified as belonging to the genus *Kallymenia*, were collected from shallow and mesophotic depths to contribute to the creation of a more comprehensive biodiversity catalog, with these specimens also providing an opportunity to examine a largely unexplored community at depths as great as 118m. Our multi-gene phylogenetic assessment suggests 2 species from mesophotic depths assignable to the newly erected genus documented in the western Pacific and Indian Ocean in Australia, *Leiomenia* Huisman & G.W. Saunders, and another mesophotic specimen assignable to a New Zealand endemic genus, *Psaromenia* W.A. Nelson & Zuccarello. With use of multi-gene analyses, our understanding of the composition of the Hawaiian red algal flora is altering.

ECOLOGICAL SPECIALIZATION PROMOTES SPECIATION IN SYMBIOTIC MICROALGAE

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Genetic evidence provides insight into the influence of natural selection on processes of speciation which yields a more precise understanding of species diversity, especially among morphologically cryptic organisms. Investigating processes of speciation among micro-eukaryotes using genetic methods is challenging due to limitations on obtaining pure samples from across species ranges. The hosts of symbiotic micro-eukaryotes provide means by which to routinely sample in different physical and environmental contexts. For instance, most dinoflagellate mutualists in the family Symbiodiniaceae exist mono-clonally in coral host tissues. The use of several genetic markers indicate the existence of hundreds of symbiont species across multiple genera, including within the most ecologically dominant genus, *Cladocopium*. However, most all species remain undescribed and thus the study of these organisms is limited by no formal taxonomy. We investigated the *Cladocopium* associated with common branching corals (genus *Pocillopora*) across the Indo-Pacific to test whether these symbionts represented distinct species. We delimited two independently-evolving lineages based on time-calibrated phylogenetic and population genetic evidence. These candidate species associated with distinct host species. The divergence of these dinoflagellates and the evidence for adaptation to distinct niches highlights the importance of ecological specialization influencing speciation. Symbiotic dinoflagellates represent a model system to study processes of speciation in micro-eukaryotes

CORALLINA OFFICINALIS VAR *CHILENSIS* (CORALLINALES RHODOPHYTA) NOT A “VARIETY” AND DISCOVERED IN BOTH HEMISPHERES.

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Genuiculate coralline algae are notoriously challenging to identify in the field due to cryptic speciation and few distinguishing characteristics. Historical species delimitations based on morphology are often unsupported by sequence-based phylogenies. In 1902, Yendo reported *C. officinalis* var *chilensis* (Decaisne) Kuetzing in British Columbia, Canada. Unfortunately, Yendo's collections of articulated corallines have not been found, making it impossible to verify Yendo's report. In attempt to determine if the name was applied correctly, we sequenced Darwin's type specimen, the Chilean basonym *C. chilensis* (Decaisne), using *rbcL* (263 bp). Darwin's type sequence corresponded with a British Columbian species congeneric to, but not synonymous with, *Corallina officinalis*. We propose reversing Kuetzing's synonymization that designated *C. chilensis* as merely a variety of *C. officinalis*, retiring the name *C. officinalis* var *chilensis* and restoring the name *C. chilensis* in its place.

DIVERSITY OF THE GENUS *SHEATHIA* (BATRACHOSPERMALES, RHODOPHYTA) IN NORTHEAST INDIA AND EAST NEPAL

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Freshwater red algae of the order Batrachospermales were surveyed in northeast India and east Nepal and six populations of the genus *Sheathia* were found. All were grouped in a large clade with *S. arcuata* in the phylogenetic analyses based on the *rbcL* gene sequences of our material and those available in GenBank. However, *S. arcuata* represents a species complex with a high sequence divergence with several smaller groups. Samples from India and Nepal were grouped in three distinct clades with high support. Two samples from India formed a clade, whereas one sample from India and one from Nepal consisted of another clade, both representing new species. Two samples from Nepal grouped with sequences from Hawaii and Indonesia (both represented only by the 'Chantransia' stage) and sequences of gametophytes from Taiwan. This clade also represents a new species, which requires further analyses to determine the morphological traits of the gametophytic stage. Morphological characters of the specimens from these three clades fit within the circumscription of *S. arcuata*, except that they lack heterocortication, i.e. presence of bulbous cells in the cortical filaments, typical of most species of the genus *Sheathia*. Although the region sampled is relatively restricted, the genetic diversity among specimens of these three groups was high and the phylogenetic relationships with the other clades of *S. arcuata* complex were variable. These data corroborate data from other groups of organisms that those regions are hotspots of biodiversity.

Contributed Session: Phylogeny and Systematics II

A NEW CLASSIFICATION FOR THE GRACILARIALES (RHODOPHYTA) INCLUDING NEW SUBFAMILIES, TRIBES, SUBGENERA, AND TWO NEW GENERA, *AGAROPHYTON* AND *CRASSIPHYCUS*

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Gracilariales is a red macroalgal order and the main global source of the economically important agar, a marine phycocolloid. Independent comparative morphological and molecular phylogenetic studies over the last 20 years have revealed the existence of seven major clades recognizable as distinct genera. Of these major clades only four free-living genera have been widely accepted taxonomically: *Curdia*, *Melanthalia*, *Gracilariopsis*, and *Gracilaria*. Three other clades comprise the reinstatement of the genus *Hydropuntia* and the proposal of two new genera, *Agarophyton* and *Crassiphycus*. Based on new *rbcL* DNA sequences, and along with a reassessment of published comparative morphological and molecular phylogenetic studies, we argue that the latter three genera represent distinct evolutionary lineages in the Gracilariaceae worth recognizing as distinct genera, and propose a new classification for the order Gracilariales. Our new proposal incorporates the most current understanding of the evolutionary history of the order, establishes a natural and stable classification system, and provides the basis for the recognition of intra-family ranks. Our classification scheme reconciles all molecular phylogenetic studies published to date, including newly published phylogenomic trees.

MARTENSIA (DELESSERIACEAE RHODOPHYTA) FROM SHALLOW AND MESOPHOTIC HABITATS IN THE HAWAIIAN ARCHIPELAGO: DESCRIPTION OF FOUR NEW SPECIES

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Sixty-eight specimens of the red algal genus *Martensia* from the Main and Northwestern Hawaiian Islands, representing both shallow (47 specimens from 0-2 m depth) and mesophotic habitats (21 specimens from 62-93 m depth), were collected and analyzed using morphological and molecular analyses. Phylogenetic analyses of the *rbcL* gene resolved five distinct clades of *Martensia*, of which none could be attributed to the two taxonomic names previously attributed to this flora (*M. fragilis* and *M. flabelliformis*). Analyses of the COI barcoding region were consistent with *rbcL* trends, although fewer specimens amplified and sequenced for this marker. Four *rbcL* clades (lineages 1-4) were distinct from each other and from other described species of *Martensia* based on both phylogenetic position and morphological characters, and will be proposed as new species. The remaining clade (lineage 5) corresponds to *Martensia albida*, which was described from Korea in 2006, and is thus recorded from both shallow and mesophotic habitats in the Main and Northwestern Hawaiian Islands for the first time. All five species in the Hawaiian flora occur in mesophotic habitats, while three are also represented by substantial numbers of collections from shallow waters of the Main Hawaiian Islands. This study provides further support for the large amount of uncharacterized biodiversity from both the shallow and mesophotic depths in the Hawaiian Archipelago.

TOWARDS UNDERSTANDING THE HOST AND HOLOBIOMES OF THE CARRAGEENOPHYTE RED ALGAE

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Seaweeds co-exist with an associated community of prokaryotic and eukaryotic co-localized and co-evolving taxa, including bacteria, protists, fungi and other algae. This holobiome is increasingly recognised as influencing host health status, particularly bacteria which can be beneficial, modifying the host's interaction with grazers, epiphytes and abiotic factors. Other members can be pests (endobionts and epibionts, including other seaweeds) and pathogens (bacteria and micro-eukaryotes). Little is known about the interactions between these taxa and how they are influenced by environmental conditions and host. Understanding this is potentially relevant to seaweed aquaculture success. Carrageenophytes are an important source of carrageenan, a polysaccharide used for thickening foods and in other industrial processes, e.g. cosmetic and pharmaceutical production. Commercial carrageenan is mainly from *Kappaphycus* and *Eucheuma* grown in the tropics. Yield is limited by epiphyte and disease outbreaks but factors affecting these are poorly understood. *Chondrus crispus*, a traditional North Atlantic source of carrageenan, is a potential model in which to study carrageenophyte holobiome variation. High-throughput amplicon sequencing of prokaryotic and eukaryotic components, paired with light microscopy, are being used to study composition across seasons in individual host tissues of life stages of UK *C. crispus*. Understanding the nature of the holobiome is critical for interpreting the health and disease role of the holobiome in these algae.

TAXONOMY AND BIOCHEMISTRY OF A NEW PLEUROCAPSAELEAN CYANOBACTERIUM ISOLATED FROM LAGUNA MADRE

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Laguna Madre (TX, USA) is a unique hypersaline ecosystem well known for its commercial fisheries and role in providing refuge for overwintering birds. About half of its area is covered by tidal sand flats dominated by *Lyngbya* spp. and *Coleofasciculus* spp. In addition to these dominant species, other cyanobacterial taxa are present on atypical substrata, e.g. plant's roots/stems and seashells. During our expeditions to Laguna Madre, we found a peculiar pseudofilamentous cyanobacterium growing on the surface of *Anomalocardia auberiana*. This "cyano" was initially identified as *Pleurocapsa minuta*. Sheaths of the natural populations were colored by scytonemin, with rare blackish patches containing gloeocapsin (?)- its presence will require confirmation by chemical analysis. Our cultivated morphospecies lost its robustly colored sheath in the transition from natural populations to culture. Cultures show chromatic adaptation with reddish cells in the stationary phase versus blue-green cells in exponential phase. Applied molecular methods including 16S rRNA megaphylogeny and rpoC1/rbcX phylogeny showed that "*Pleurocapsa minuta*" belongs to its own independent lineage at the genus level within the order Pleurocapsales. We have not found baeocytes in our isolate, which is atypical for Pleurocapsales. Perhaps the presence of baeocytes is not a synapomorphy for the order. Pleurocapsales is a problematic cyanobacterial order with urgent need for more studies. We hope that the application of megaphylogenies can help resolve this confusing group.

PRELIMINARY ASSESSMENT OF ANTARCTIC CORALLINE ALGAE (CORALLINOPHYCIDAE, RHODOPHYTA) BASED ON DNA SEQUENCING, INCLUDING SEQUENCING OF TYPE SPECIMENS

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The Antarctic is one of the most vulnerable regions to climate change because its geographic isolation and unique climate history drive high endemism in its flora and fauna. To date, Antarctic coralline algae have only been identified using morpho-anatomical characters. Worldwide, these characters are often inadequate to segregate coralline algal species and even genera. Nearly all of the names applied to Antarctic corallines are based either on Subantarctic type specimens, e.g., *Clathromorphum obtectulum* (type locality Kerguelen Island), *Hydrolithon subantarcticum* (type locality Dusen, Argentina) or Arctic type specimens, e.g., *Leptophytum foecundum*. Sequencing a 3' portion of the rbcL gene of Subantarctic or Arctic type specimens has shown that, thus far, none of those specific epithets apply to Antarctic specimens. Of all the currently accepted specific epithets used for Antarctic coralline algae, only *Lithothamnion coulmanicum* (type locality: Cape Wadsworth, Coulman Island, Antarctica) is correctly applied, and its type locality is in Antarctica. DNA sequencing also shows that no generic name with a northern hemisphere type species applies to Antarctic coralline algae. Based on what has been reported in the literature, undescribed species also are present. Because Antarctic corallines may be particularly susceptible to the dual threats of global warming and ocean acidification, a thorough description of these species and their phytogeography is key to our understanding of species-specific and ecosystem-wide responses.

THE POWER OF POINTS: MAXIMISING THE POTENTIAL OF CHAROPHYTE HERBARIUM DATA

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Freshwater algae in family Characeae (charophytes) occur in water-bodies world-wide, and have long been regarded as 'honorary angiosperms' because of their similarity with plants in the genus *Equisetum*. The Natural History Museum in London (BM) has one of the most comprehensive collections of this group in the world, with only New York (NY) and Melbourne (MEL) containing collections of equal or superior significance. Recently the collection has been databased and geo-located, so it can be accessible to scientists and the general public. This can allow them to know what the entire collection contains, and see when and where collections were obtained. The information can be used to: a) locate important historical material for systematic studies, b) target places for new collections, hot-spots and poorly-collected countries or regions, and c) recreate the historical, environmental, and social context of the collectors. Similarly, a knowledge of charophyte ecological tolerances and requirements can allow us to infer the environmental and physico-chemical conditions of water bodies at different times and places. In this way curatorial, ecological and historical studies can interact to make us better informed and assist with future planning. Examples of how this data can be used in UK and New Zealand are given. Collections provide a resource not just for dry and dusty documentation of biodiversity, but a stimulus for further research and understanding.

Contributed Session: Ecology I

POTENTIAL MECHANISMS DRIVING THE GEOGRAPHIC DISTRIBUTION PATTERN OF DEFENSIVE SECONDARY METABOLITES IN THE RED SEAWEED *PLOCAMIUM* "CARTILAGINEUM"

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Inter- and intraspecific interactions between organisms can be a form of communication, environmental sensing, or defence and are often mediated by chemicals like secondary metabolites. Sessile marine organisms such as macroalgae commonly produce chemical defences against grazers, pathogens, and biofoulers. *Plocamium* “*cartilagineum*” is a finely branched red understory alga that is common in Antarctic macroalgal forests. It supports a high abundance of amphipods of which most are not able to feed on the heavily chemically defended *P. “cartilagineum”* except for *Paradexamine fissicauda*. Different *P. “cartilagineum”* individuals produce differing mixtures of halogenated secondary metabolites which are referred to as chemogroups. Around Palmer Station from 2016 to 2018 a total of 16 different chemogroups were identified. The 16 chemogroups fit well into two distinct genetic groups (not different enough to be considered different species) identified by the *cox1* and *rbcL* genes. These data suggest that chemogroups are to some extent site specific, they have some correlation with depth and that there is an underlying genetic differentiation. In order to determine the mechanisms driving the geographic pattern of secondary metabolites in *P. “cartilagineum”*, a variety of different approaches were taken. Transplant experiments were conducted to assess the role of environmental factors. Additionally, transects were run in order to describe fine-scale distribution of chemogroups and the associated population genetics.

WHEN FORM DOES NOT PREDICT FUNCTION: EMPIRICAL EVIDENCE VIOLATES FUNCTIONAL FORM HYPOTHESES FOR MARINE MACROALGAE.

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Functional groupings are widely utilized to reduce complexity and generalize across communities in many ecosystems. These models assume species within functional groups perform similar functions and thus will respond similarly to key ecological drivers. We tested predictions of the widely used Functional Group Model (FGM) for marine macroalgae, which groups species initially on morphological complexity, to validate its underlying assumptions. The FGM predicts increased resistance to disturbance and herbivory as morphological complexity (and thallus toughness) increases. The FGM also predicts a tradeoff between complexity and growth. To test predictions, we measured: 1) thallus toughness (force to penetrate), 2) tensile strength (force to break) and 3) relative growth for both tropical and temperate macroalgae from different functional groups. Penetration strength followed model predictions at the functional group level, though there was significant variability among species. The model did not predict tensile strength at any level for either tropical or temperate macroalgae. Further, relative growth did not follow predictions; rather it was highly variable among species and functional groups. Thus, the assumptions that morphology is indicative of ecosystem function and species within functional groups are more similar than between groups were violated, providing strong evidence that individual species need to be considered when predicting community responses to ecological drivers and challenging the usefulness of functional form groupings for marine macroalgae.

TISSUE WATER POTENTIAL REGULATION AND PHOTOSYNTHESIS BY *GRACILARIA SALICORNIA* IN A SUBMARINE GROUNDWATER DISCHARGE INFLUENCED SYSTEM

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While submarine groundwater discharge (SGD) has been linked to algal bloom conditions, physiological responses by macroalgae to SGD conditions are not well understood. A cryptic yet common feature on basaltic coastlines, SGD delivers a tidally-driven diurnal pulse of fresh, nutrient rich basal groundwater to the nearshore ecosystem. Natural conditions of SGD are likely to have selected for niche partitioning by macroalgal species across gradients of SGD influence. Under anthropogenically impacted conditions land use derived nutrient loading of SGD strongly influences coastal nutrient availability, leading to increased algal growth. In this study, field characterization across a gradient of SGD influence measures physiological responses in photosynthesis and tissue water potential regulation by invasive *Gracilaria salicornia* to SGD associated changes in salinity and nutrient availability. *G. salicornia* exhibits measurably different physiological responses across locations of strong, intermediate, and zero SGD influence. This differential physiological response to SGD conditions is tied to seasonal benthic community composition of SGD influenced sites, where *G. salicornia* is often dominant at sites of strong SGD influence, while diverse native species assemblages dominate sites of zero SGD influence.

THE IMPORTANCE OF THE CHLOROPHYTE *OSTREOBIUM* SPP. DURING CORAL BLEACHING RECOVERY

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Corals in symbiosis with Symbiodinaceae dinoflagellates confers corals the capacity to build reefs in oligotrophic environments. The optical properties of the coral skeleton allow corals to be one of the most efficient light collectors in nature. This high light absorption efficiency combined with high solar tropical irradiance makes corals particularly vulnerable to increases in temperature. Any reduction in coral optical cross-section produces a large increase in the light availability due to the multiple light scattering by the coral skeleton. A considerable reduction in the optical cross section can surpass the limits of tolerance for the coral-dinoflagellate symbiosis, causing a positive feedback loop that may result in the breakdown of this symbiosis (i.e. coral bleaching). Excessive light stress makes recovery of the remaining dinoflagellates impossible within the coral tissue. This raises the question about how different mechanisms by which corals can recover after a bleaching event. In the current study, I will explore how the endolithic algae *Ostreobium* spp. found within the coral skeleton helps corals recover from a bleaching event. The reduction in the dinoflagellate population within the coral tissue during a bleaching event increases the light availability within the coral skeleton, allowing the *Ostreobium* to bloom near the coral skeleton surface. As a result, the *Ostreobium* bloom within the coral skeleton reduces the effect of coral skeleton multiple light scattering on the coral tissue, allowing for the recovery and repopulation of the dinoflagellates.

THERMAL PLASTICITY IS INDEPENDENT OF ENVIRONMENTAL HISTORY IN THE INTERTIDAL CORALLINE ALGA *ELLISOLANDIA ELONGATA*

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Strong gradients in thermal stress across the intertidal zone present an opportunity to test whether thermal tolerance is a plastic or canalized trait in intertidal macroalgae. Here, we studied the intertidal pool-dwelling calcified alga, *Ellisolandia elongata*, under near-future temperature regimes, and the dependence of its thermal acclimatization response on environmental history. Two timescales of environmental history were tested during this experiment. The pool of origin was representative of long-term environmental history over the alga's life (including settlement and development), while the pool it was transplanted into accounted for recent environmental history (acclimation

over many months). Unexpectedly, neither long-term nor short-term environmental history, nor ambient conditions, affected photosynthetic rates in *E. elongata*. Individuals were plastic in their photosynthetic response to laboratory temperature treatments. Further, replicate ramets from the same individual were not always consistent in their photosynthetic performance from one experimental time point to another or between treatments, and exhibited no clear trend in variability over experimental time. High variability in climate change responses between individuals may indicate the potential for resilience to future conditions, and thus may play a compensatory role at the population or species level over time.

DECIPHERING CHEMICAL SIGNALING IN ECOLOGICAL INTERACTIONS IN MARINE BENTHIC CYANOBACTERIA

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Black Band Disease (BBD) is the first reported coral disease and the most widely distributed polymicrobial disease of corals. In BBD, a disease consortium dominated by the filamentous cyanobacterium *Roseofilum reptotaenium* displaces members of the corals' microbiome and can be lethal to corals. We investigated the natural products chemistry and chemical ecology of BBD and nonaxenic cultures of *R. reptotaenium* to determine what role these compounds play in the disease consortium. We are also currently investigating cyanobacteria that cause diseases in crustose coralline algae (CCA) and the role of cyanobacterial natural products in toxicity to CCA.

Contributed Session: Applied Phycology

ECOLOGICAL EFFECTS OF HARVESTING: A CASE STUDY OF HARVESTING AND POPULATION DYNAMICS OF THE CARRAGENOPHYTE *MAZZAELLA LAMINARIOIDES* IN MATANZAS, CHILE

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Worldwide seaweeds are cultivated and wild-harvested for industrial purposes, as extraction of the polysaccharides present in their cell walls. To test the effects of harvest on population growth we used a case study of *Mazzaella laminarioides*, an intertidal seaweed endemic of Chile. This species is increasingly wild-harvested for carrageenan production, and the ecological effects of current harvesting practices are unknown. We assessed three treatments, simulating current harvest methods: (1) pulling fronds by hand monthly, (2) pulling fronds at the beginning of the season, and (3) scraping all fronds at the beginning of the season. Using a random block design we established 13 experimental units, containing four plots each, which were subjected to one of the three treatments, or left as a control. Monthly, during one harvesting season (December 2016 - May 2017), we monitored holdfast density, and frond density and size. For statistical analysis, we used linear mixed effect models with three response variables: density of holdfasts, fronds, and harvestable fronds (>5cm). The treatment that showed a most rapid recovery of the variables studied was hand-pull once. By the end of the experiment, plots hand pulled monthly had significantly more holdfasts and same number of fronds as the control, but significantly fewer harvestable fronds. Plots scraped once had more holdfasts, but significantly fewer fronds than the control. Our results suggest that the impact of harvest on the population could be reduced by strategies as hand-pull and rotation of harvesting areas.

UNIVERSAL PCR PRIMER SUITES FOR THE RAPID DETECTION OF ANATOXIN-A AND MICROCYSTIN-RELATED GENES IN FRESHWATER CYANOBACTERIAL COMMUNITIES

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Cyanobacterial blooms pose several threats to freshwater systems around the world. The ubiquity of this group and their ability to produce a variety of toxins make it difficult to predict and manage toxic bloom-forming genera. There is a lack of reliable tools to test the potential toxicity of diverse cyanobacterial communities. The aim was to develop gene-specific PCR primers for the suite of microcystin and anatoxin-a biosynthesis genes, which would function regardless of which genera contained the targeted genes. We designed and tested universal primers for the detection of microcystin and anatoxin-a genes using known sequences from genera in the NCBI database. These primers were tested across several cyanobacterial genera from the UTEX Culture Collection of Algae to evaluate the specificity of the primers and to screen for potentially toxic strains to use in future research. The anatoxin-a primers were verified against *Lyngbya kuetzingii* UTEX B 1547 and successfully tested against other genera of the Oscillatoriales and Nostocales. Published genera-specific primer sets were used to identify toxin-producing strains of the genus *Microcystis* for the verification of our designed primers. The universal microcystin primers were difficult to validate since the genetic diversity of toxin-producing genera required the use of highly-degenerate primer sets. These data and the development of universal gene-specific primers will be presented along with future directions for the rapid in situ detection of these biosynthesis genes.

OBSERVATIONS OF TWO RESERVOIRS IN CENTRAL TEXAS, USA DURING A DROUGHT: STATISTICAL STRATEGIES FOR DETECTING HARMFUL ALGAL BLOOMS

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Eutrophic bodies of water enriched by drought conditions are more susceptible to algal blooms, including potentially harmful species. Two reservoirs in the Highland Lakes of central Texas were observed during an extended drought (2010-2015). A suite of physiochemical characteristics was examined to identify which factors had the most significant impacts on eutrophication coupled with the abundance of microalgae, including cyanobacteria. Statistical models incorporated archived water quality data, including chlorophyll-a concentration as a proxy for phytoplankton abundance; samples were taken every other month. Each reservoir responded differently to the drought – Lake Lyndon B. Johnson (LBJ) became eutrophic while Lake Travis remained mesotrophic. Corrected Akaike Information Criterion linear models were applied to determine the best fit for predicting bloom conditions for each reservoir. Total nitrogen was the primary indicator in LBJ; the indicators for Travis were elevated chloride, sulfate, and conductivity due to a lack of rainfall. While the biovolume varied significantly, cyanobacteria were present in both lakes. *Aphanizomenon* and *Limnothrix* were the dominant cyanobacteria in LBJ and Travis, respectively. The models support that an increase in total nitrogen in a period of drought amplified the potential for blooms of *Aphanizomenon* in the upper Highland Lakes. It was postulated that *Aphanizomenon* used free nitrogen rather than fixing nitrogen, allowing for rapid growth and leaving less free nitrogen for downstream communities.

NEW TOOLS FOR SELECTIVELY IMPROVING STRAINS OF SUGAR KELP *SACCHARINA LATISSIMA* FOR FOOD AND FUEL

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As part of ARPA-E's (DOE) MARINER program, we are pursuing a selective breeding project to improve the productivity and composition of *Saccharina latissima* that could ultimately serve as feedstock for biofuels. While current markets for kelp are human food, animal feed and phycocolloids, MARINER's goals are to develop a scalable pathway toward low-cost bio-energy feedstock. To facilitate swift cloning of gametophytes, we have developed efficient isolation by cell-sorting methods. We are employing PacBio and Illumina sequencing to create a deep-sequenced reference genome and establish a variant catalog for our founding populations and families. We have a team overseeing field trials of hundreds of unique sporophytes created from crosses generated from hundreds of gametophytes isolated from sporophytes collected from 14 locations in New England. These were outplanted in late 2018 and January 2019 on farm sites in Southern New England and in the Gulf of Maine. We will report on managing multiple crosses in the hatchery, field-planting, and early family phenotypic data. One of our goals is to develop methods to predict offspring (sporophytes) performance based upon genotype and breeding values of parents (gametophytes) as a short cut around extensive and expensive field-testing. Ultimately, our project goal is to select sugar kelp genetically suited to offshore farm environments and possessing qualities of increased dry matter yield per unit area (up to 10% per generation) and improved composition for use as food and eventually as a bioenergy feedstock.

Contributed Session: Evolution

GENE TRANSFER ACCOMPANYING THE SECONDARY ENDOSYMBIOSIS OF EUGLENID PLASTID

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Euglenophytes form a monophyletic group with secondary chloroplasts derived from a green alga, which was most probably acquired by a common ancestor of autotrophic euglenids. The process of organelle acquisition is accompanied by the transfer of genes from the endosymbiont to the host nucleus (EGT), the presence of such genes in euglenids provides a footprint of past endosymbioses. To investigate the process of EGT influx into the euglenid

lineage, we have analyzed transcriptomes of four autotrophic and five heterotrophic euglenids using an automatic pipeline, which enable us to select transcripts of genes putatively related to other algae. As expected, the percentage of green-algal-related genes is higher in autotrophic as compared with heterotrophic euglenids. We have also confirmed the previous notion that euglenids contain a relatively high number of genes related to ochrophytes and haptophytes, which are not related to their plastids. Finally, we have mapped the entries of algal-related genes on the nodes of consensual euglenid phylogeny using orthoMCL and Dollo parsimony approach. Origin of approx. 213 such genes was mapped on the common ancestor of *Euglena* and *Eutreptiella*, in which the euglenophyte plastid is expected to originate. Astonishingly, 406 such genes were mapped on earlier and 52 on later internal nodes suggesting that the acquisition of the plastid protein repertoire was a continuous process rather than a sudden event. It is also possible that the endosymbiosis took place earlier and involved more partners than expected.

SUBTLE DIFFERENTIATION MAINTAINS HAPLODIPLONTIC LIFE CYCLES ... UNTIL IT DOESN'T

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Genetic models suggest haplodiplontic life cycles are transitory states on the way to diploidy or haploidy. The diversity of lineages maintaining haplodiplontic life cycles suggests they are not transitory states, but evolutionarily stable. Here, we used the widespread, non-native macroalga *Agarophyton vermiculophyllum*, which throughout the Northern Hemisphere has been shown to undergo dramatic demographic shifts following the invasion of soft-sediment habitats. Almost all soft-substratum habitats in the non-native range are dominated by tetrasporophytes, despite the likelihood that both tetrasporophytes and gametophytes were introduced together. We subjected male and female gametophytes and tetrasporophytes to a factorial combination of temperature, salinity, and light levels. The combined stress of high temperature and high salinity reduced growth and increased bleaching risk. Females and tetrasporophytes tolerated these conditions better than males. Less stressful environments led to higher tissue quality. The invasion of soft-substratum habitats uncouples the life cycle in which tetrasporophytic phenotypes are consistently more robust. These differences, however, are subtle and may not be captured accurately if the wrong phenotypes are investigated.

ESTIMATING THE SHIFT TO MULTICELLULARITY AND THE EMERGENCE OF SHALLOW COASTAL ECOSYSTEMS USING HETEROKONT ORGANELLAR GENOMES

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Brown algae (Phaeophyceae) are important architects of coastal marine ecosystems and represent one of the last lineages to transition to complex multicellularity in the Eukaryotic Tree of Life. Brown algae also form one of the only multicellular lineages in one of the largest and most heterogeneous assemblages of organisms on earth, the heterokonts (Stramenopiles). Heterokonts span both terrestrial and aquatic habitats and include photosynthetic planktonic lineages (e.g., diatoms), and non-photosynthetic lineages like the pseudofungi (oomycetes). We proposed that the origin of brown algae correlated with the emergence of shallow benthic coastal ecosystems. Evaluating this hypothesis required a robust estimate of the timeframe for the origin of multicellularity in the Gyristan heterokonts and the diversification of brown algal taxa, like the kelps. Relaxed clock analyses which included organellar data

from the closest extant relative of the brown algae, *Schizocladia ischiensis* and other important heterokonts enabled robust estimations of these timeframes.

TRANSCRIPTOMICS AND POPULATION GENETICS REVEAL THE ROLE OF POLYPLOIDY AND LIFE HISTORY IN MICRASTERIAS ROTATA (DESMIDIACEAE)

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Micrasterias (Desmidiaceae) is a diverse single-celled clade of algae with a haplontic life cycle driven by frequent asexual and infrequent sexual modes of reproduction. In addition to being morphologically diverse, species of *Micrasterias* show diversity in chromosome number which may result from complex polyploid histories within the genus. The goal of this research is to understand the role of polyploidy on the evolutionary genomics and population genetics of species of *Micrasterias* with a focus on *Micrasterias rotata*, a species with high chromosome counts. Using transcriptome data from stock culture collections and molecular phylogenetic evolutionary analyses of substitution rates the presence of ancient whole genome duplications is inferred for *M. rotata*, *M. radiata*, *M. thomasi*, and *M. fimbriata*. A unique method of DNA extraction from single-cells, whole genome amplification to generate template DNA, and chloroplast, mitochondrial, and nuclear markers developed from transcriptome data is used to study the population genetics of *M. rotata* from streams and lakes of North American Pacific Northwest. The transcriptome data weakly support an ancient whole genome duplication in *M. rotata* whereas the population genetic data indicate that *M. rotata* are diploid with tetraploid zygospores. The population genetic analyses also show that *M. rotata* harbors high heterozygosity and that populations may be sustained through asexual clonal reproduction.

Contributed Session: Ecology II

PERIPHYTON COMMUNITIES IN THE ATCHAFALAYA FLOODPLAIN

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Periphytic algae are important sources of carbon in freshwater communities and contribute to the bulk of primary production in lakes and rivers, but little is known about their role in floodplain systems. The Atchafalaya River Basin (ARB) is the largest tributary of the Mississippi River and the largest remaining bottomland hardwood river system in North America. The annual flood pulse likely plays a role in floodplain periphyton dynamics, influencing shifts in community composition and productivity. Starting in August 2017, we deployed 42 glass slide periphytometers at 14 ARB sites differing in their position relative to floodplain water inputs. Slides were harvested biweekly and algae were classified into eight taxonomic groups. *In situ* chlorophyll and phycocyanin, HPC, and TOC/TN were also determined at all sites. For nearly all months sampled in 2018, site location influenced periphyton abundance (diatoms and chlorophytes; all $p < 0.01$), with diatoms having the highest total abundance. Chrysophytes appeared in September, likely due to falling temperatures. Xanthophytes rose in November, likely due to temperature shifts or rises in DOM with receding water. Water levels began to rise in December, with floodplain inundation peaking in April 2018. The movement of water on and off the floodplain appears to be important to periphyton assemblages in the ARB. Conditions outside the ARB for comparison of periphyton dynamics in flood pulse and non-flood pulse environments will also be discussed.

LOSING LARGE BROWN ALGAE: DRAMATIC SHIFTS IN MACROALGAL ASSEMBLAGES OVER 50 YEARS IN WAIKIKI, SOUTH OAHU

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Long-term quantitative datasets in marine tropical areas are rare, yet needed for comparisons to present communities to identify temporal patterns and inform management about the status of culturally and ecologically important species. From 1966 to 1969, M. Doty and colleagues surveyed the biomass and species composition of algae in 12 plots from 0 to 230 m offshore of south O‘ahu. In conjunction with the undergraduate research program Our Project in Hawai‘i’s Intertidal (OPIHI), we resurveyed three plots (10, 110, and 210 m) using the same methodology to identify spatial changes in macroalgal species composition and abundance. In 1967, the most abundant nearshore (10 m) species were *Ulva* spp., *Dictyosphaeria cavernosa*, *Valonia aegagrophila*, and the invasive *Acanthophora spicifera*, while the offshore sites (110 and 210 m) were dominated by a high abundance of the native brown algae *Sargassum* spp., *Dictyopteris plagiogramma*, and *Padina* sp. The species composition in 2018-2019 dramatically shifted to a high abundance of invasive *Gracilaria salicornia* and *A. spicifera*, low abundance of the invasive *Avrainvillea* sp., and absence of large brown algae such as *Sargassum* spp. and *D. plagiogramma*. The loss of these culturally-important native species and increase in invasive species suggests this area has undergone a dramatic shift in community assemblage structure, with unknown ramifications for this area’s food web dynamics, fisheries habitat function, and overall ecology.

LIGHT REDUCTION INSIDE KELP FORESTS CAN CONSTRAINT THEIR INVASION BY THE EXOTIC SEAWEED *UNDARIA PINNATIFIDA*

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The physiological plasticity behind the invasiveness capacity of the exotic seaweed *Undaria pinnatifida* is still not well understood. Kelp monitoring programs in Baja California, Mexico, suggest that light availability within the iconic giant kelp forests (*Macrocystis pyrifera*) determines the presence and growth of *U. pinnatifida* in the understory. To test if limited photoacclimation capacities agree with these observations, we performed an in situ experiment where we transplanted juvenile sporophytes of *U. pinnatifida* to the understory of a thriving forest, where light was 8% of the surface irradiance. We measured a wide range of photobiological descriptors and other key plant traits such as nitrate uptake, oxidative stress, and growth after 7 days period. Generally, *U. pinnatifida* showed a limited capacity to acclimate to severe light scarcity, since it was unable to modify its photosynthetic efficiency, maximum photosynthesis, blade absorptance, compensation/saturation irradiances, or pigments (except for fucoxanthin). The absence of photoacclimation lead to severe plant carbon unbalance, a reduction in nitrate uptake capacity, and a general decrease in algae fitness. Results indicated that light scarcity within giant kelp forests negatively influence the photosynthetic performance of *U. pinnatifida* and therefore can potentially limit its invasiveness capacity. Stressful conditions such as extreme warming events can affect the structure of kelp canopy, making these forests more vulnerable to invasive seaweeds.

WHY ARE THERE SUCH UNUSUALLY DENSE POPULATIONS OF *ACETABULARIA* AND *BATOPHORA* IN ANCHIALINE LAKES OF THE BAHAMAS?

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The islands of the Bahamas are home to a number of anchialine lakes, attached to the sea by subterranean connections. Due to these connections, we might expect the community composition of these lakes to mirror those of other nearby shallow marine environments such as reefs or estuaries. However, many of the lakes we've sampled are dominated by large "mats" of dasycladacean seaweeds (primarily *Acetabularia crenulata* and *Batophora oerstedii*) far exceeding the bottom coverage of other nearby shallow marine habitats. What is it about these lakes that make them such prime habitat for dasyclads? Some of these ponds do exhibit extreme fluctuations in salinity; Reckley Hill Settlement Pond on San Salvador Island has been measured at half to twice the average salinity for seawater and hosts large mats of dasyclad seaweed. An undergraduate study using Florida *A. crenulata* suggested best growth at 35-52ppt, with a growth rate reduced by more than sixty-percent outside that range. Biotic factors could also be at work on these dasyclads. We are also in the process of characterizing the rest of the biota associated with dasyclad seaweeds in Bahamian anchialine lakes, such as the gastropod grazers and epiphytic diatoms, for comparison to dasyclad assemblages outside of these lakes. We suggest that these anchialine dasyclad communities could be natural stress labs for investigating community and ecosystem effects of climate change and other anthropogenic threats to near-shore marine environments.

Contributed Session: Harmful Algal Blooms

IS THERE AN ECO-FRIENDLY TREATMENT TO CONTROL CYANOBACTERIAL HARMFUL ALGAL BLOOMS?

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In February 2017, a *Microcystis aeruginosa* bloom (maximal biomass of 55 µg/L chl a and microcystin concentration of 40 µg/L) occurred in a freshwater pond in Padre Island National Seashore, Texas. This bloom caused mortalities including migratory redhead ducks. To treat the pond without further damage to the ecosystem, we proposed use of peroxide. A nomograph of peroxide required for oxidizing different initial cyanobacterial biomass levels to achieve desired final microcystin and chl a concentration was developed, then an outdoor mesocosm experiment with four treatment levels were tested. With chl a concentration >50 µg/L, the nomograph predicted >97% removal efficiency if 50 mg/L peroxide was used. In the mesocosm experiment, discrete samples assessed cell morphology, pigment, and toxin content (n = 3) at six different time intervals during the 48 hr treatment period. In the 50 mg/L peroxide treatment, change in cell morphology was evident at 4 hrs, with a significant decrease in filter-retained toxin and pigment concentration, with a significant increase in dissolved toxin (p-value <0.05). Over 75% of microcystin and >80% of chl a was destroyed after 48 hrs exposure to the highest treatment and at the lower dose (10 mg/L), 34% of chl a and 19% of microcystin were destroyed. The pond was treated with 10 mg/L H₂O₂ which reduced chl a by 60% and microcystin by 35% after 2 days. Control of the

cyanobacterial bloom using peroxide was effective and peroxide residual was depleted by biological and physical oxidation resulting in no long-term damage to the environment.

DIFFERENCES IN XANTHOPHYLL DE-EPOXIDASE ACTIVITY IN HIGH AND LOW TOXIC STRAINS OF *KARENIA BREVIS*

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The marine dinoflagellate *Karenia brevis* produces a suite of poly-ether ladder neurotoxins known as brevetoxins (PbTx). The endogenous function of brevetoxin remains unknown. Hypotheses have included a role as a feeding deterrent or mediator of osmotic regulation. We have previously reported that PbTx localizes to the thylakoid membrane and interacts with light harvesting complex II (LHC II) and thioredoxin (Trx). This may indicate a role in photosynthesis or redox regulation. High and low-toxic strains differ considerably, not only in their production of brevetoxin, but in their ability to perform non-photochemical quenching (NPQ) which involves the dissipation of excess light energy as heat. However, it is unknown whether the deficiency of NPQ is a result of low toxin production, or low toxin production a result of low NPQ. The xanthophyll cycle is central to energy dependent NPQ (qE). In dinoflagellates, diadinoxanthin is converted to diatoxanthin by enzymatic de-epoxidation of diadinoxanthin via diadinoxanthin de-epoxidase (DDE). The glycolipid monogalactosyl-diacylglycerol (MGDG) is vital to proper function of the xanthophyll cycle. We have shown that the low toxic strain of *K. brevis* is deficient in performing this de-epoxidation. However, the source of this deficiency is not understood. Our results will show the RT-qPCR studies done in our lab to quantify differences in relative amounts of DDE expression at the mRNA level in high and low toxic strains of *K. brevis*. The glycolipid profile of the high and low toxic strains will be compared.

EFFECT OF DIFFERENT MINIMUM SAMPLING AREAS ON THE ASSESSMENT OF SPATIAL VARIABILITY: A CASE STUDY IN A GREEN TIDE

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Blooms of green seaweeds, mainly *Ulva*, are called green tides. The study of spatial patterns of variability may elucidate factors controlling the development of green tides. Previous studies of green tides have used different minimum sampling area sizes (MSAs) ranging from 625 cm² to 2500 cm². This study's main objective was to investigate the effects of different MSAs in assessing relevant spatial scales of variation in a green tide located in the Argideen Estuary, Co. Cork, Ireland. Two MSAs (Small - 625 cm²; Large - 2500 cm²) were used to assess abundance and distribution of dominant *Ulva* morphologies (tubular and laminar). In addition, associated benthic epifaunal communities for both MSAs were collected. Tubular *Ulva* had a higher abundance than laminar *Ulva*. Both MSAs highlighted position (or tidal ranges) as the most relevant spatial scale of variation for tubular *Ulva*. For laminar *Ulva*, only the small MSA outlined section (or 1000 m scale) as the most relevant spatial scale of variation. Overall, similar results were obtained independently of the MSA used for the spatial scales of variability assessed for *Ulva* biomass. For the epibenthic fauna, *Peringia ulvae* was the most abundant species. The small MSA highlighted that its abundance and distribution was primarily explained by position, with significant interactions between position and section. Similar observations were made for the large MSA, with section by itself also a significant factor.

COULD THE LOSS OF DMA PROVIDE A SIGNIFICANT AMOUNT OF NITROGEN (N) AND PHOSPHORUS (P) TO SUPPORT THE SUPER BLOOM IN THE INDIAN RIVER LAGOON, FLORIDA?

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Catastrophic loss of seagrass occurred in the Indian River Lagoon (IRL), Florida, due to two consecutive years (2011-2012) of unprecedented phytoplankton “super blooms”. This seagrass decline was preceded by a large loss of drift macroalgae (DMA). Could the loss of DMA provide a significant amount of nitrogen (N) and phosphorus (P) to support the super bloom? To determine tissue N and P, 8 collections of DMA were made between July 2014 and August 2015 at 6 sites, 3 in the Northern IRL and 3 in the Banana River Lagoon (BRL). The annual mean N content of DMA was 2.11% dw; the monthly mean (all sites) N content of DMA ranged from 1.81% (August 2014) to 2.78% dw (December 2014) and varied little among sites. The annual mean P content of DMA was 0.09% dw. The overall monthly mean (all sites) P content of DMA ranged from 0.06% (June 2014) to 0.11% dw (December 2014). Mean P composition varied more than N composition among sites over the whole year, with the monthly mean P content at site BR 3 (0.16% dw) three times that at site BR1 (0.05% dw). In both the NIRL and BRL, the P content of DMA increased from north to south. Given historical DMA biomass present before the blooms and the measured N and P tissue nutrients, the loss of DMA in 2010-2011 did provide a significant amount of these important nutrients to the super bloom. This study has provided a better understanding of macrophyte nutrient cycling in the IRL and how the disruption of this role may have contributed to the development and persistence of severe phytoplankton blooms, which have reoccurred since 2011.

NUTRIENT DYNAMICS AND ECO-PHYSIOLOGY OF OPPORTUNISTIC MACROALGAL BLOOMS IN IRISH ESTUARIES AND COASTAL BAYS (SEA-MAT PROJECT)

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Sea-MAT aimed to understand the role of local environmental conditions in the development of green tides in Ireland. Five of the largest macroalgal blooms in Irish estuaries were studied and monitored using innovative methodologies. Molecular tools revealed the multi-specific composition of the green tides (8 species of *Ulva*), confirmed the presence of *Gracilaria vermiculophylla* and identified *Pylaiella littoralis* as the main species producing the golden tide at Killybegs. Remote sensing techniques were used to reconstruct the invasion of *G. vermiculophylla*. Assessment of spatial and temporal scales of biomass variability suggested a photoperiod and temperature were key in the annual development and composition of red and green blooms, revealing a temporal succession between *Ulva* species. Seawater physicochemical parameters differed between different seaweed tides (i.e. green, golden and red), indicating relevant differences in ecophysiological traits. Tissue N content (>2% N) suggested that seaweed tides are not limited by N, since these values were higher than the critical quota (approx. 2%). Various experiments were conducted in order to identify the mechanism(s) determining the seasonal succession observed in Irish green tides between tubular (i.e. *U. compressa*) and laminar (*U. rigida*) morphologies and predict the future development of Irish green tides in the context of global warming and eutrophication. Recommendations to reduce the impact of seaweed tides and control their development are proposed.

VITAMIN B12 ECOLOGY AND PHYSIOLOGY OF *KARENIA BREVIS*

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Recent evidence has highlighted the diversity of vitamin B12 molecules and the potential implications for phytoplankton dynamics. Specifically, in contrast to true vitamin B12, many cyanobacteria produce only pseudo-vitamin B12, which cannot be used effectively by numerous diverse eukaryotic phytoplankton. On the other hand, the diazotrophic filamentous cyanobacteria *Trichodesmium*, appears to have the genes to synthesize vitamin B12. Moreover, another diazotrophic cyanobacteria has been shown to excrete an order of magnitude more B12 into the environment compared to *Synechococcus*. Consequently, we developed a vitamin B12-bioassay using *K. brevis* to quantify the bioavailability of B12 excreted by local isolates of *Trichodesmium* and *Synechococcus*. Neither cyanobacteria needed exogenous B12 in culture. Both *Synechococcus* and *Trichodesmium* cultures excreted vitamin-B12 equivalents into the medium, but *Synechococcus* excreted them at a rate 3x faster than *Trichodesmium*. Bacterial community fingerprints did not show dramatic shifts over batch growth of *Synechococcus*. This suggests pseudo-vitamin B12 remodeling may be most important to *K. brevis*. *Karenia brevis* culture decline was more rapid when limited by B12 compared to nitrogen. To evaluate how vitamin B12 might limit *K. brevis* growth in the environment, we applied the B12-bioassay to samples collected from 6 coastal sites over 4 weeks during event response sampling for the 2017-2018 *K. brevis* bloom. The sites >30 Km offshore had consistently the lowest vitamin B12 levels (1-3 pM), coinciding with the lowest *K. brevis* counts.

Contributed Session: Biodiversity

MORPHOMETRIC ACCOUNT OF *CALOGLOSSA* (DELESSERIACEAE, RHODOPHYTA) INCLUDING FOUR NEW RECORDS FROM THE SUNDARBANS, BANGLADESH

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Mangrove-associated red algal species of the genus *Caloglossa* were collected from the estuarine waterbody during the low tide while adhering to pneumatophores, barks of mangrove trees and other solid substrates in the Sundarbans forest of Bangladesh in February and March (dry season), November and December (wet season), 2018. Anatomical structure, branching patterns, rhizoidal arrangements, apical cells, constriction at the node, midrib and reproductive traits were examined. In addition, only two species *Caloglossa bengalensis* and *C. vieillardii* reported in 1973, four new records for Bangladesh were found: *C. adhaerens*, *C. beccarii*, *C. stipitata* and *C. leprieurii*. While *C. bengalensis* was recorded from all sampling spots throughout the year, *C. adhaerens* was recorded during the wet season and only at the highest tidal zone where it receives more sun. *C. beccarii* occurred predominantly upstream away from the Bay of Bengal while *C. stipitata* seemed more common downstream. *C. leprieurii* was apparently rare and collected only in a few sites. However, *C. vieillardii* was not encountered during the study period. This study provided further evidence in documenting the rich diversity of epiphytic algae in the Sundarbans.

DNA SEQUENCING OF TYPE SPECIMENS REVEALS TWO HOMOTYPIC SYNONYMS FOR THE CORALLINE SPECIES *HARVEYLITHON MUNITUM* (METAGONIOLITHOIDEAE, CORALLINALES)

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Harveylithon A. Rösler, Perfectti, V. Peña & J.C. Braga (Metagoniolithoideae, Corallinales) is a recently described genus that currently includes six species worldwide. Comparative DNA sequence analyses of a short portion (118-276 base pairs) of the 3' end of *rbcL* from type specimens revealed that *Harveylithon munitum* (basonym *Lithophyllum munitum* Foslie & M. Howe, described in 1906 from Cave Cays, Exuma Chain, Bahamas) is conspecific with both *Goniolithon accretum* Foslie & M. Howe and *Goniolithon affine* Foslie & M. Howe, described in 1906 from Sand Key, Florida and 1907 from Culebra Island, Puerto Rico, respectively. *L. munitum* and *G. accretum* were described in the same 1906 publication. Because there is no priority based on page number, we have chosen to apply the currently accepted and taxonomically up to date name *H. munitum*. Comparative analyses of *rbcL* and *psbA* sequences from contemporary field-collected specimens revealed that *H. munitum* currently inhabits mesophotic rhodolith beds in the Northwestern Gulf of Mexico, the intertidal zone in the Florida Keys, Caribbean Panama, and the Great Barrier Reef. Two new species of *Harveylithon* from the Northwestern Gulf of Mexico were also identified in the analyses. Further DNA sequence analyses of additional markers need to be conducted to clarify the relationship between the Western Atlantic and Australian *H. munitum* populations.

BIOGEOGRAPHICAL PATTERNS OF INDONESIAN SAR CLADE COMMUNITIES IN RELATION TO WALLACE'S LINE

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Indonesia is home to some of the most biodiverse ecosystems in the world, and yet outside of animal systems, few marine biodiversity studies have taken place there. Over the years, biogeography studies on terrestrial animals found that there was a barrier, which became known as Wallace's line, separating terrestrial Asian fauna from terrestrial Australian fauna in the Indo-Pacific. Since the proposal of Wallace's line, the boundary has been redrawn and evaluated by a number of scientists but has rarely been applied to marine ecosystems within this region. More recently, a new barrier has been hypothesized for marine communities based on direction of surface currents in this region. Using metabarcoding of the V3 and V9 variable regions of 18S rDNA the SAR clade communities in three coastal marine environments located on either side of this proposed line have been characterized. Beta diversity shows significant difference between communities in each sampling region, while Shannon diversity remains statistically the same across regions. Possible environmental drivers behind these community shifts will be discussed.

A BIODIVERSITY EVALUATION OF INTERTIDAL ALGAL COMMUNITIES FROM THE ALABAMA GULF COAST VIA METABARCODING

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The recent progress of molecular techniques made possible to develop a new approach for faster and more accurate identification of species richness. Metabarcoding is a relatively new technique and few studies reported its application for assessment of algal communities. The most efficient barcode(s) as well as the standardized bioinformatics pipeline for algal metabarcoding studies have not been established yet and requires further research. This study will present the first implementation of DNA metabarcoding for studying intertidal algae community composition and horizontal zonation patterns in the coastal zone of the Northern Gulf of Mexico (NGoM). Our results indicated that implementation of Trimmomatic software as the preprocessing step before the application of the major USEARCH pipeline can highly increase the number of usable reads after the filtering stage. This step allows the benefit from high reliability of USEARCH pipeline as the core tool for data processing and reduce the negative effects of the USEARCH's aggressive sequence filtering algorithm. Our modified pipeline was able to taxonomically assign 90% and 42% of unique operation taxonomic units (OTUs) to genus and species levels, respectively. To the best of our knowledge this is the highest percentile of OTUs assigned to low taxonomic ranks up to date for algal metabarcoding studies. Overall, our analyses recovered 128 unique algal genera and 112 unique algal species, with 68 species never reported previously for the Gulf of Mexico

THE IMPORTANCE OF RHODOLITHS FOR MACROALGAL BIODIVERSITY IN GULF OF MEXICO MESOPHOTIC HABITATS

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In the northwestern Gulf of Mexico, unique deep bank habitats associated with salt domes occur at ~50-90m on the continental shelf offshore Louisiana and Texas. In these mesophotic rubble habitats, rhodoliths, accreted predominantly by calcified crustose coralline red algae, are the main hard substrata for the attachment of benthic macroalgae. Metabarcoding of environmental DNA using molecular markers (16S gene V4 region and tufA gene) for endolithic portions of rhodoliths has revealed hidden cryptic algal diversity and unsuspected life history stages (e.g., dinoflagellates, haptophytes, unicellular red algae). We explored cryo-SEM as a potentially more informative method than regular SEM to effectively explore endolithic rhodolith microhabitats and minimize artefacts of sample

preparation in the study of cell inclusions which brought to light a suite of microalgal stages. Analyses of combined 16S V4 metabarcodes and 16S Sanger sequences of several macroalgal orders increased the established record of diversity in the region. Progress is underway to link the eukaryotic component of the rhodolith holobiont (“total organism”) with its co-occurring prokaryotic component. Rhodoliths are marine biodiversity hotspots that may function as seedbanks, temporary reservoirs for life history stages of ecologically important eukaryotic microalgae, or as refugia for ecosystem resilience following environmental stress.

THE ARCTIC OCEAN BIOME AND PHYTOPLANKTON ENDEMICITY.

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The Arctic Ocean is colder, fresher and more isolated than any other ocean. The limited number of inflows and outflows suggest barriers to species colonization and the extreme seasonal dark / light cycle is a strong environmental filter. For example, arctic phytoflagellates have a number of genes and pathways that compensate for living much of the time in the dark and under low light. Consistent with strong evolutionary pressure to adapt to Arctic conditions, recent 18S rRNA surveys and culturing efforts are pointing towards widespread endemicity of Arctic phytoplankton and other protists. The molecular surveys repeatedly find rRNA gene reads that cluster apart from temperate ocean representatives, suggesting widespread endemicity across multiple algal phyla. As sampling effort across the Arctic increases it is clear that many of these uniquely arctic species are pan-arctic. These endemic pan-arctic phytoplankton are just as indicative of the Arctic Ocean Biome as larger iconic species and the seasonal and spatial patterns of select species are starting to fill knowledge gaps into the functioning and vulnerability of the Arctic Ocean Biome.

GETTING INTO THE WEEDS – EYES ON SEAGRASS CITIZEN SCIENTISTS DOCUMENT MACROALGAL DISTRIBUTION PATTERNS IN A FLORIDA ESTUARY

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Coastal communities are concerned about the observed increase in macroalgae in their waterways. Macroalgae often display marked seasonal abundance patterns, peaking in spring and declining in the summer. These patterns may be related to salinity, temperature and light conditions. In Charlotte Harbor, on the west coast of Florida, there is an anxiety that increasing macroalgal abundances are damaging seagrass habitats and their associated economic value by outcompeting for light and nutrients, creating hypoxic conditions, and interfering with boating, fishing and tourism. Despite these concerns, a comprehensive monitoring program to evaluate macroalgal trends is lacking. To fill this gap, we developed a citizen science monitoring program to observe seagrass and macroalgal distribution patterns. Piloted in 2019, each year, during April and July, volunteer snorkelers will complete standardized data reports that we compile and submit to management. The goal of this study is to improve our understanding of macroalgal bloom dynamics in shallow seagrass areas. Extension efforts in collaboration with citizen scientists allow for coordinated data collection over broad areas within short time periods. Trained volunteer monitors will become advocates for their estuary and generate information needed by scientists. Long-term, survey results can provide documentation of macroalgal distribution patterns, and aid in distinguishing between interannual variability and management-linked changes in macroalgal biomass.

Posters - Alphabetical by presenter's last name. (#Eligible for PSA Student Lewin Award)

P1

IMPACTS OF MACROALGAL-ASSOCIATED GASTROPODS ON EPIPHYTIC MICROALGAE ON THE ECOLOGICALLY IMPORTANT ANTARCTIC BROWN ALGA *HIMANTOTHALLUS GRANDIFOLIUS*

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Benthic macroalgae that dominant shallow, hard bottom communities along the western Antarctic Peninsula support very high densities of mesograzers, particularly amphipods but also small gastropods. Previous studies have demonstrated that the macroalgae and amphipods form a mutualistic relationship. Most of the macroalgae are chemically defended from predation which benefits the associated amphipods by providing a refuge from predation while the macroalgae benefit from the amphipods greatly reducing fouling of their surfaces by smaller algae. One of the three most important macroalgae in terms of overstory cover, *Himantothallus grandifolius*, forms huge blades which carpet the benthos in deeper water. Field observations suggest that gastropods may be higher in relative abundance in proportion to amphipods on *H. grandifolius* than they are on other overstory macroalgae which are more finely branched. The present study documents that natural abundances of gastropods on *H. grandifolius* in mesocosms reduce fouling by microscopic algae, primarily diatoms. However, amphipods are probably also important in keeping them clean of diatoms in nature. In a smaller scale experiment, three different gastropod species were differentially effective at reducing diatom coverage on *H. grandifolius*.

P2

A PRELIMINARY FLORA OF THE BENTHIC, CORAL-ASSOCIATED DIATOMS OF GRAY'S REEF NATIONAL MARINE SANCTUARY, GEORGIA, USA

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Diatoms have been used as indicators of environmental change in many freshwater systems, such as lakes and rivers. The heterokont microalgae are highly diverse, with tens of thousands of described species, many of which have adapted to specific environmental conditions and can be identified by species-specific siliceous shells which persist long after cell death. This provides a stratigraphic record of environmental conditions inferred from the diatoms present. Despite the demonstrate potential in freshwater habitats, diatoms have not been used in this manner for coastal ecosystems. This includes threatened coral reef systems where the relatively quick diatom generation time could forecast environmental changes which could eventually harm the slower-growing corals. However, the fact that we do not have a strong knowledge base of benthic marine diatom taxonomy, especially benthic diatoms associated with coral reefs, presents a significant hurdle to utilizing diatoms in this fashion. Building off floristic efforts from reefs in Guam and the Red Sea, we have begun assembling a flora of coral reef-associated benthic diatoms off the continental US—specifically Gray's Reef National Marine Sanctuary (GRNMS) off the coast of Georgia. Sediment samples from around 20 m depth were collected no further than 1 m from coral heads both inside and outside of the marine sanctuary. This poster reports our progress so far in cataloging the described and

undescribed benthic diatom diversity for comparison to samples collected near coral heads at similar depths in the Red Sea.

P3

SYSTEMATIC IDENTIFICATION AND ECOLOGY OF *CHARA* (CHARALES) IN STORMWATER TREATMENT AREAS OF SOUTH FLORIDA: A PRELIMINARY STUDY

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Chara (aka stoneworts and muskgrass) is a genus of green algae in the class Charophyceae. This alga is generally associated with clean waters and can serve as a bioindicator of water quality. The genus is widespread in South Florida, and is planted and used for nutrient uptake (especially phosphorus) in the Storm Water Treatment Areas (STAs) of the South Florida Water Management District (SFWMD). In the STAs, massive die-offs of *Chara* can occur that undermine the efficacy of the water treatment process. In order to attain a better understanding of these die offs, research on the phylogenetic and ecological characteristics is necessary. We conducted morphological, phylogenetic and ecological analyses to further our understanding of *Chara* in the STAs. Two species were found in our investigation: *Chara haitensis* Turpin and *C. zeylanica* Klein ex Willdenow. These species are morphologically similar and appear cryptic, which complicates field identification. We were able to identify that both species were co-occurring, even in single beds, by phylogenetic analyses of the *rbcL* and *matK* genes. *Chara* growth patterns were analyzed using mesocosms. From these experiments, we observed that the flow and depth of water has a major role in the success of *Chara* growth. Future work is directed at analyzing the physiological responses of these species under varying nutrient, pH and flow scenarios.

P4

EFFECTS OF GLYPHOSATE (RODEO) ON THE GROWTH OF *MICROCYSTIS AERUGINOSA* (CYANOBACTERIA)

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The widespread application of glyphosate as an aquatic herbicide has been disputed based on its potential secondary effects on aquatic algae, especially those that form harmful algal blooms (HABs). Glyphosate, the active ingredient in the commercial aquatic herbicide Rodeo, is thought to stimulate algal growth, primarily of cyanobacteria, with an inorganic form of phosphorus (P). In order to investigate the role of glyphosate (Rodeo) on the growth of *Microcystis aeruginosa*, BG11 supplemented with glyphosate was applied to cultures within 24-well plates using relative field application rates (1, 3, and 30ppm) together with both normal BG11 and BG11 without P. Cultures were incubated at 25°C, on a rotary shaker (120 rpm) for two weeks. Growth was monitored using a plate reader for in situ chlorophyll a quantification. Preliminary results suggest that the addition of glyphosate to BG11 can stimulate the growth of *M. aeruginosa*. Further research aims at testing the effect of glyphosate on other planktonic cyanobacteria and benthic cyanobacteria due to the possibility of differing responses based on evolutionary history, physiology, and location in the aquatic system. In addition, experiments at mesocosm scales are planned.

P5

PHYSIOLOGICAL DIFFERENTIATION AMONG GREEN ALGAL TURF SPECIES ON SOFT SEDIMENTS IN MANGROVE FORESTS IN TAMPA BAY, FL.: A CASE OF LIGHT NICHE PARTITIONING?

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Mangals are highly productive coastal communities with essential ecosystem services. Macroalgae have been shown to contribute significantly to mangal primary production. Turf forming macroalgae are found in the soft sediments under mangrove canopies. A limited number of previous studies largely consist of species inventories or the occasional assessment of productivity of this community as a whole. This study was conducted to explore the potential physiological differences of macroalgal species found in these turfs in Tampa Bay as well as to examine the impact of sedimentation on these turfs. Samples were randomly collected and analyzed for pigment concentrations, photosynthetic performance, and community composition by taking 5 cm deep sediment cores (N=360). Regardless of sampling site, *Boodleopsis pusilla* dominated turfs were shade acclimated where as *Chaetomorpha brachygona* and to a lesser extent *Cladophora coelothrix* dominated turfs were sun acclimated. This physiological performance appears to mirror the spatial distribution of these algae in the forest understory indicating the potential for these turfs to partition this niche based on available irradiance which can vary from 40 down to 4% of irradiance incident on the forest canopy. Lastly, pigment concentrations and photosynthetic performance within the top 1 cm of the turf declined significantly with depth indicating rapid deterioration with sediment accumulation. The role of these macroalgal turfs in stabilizing mangal sediments will be explored in future work.

#P6

THREE NEW GENERA OF MARINE CYANOBACTERIA FROM THE COAST OF SOUTH FLORIDA

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Marine non-heterocytous filamentous cyanobacteria represent a double-edged sword in marine ecology where they compete with benthic organisms by forming benthic cyanobacterial mats (BCMs), potentially house numerous bioactive compounds. The BCMs are an integral component of benthic communities in tropical marine waters that can develop into massive proliferations that are at risk of global expansion in lieu of climate change. These BCMs are widespread phenomena and often are very diverse. The extent of phylogenetic diversity occurring within these mats, though, remains largely unexplored, especially in Florida. To elucidate this diversity, coastal environments of South Florida were sampled and subsequently processed for isolation and identification. Unialgal cyanobacterial 16S rRNA and 16S-23S ITS gene phylogenetic relationships were evaluated using both Maximum likelihood and Bayesian inferencing. Three new genera are proposed based on the polyphasic approach. These new genera are characterized by curved, tapered apical cells that twist and rotate to facilitate mobility. These taxa also generate a similar morphological feature of linked and repeating barrel-shaped cells along individual filaments. A novel molecular fingerprint including a nine base pair insert within the 16S rRNA gene sequence facilitates the delimitation of these genera. Based on morphometric and phylogenetic relationships along with secondary structure of the ITS region, our research presents three new genera of non-heterocytous filamentous cyanobacteria occurring in coastal ecosystems of South Florida.

P7

PERFORMANCE OF 3D MANUFACTURED SUBSTRATA IN THE ALGAL TURF SCRUBBER APPROACH

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The performance of Algal Turf Scrubbers (ATS) rely upon the attachment of benthic filamentous algae to a substratum for remediation of aquatic pollution. The ATS process results in a mixed algal community of multiple phyla, providing a non-specific biomass product of varying quality for post-harvest utilization. This is a factor that has hindered the economic viability of the ATS approach for water remediation in most cases. Among possible process-based approaches for affecting algal community selectivity through competitive exclusion, re-engineering of the substratum for species-specific early colonization shows promise for positively affecting the process. We report on activities researching and developing novel substrata for use in ATS systems. Studies include investigation into advanced rates of early algal colonization using 3D-printed substrata forms, both idealized and reverse-engineered from natural substrata; optimization to increase biomass accrual rates on novel fibrous substrata; and design of new polymer composite materials that are species-selective through manipulation of surface free energy characteristics. Resulting substrata technologies have been tested in the laboratory, and demonstrate promise for understanding fundamental properties of the colonization ecology of attached benthic filamentous algae. Field applications of the materials technologies show advancements in biomass productivity that argue for considerations for scale-up for economic viability of ATS cultivation of algae.

P8

COMPOSITION AND DOMINANCE OF BEACH CAST SEAWEEDS ON THE SOUTHEAST AND NORTHEAST COAST OF BRAZIL

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The beach cast seaweeds are frequently found in Brazil, but research on them is still insufficient. The present study analyzed the composition and dominance of beach cast seaweeds on the northeast and southeast coast of Brazil. The studies were carried out on the beaches of Candeias, PE and Emboaca, CE (northeast), Pontal and Itaoca, ES (southeast). Samples were taken using the transect and square (25 cm²) method of in three replicates and the identification was based on morphological characters. A total of 140 taxa were identified, 105 Rhodophyta, 14 Ochrophyta and 21 Chlorophyta. These taxa were classified in five morpho-functional groups. In both regions Rhodophyta were the most representative group. Species diversity was greatest in northeast than southeast. Results of the nMDS based on biomass revealed a spatial separation in the distribution of the samples. The sites differed significantly in biomass of species (PERMANOVA, $p < 0.05$). According to SIMPER, the macroalgae species that most contributed to the dissimilarities of biomass between the sites were *Zonaria tournefortii*, *Dictyopteris jolyana*, *Spatoglossum schroederi* and *Codium isthmocladum*. Biomass comparisons of the morpho-functional groups between the beaches were significantly different, except for articulated calcareous. Most of the species were grouped in the corticated that obtained the highest biomass, in relation to the others.

P9

A POLYPHASIC ASSESSMENT OF PHYLLOSHERE ASSOCIATED CYANOBACTERIA COLLECTED FROM NORTHEAST JACKSONVILLE, FLORIDA (USA).

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Cyanobacteria are photosynthetic prokaryotes found throughout a diverse range of both aquatic and terrestrial habitats. Due to their ability to fix inorganic carbon and nitrogen, cyanobacteria play an important ecological role often involving symbiotic relationships with other organisms. This includes growing epiphytically on a variety of plant species. This study explores the diversity of epiphytic cyanobacteria from the campus of the University of North Florida (Jacksonville, Florida, USA). Seventeen isolates were collected from six plant surfaces and subsequently cultured on Z8 medium. Individual colonies were isolated and identified through morphology and sequencing of the 16S rDNA gene, which was employed in subsequent phylogenetic reconstruction employing MEGA v7 software. Folding patterns of the secondary structures from the 16S-23S ITS region were used to differentiate species. Samples fell under the genera *Nostoc*, *Komarekiella*, and *Kryptousia*, whose members possess the ability to differentiate into nitrogen fixing heterocysts and whose motile filamentous cells are typically enclosed by a protective sheathes. These traits combined give the members an advantage both as symbionts and as survivors of environments subjected to high levels of UV radiation and desiccation, which explains their ability to outcompete other cyanobacteria as epiphytes.

P10

PHYMATOLITHON CONCAVUM SP. NOV. (HAPALIDIACEAE, RHODOPHYTA) FROM THE NORTHEAST ATLANTIC OCEAN

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Phymatolithon is distinguished from other members of Hapalidiaceae by monomerous construction, cells of adjacent filaments joined by cell fusions, the absence of flared epithallial cells, subepithallial initials that are usually as short as or shorter than their immediate inward derivatives, adventitious and deep conceptacle primordium (more than 10 cells), absence of protective cells in male conceptacles, mature carposporophytes with discontinuous fusion cells, gonimobalst filaments developing across the entire upper area of the fusion cells, and multiporate tetra/bisporangial conceptacles. Worldwide, 21 *Phymatolithon* species are currently listed from the worldwide. We collected unidentified samples from the intertidal zones of United Kingdom and France. We analyzed the DNA sequences of them using *psbA* and COI-5P genes and also observed their morphology and anatomy of vegetative and reproductive thalli. In this study, we describe our unidentified samples as a new species, *Phymatolithon concavum* sp. nov. based on morphological and molecular data. *P. concavum* sp. nov. is characterized by encrusting to lumpy thalli, female conceptacles with raised rims, pitted tetra/bisporangial conceptacle roof with depressions, and degenerated uppermost cell of tetra/bisporangial conceptacle roof. We also provide evidence of their phylogenetic relationships with other similar species based on sequencing analyses. Our *psbA* and COI-5P sequences revealed sufficient divergence to warrant recognition of *P. concavum* as a new species.

P11

MORPHOLOGICAL AND MOLECULAR ANALYSES UNCOVER A NEW SPECIES OF DIGENEA (RHODOMELACEAE, RHODOPHYTA) FROM TROPICAL WESTERN ATLANTIC

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The number of algal species has increased since the use of molecular data in taxonomic studies. Three new species previously known as *Digenia simplex* were recently segregated and described using molecular evidence *D. arenahauriens*, *D. mexicana* and *D. rafaellii*. In this study, using morphological and molecular analyses of mitochondrial COI-5P and plastid *rbcL* DNA sequences we report a new species of *Digenea* from Florida and Cuba. This species is a small size, up to 2 cm high, determinate branches reaching 1 cm long; one to two layers of cortical cells and 12 pericentral cells. The COI-5P analysis resolves *Digenea* sp. in a sister clade with *D. cymatophila* from Hawaii, with interspecific divergence of 4.6%. The sequence divergence between *Digenea* sp. and *D. simplex* from Europe (including type locality) was 4.1%. The *rbcL* analysis shows that *Digenea* sp. was phylogenetically distinct from all other *Digenea* species and sister to *D. rafaellii* from Mexico, with 1.8% of interspecific genetic distance. *Digenea* sp. from Florida and Cuba showed an *rbcL* sequence divergence of 2.4% with *D. simplex* from Greece. Our data support the recognition of a new species of *Digenea* to accommodate specimens previously identified as *D. simplex* in South Florida and Cuba. Morphological features related to determinate branchlets and surface cortical cells deserve a more detailed study, since they seem useful in the *Digenea* species delimitation.

P12

THE NAGOYA PROTOCOL: WHAT IT IS AND WHY PHYCOLOGISTS SHOULD CARE

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The Nagoya Protocol is an international treaty that implements key concepts identified in the 1992 Convention on Biological Diversity, such as fair and equitable sharing of benefits from biological diversity (<http://cbd.int>). Although neither the USA nor Canada is currently a party to the Nagoya Protocol, 116 nations are, and in practice it defines international procedures for the exchange of genetic resources and traditional knowledge of those resources, and researchers who transport specimens across international boundaries cannot afford to ignore it. At present biological resources from the open ocean are not covered by the Protocol, but negotiations are currently underway to do so. The Protocol does not give governments any rights they did not already have, but requires a clear process, a domestic regulatory regime covering “mutually agreed terms” and “access and benefit sharing”, along with mechanisms to document compliance. Benefit sharing can be interpreted broadly, and can include activities such as speaking at local universities, training local students, and forming research partnerships. To facilitate documentation of compliance, the protocol established the Access and Benefit Sharing Clearinghouse (<https://absch.cbd.int/>), which is a key resource for researchers. Under the Protocol it is now necessary to have both a national permit (collecting permit) and an internationally recognized certificate of compliance (IRCC). Note that even after specimens have been collected, use must only be within the pre-negotiated terms; other uses require new approval.

P13

CAN PHOSLOCK® BE USED TO BIND AND SEDIMENT MICROCYSTIN-LR IN AQUATIC SYSTEMS?

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Microcystins [and its congener microcystin-LR (MC-LR)] are considered the most common cyanotoxin produced by cyanobacterial harmful algal blooms. The intracellular MC-LR is released into the water column upon cell lysis during treatment or senescence, where it can remain stable for weeks and lead to adverse health effects. The ideal treatment method for MC-LR-producing strains is one that can remove or degrade both cells and toxins from the water column. Many treatment methods result in only cell lysis and consequent release of toxins; therefore, targeted toxin removing methods are desired. We tested the hypothesis that Phoslock® can bind to MC-LR, removing it from the water column by sedimentation. In order to test this, MC-LR was dissolved in deionized water and diluted to 5, 20, 50, 100, and 500 ppb. A stock solution of Phoslock® (1 gL⁻¹) was used and kept homogenized on a magnetic stirrer and applied into solutions containing MC-LR at concentrations of 50, 100, and 150 ppm (in triplicate) including a control without Phoslock®. The tubes were incubated at room temperature for 24-48hr, and then processed for MC concentration using ELISA. Results indicate that MC-LR is removed from the water column when higher concentrations of both Phoslock® (100 and 150ppm) and MC-LR (100 and 500ppb) are present. Future work aims at deciphering the *in situ* effects of Phoslock®, in combination with other algaecides and flocculants to improve the efficacy of toxin removal.

P14

DOES THE PRESENCE OF EYESPOTS INFLUENCE PLASTID-ASSOCIATED GALACTOLIPID COMPOSITION IN DINOFLAGELLATES?

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Few dinoflagellates possess eyespots thought to act in phototactic responses. In many cases, the proteins comprising eyespots are positioned in or near chloroplast membranes and are composed primarily of two galactolipids, mono- and digalactosyldiacylglycerol (MGDG and DGDG). As part of our lab's continuing characterization of these dinoflagellate galactolipids, we have conducted an examination of published data on MGDG and DGDG in both eyespot-containing and lacking, peridinin-containing, photosynthetic dinoflagellates with secondary plastids to address the question: do eyespots influence galactolipid composition? As MGDG/DGDG are important structural lipids in plastid membranes which house eyespots, we hypothesized that the presence of eyespots would impact the overall composition of these galactolipids to allow their placement within a membrane(s). Included are new data on the eyespot-containing dinoflagellate *Margalefidinium polykrikoides*. We have observed that within *M. polykrikoides* and taxa such as *Symbiodinium* spp., the presence of eyespots appears to have no effect on galactolipid composition when compared to eyespot-lacking taxa. *M. polykrikoides* produces C20/C18 forms of MGDG and DGDG that are indistinguishable from those produced by eyespot-lacking C20/C18 taxa. For example, *Symbiodinium* spp. produce C18/C18 (sn-1/sn-2 fatty acids) forms that are indistinguishable from those of a cluster of eyespot-lacking C18/C18 taxa. We conclude that despite the close association of eyespots with plastid membranes, their presence does not influence galactolipid composition.

P15

MELANOTHAMNUS MANITICOLUS SP. NOV., AN EPIZOIC SPECIES EVOLVED FOR LIFE ON THE WEST INDIAN MANATEE

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Epizoic organisms are known to grow on marine megafauna. Numerous macroalgae have been documented growing on sea turtles and species are also known to grow on the West Indian Manatee, but the number and identification of these species have not been determined. Analysis of DNA sequences of 11 specimens collected from different manatees captured in three areas of Florida indicated that they represented a single undescribed species within the Rhodomelaceae genus *Melanothamnus*. Morphological analysis revealed *Melanothamnus* characteristics but also previously undescribed character states. These include heavy cortication restricted to the basal holdfast, and a sharp transition between the corticated and ecorticated section of the thallus; tetrasporangia that develop in both straight and spiral series, ostiole cells the same size as cells below, and robust rhizoidal holdfasts that originated from the longitudinal extension of basal pericentral cells with surrounding cortical cells extending into upper rhizoid. This species is described as *M. maniticolus* sp. nov.

P16

OVERVIEW OF *LAURENCIA* COMPLEX (CERAMIALES, RHODOPHYTA) DIVERSITY IN CUBA ASSESSED THROUGH MOLECULAR MARKERS

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Laurencia complex (Rhodomelaceae, Rhodophyta) comprises 208 species accepted taxonomically worldwide of which only 18 names have been mentioned for Cuba. These species recorded for Cuba are mainly based on morphological characters. However, relatively recent molecular techniques using mitochondrial DNA barcoding and other plastidial markers have been key to identifying the biodiversity of the species that make up this complex. Here, we provide an overview of the diversity of algae in Cuba based on DNA markers of phylogenetic importance. We recovered the sequences of the species that were registered for Cuba in GenBank. A Maximum Likelihood phylogeny based on *rbcL* illustrates the eight genera currently recognized for the *Laurencia* complex, including Cuban species. A total of 87 sequences were recovered. *rbcL* is the most representative marker with 67 sequences, 47 for *Laurencia*, 16 for *Palisada* and 4 for *Yuzurua*. Only 4 sequences of the species reported for Cuba appear in GenBank. One of them is *Laurencia intricata* and corresponds to the type locality of the species. *Palisada corallopsis* is another species with a type locality registered for Cuba. This species has only two sequences in Genbank and none is Cuban. *Laurencia chondrioides*, *L. microcladia* and *L. minuscula* do not possess any sequence in GenBank confirming the need to deepen the studies of this complex of red algae for the Cuban archipelago.

P17

DIFFERENTIAL GENE EXPRESSION IN GREEN ALGAL COMPETITION

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As part of a larger collaborative effort to determine the potential for phylogenetic relatedness to predict outcome of competition among planktonic green algae, RNAseq data were collected to track gene expression through the growth curve. Eight freshwater algal species spanning the Chlorophyte and Charophyte lineages were grown as monocultures and in all possible biculture combinations, in triplicate. For each condition and repeat, RNA samples were sequenced from early, pre and post-inflection log, and carrying-capacity stages of the growth curve. Here, we present eight de novo transcriptome assemblies and corresponding timecourse differential gene expression analyses from species broadly distributed across the green-algal tree. Assemblies were filtered for non-algal, duplicate, and incomplete transcripts, and the resulting reference transcriptomes ranged from 12,767 to 29,743 complete and non-

redundant complete coding regions. Levels of gene expression were estimated for each of these coding regions for all 96 monoculture time-point samples. Our results show distinct phases of gene expression across the monoculture growth curves, reflecting the effects of intraspecific competition. In addition, they indicate substantial differences among species in patterns of gene expression within commonly shared orthogroups. These observations provide baseline patterns of expression for subsequent analysis of biculture competition data.

P18

HARMFUL MACROALGAL BLOOMS: SOCIAL IMPACTS OF THE *SARGASSUM* INFLUX IN THE CARIBBEAN

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Massive *Sargassum* blooms, or “golden tides”, in the Caribbean have become an increasingly persistent nuisance since 2011, clogging coastal waters, depositing thousands of tons of seaweed onto regional beaches, covering vast areas of coastline, and forming berms as high as 4 meters. These inundations impede navigation, alter coastal species distributions, deter coastal recreation, cause anoxia, and present health risks resulting from decomposition. Despite numerous and increasingly prominent accounts in news media and grey literature of threats to nearshore ecosystems, fisheries, tourism, public health and human well-being, relatively little has been published on the phenomenon, and of that, a majority has been devoted to forecasting and/or discovering causative influences of the blooms. While these are important contributions, very little has been published on the ecological impacts, and nothing on the social impacts of these blooms. This study evaluates the disparity between published peer-reviewed literature and news media mentions and reveals that the quantity of peer-reviewed literature is disproportionately smaller than the amount of attention it has received in news media, which can be considered a proxy of social and economic impacts. This paucity of information means that managers and policymakers must make decisions uninformed by scientific research. This work will lead to a larger assessment of the social impacts of and management responses to the current *Sargassum* “invasion”.

P19

EFFECTS OF LIGHT, NUTRIENTS AND PREY ON INGESTION AND GROWTH OF A NEWLY IDENTIFIED MIXOTROPHIC ALGA, *CHRYSOLEPIDOMONAS DENDROLEPIDOTA* (CHRYSOPHYCEAE)

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Chrysolepidomonas dendrolepidota, a freshwater chrysophyte, was described recently but little is known of its distribution, physiology or ecology. Many photosynthetic chrysophytes have been identified as mixotrophic, combining photosynthesis and phagotrophy, but this study provides the first evidence of mixotrophic nutrition in *C. dendrolepidota*, including conditions that affect ingestion of bacteria and population growth. In a 2×2 factorial experiment with high and low levels of light and nutrients, the ingestion rate was significantly higher in the high light, low nutrient treatment relative to other treatments. Growth rates and abundance increased significantly in high light conditions. In experiments with nitrogen and phosphorus modified separately, ingestion rate was significantly different from the control only in the treatment with both macronutrients reduced. Supplementing low nutrient treatments with additional bacteria led to a significant increase in algal abundance relative to controls without added bacteria. These results indicate that acquisition of macronutrients is a likely driver of mixotrophic nutrition in *C.*

dendrolepidota. Although the distribution of *C. dendrolepidota* is unknown, mixotrophic chrysophytes can seasonally dominate planktonic algal abundance in aquatic systems, and nutrient limitation is known to increase bacterivory in some of those species. Identifying and understanding how different mixotrophic species respond to changing environmental cues is crucial to understanding their roles in aquatic food webs.

P20

COMPARING LONG-TERM STANDING STOCK AND TISSUE C:N:P RATIOS BETWEEN *HALIMEDA* AND *PENICILLUS* (CHLOROPHYTA) ACROSS A TROPHIC GRADIENT WITHIN FLORIDA BAY, USA.

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Florida Bay (FB), USA is a coastal subtropical lagoon with large seagrass beds containing *Halimeda* and *Penicillus* that produce calcareous biogenic sediments recognized to be P limited. Calcareous Green Algae (CGA) communities in FB have been monitored as part of the Florida Coastal Everglades Long-term Ecological Research program for nine years (2008-2017); from the SW (Sprigger Bank SB) to the central area (Bob Allen BA) and to the NE (Duck Key DK). It is expected that these genera will show a spatial variability of N and P limitation with higher standing stock towards the SW of the bay and a high limitation of P with lower standing stock towards the NE. At SB, the only site with both genera present, *Halimeda* showed a higher standing stock (74gm⁻²) than *Penicillus* (19gm⁻²). *Penicillus* had higher standing stock at SB than BA and DK (1.63,3.50gm⁻²). *Halimeda* C:N:P (1628:78:1) and *Penicillus* (2404:133:1) showed stronger N and P limitation in *Penicillus*. However, *Penicillus* had higher N (1.67%DW) content than *Halimeda* (1.02%DW). *Penicillus* had P limitation in all 3 sites (0.03%DW) and the expected N spatial variability was not found with similar high values at all sites (N%DW 1.67, 1.58, 1.55). The C:N:P and standing stock patterns found in these CGA genera are consistent with seagrass' patterns in FB, however the differences in standing stock across sites cannot be explained by nutrient availability. These values show FB has high N availability compared with the rest of the world, while P limitation is a consistent feature of calcareous biogenic sediment tropical bays.

P21

THE COSTS ASSOCIATED WITH BEING ABLE TO EAT THE BRUSSELS SPROUTS OF THE OCEAN

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Inter- and intraspecific interactions between organisms can either be a form of communication, environmental sensing, or defence and are often mediated by chemicals such as secondary metabolites. Sessile marine organisms such as macroalgae commonly produce chemical defences against grazers, pathogens, as well as biofoulers. *Plocamium cartilagineum* is a finely branched red understory alga that is common in Antarctic macroalgal forests. It supports a very high abundance of amphipods of which most are not able to feed on the heavily chemically defended *P. cartilagineum* except for *Paradexamine fissicauda*. Different *P. cartilagineum* individuals produce differing mixtures of halogenated secondary metabolites which are referred to as chemogroups. Around Palmer Station between 2016 and 2018 a total of 16 different chemogroups were identified. A subset of these chemogroups were used to identify whether the feeding rate of *P. fissicauda* differs between individuals that vary in secondary

metabolite production. The same subset was used to assess differences in growth rate and reproductive output of *P. fissicauda* when held on a chemogroup-specific diet. These data determined whether there is a fitness cost associated with feeding on particular chemogroups and whether secondary metabolite variation impacts the grazer's feeding rate.

#P22

CORAL-ALGAL COMPETITION AND OVERGROWTH DYNAMICS OF A RAPIDLY EMERGING RED ALGA (*RAMICRUSTA* SP.) IN ST. THOMAS, US VIRGIN ISLANDS

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A rapidly emerging red alga, *Ramicrusta* sp. (hereinafter *Ramicrusta*), has recently become abundant on several coral reefs in the Caribbean. Multiple species of *Ramicrusta* are characterized by fast growth and the ability to overgrow a variety of coral species. Over the last decade, *Ramicrusta* has demonstrated widespread harm to corals in the US Virgin Islands (USVI) by overgrowing living tissue, causing bleaching and colony mortality, and impairing coral recruitment. The alga commonly outcompetes other benthic organisms and prevents coral recovery, posing a severe threat to reefs in the territory. This study used high-resolution 3D photogrammetry to measure *Ramicrusta* growth on corals in the USVI to quantify and characterize the overgrowth rates of *Ramicrusta* and determine if certain coral taxa experience faster overgrowth by the alga. 3D models of individual coral colonies (five species plus controls, N=72) competing with *Ramicrusta* were generated at two time points to measure the linear and surface area expansion of the alga over six months. The maximum linear growth rate of *Ramicrusta* reached over 3.7 cm per year, with a maximum areal growth rate of over 50 cm² per year. Growth rates of *Ramicrusta* were significantly slower on *Siderastrea siderea* than on other coral taxa, indicating that this species is a strong competitor against the alga. All other coral species exhibited little to no resistance to *Ramicrusta* overgrowth, with algal growth similar to controls.

P23

CYANOBACTERIAL BIOACTIVE METABOLITES – IS THERE A BETTER SYSTEM FOR CLASSIFICATION

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Cyanobacteria can produce a large number of secondary metabolites. Odorous metabolites affect the smell and flavor of aquatic animals, whereas bioactive metabolites cause a range of lethal and sub-lethal effects in plants, invertebrates, and vertebrates, including humans. To date, cyanobacteria are known to produce over 150 classes of bioactive compounds; however, several classes share similar structures, thereby confusing readers. A recent reanalysis reduced the current known 157 bioactive classes to 55 classes by the structure similarity and bioactivity. This reanalysis provided a basis for more formal procedures to adopt a logical naming system. This reanalysis is needed for management of water resources to effectively communicate risk of lesser known but highly abundant compounds by knowing the right class/activity associated with each compound.

P24

CONTRIBUTION OF CHLOROPLASTS TO HETEROTROPHIC METABOLISM IN *EUGLENA GRACILIS*

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Euglena gracilis has remarkable metabolic capacity and plasticity, reflecting its complex evolutionary history. Notably, *E. gracilis*, unlike green algal and plant cells, the ability to live without its chloroplasts after antibiotic bleaching raises questions about the metabolic function of chloroplasts in *Euglena* which are addressed here using network flux analysis. As a first step, the growth characteristics of wild-type and bleached *E. gracilis* strains were measured. Then steady state ^{13}C metabolic flux analysis (MFA) was used to investigate the metabolic phenotype of the two *E. gracilis* strains grown heterotrophically on AF6 medium containing [1- ^{13}C]-, [2- ^{13}C]- or a mixture of [$^{13}\text{C}_6$]- and [$^{12}\text{C}_6$]-glucose. The redistribution of ^{13}C label in the network was analysed with mass spectrometry and metabolic flux maps were deduced using the INCA software package. The flux maps showed that fluxes through the central cytosolic and mitochondrial metabolic pathways increased in bleached cells. In contrast, the flux through phosphoenolpyruvate carboxylase was significantly higher in the unbleached cells. These changes contribute to a decrease in the proportion of glucose directed towards biomass production (carbon conversion efficiency) in the strain lacking chloroplasts. We conclude that, while the bleached cells are able to maintain the same growth rate under heterotrophic condition, the absence of chloroplasts decreases their metabolic efficiency.

P25

A CITIZEN SCIENCE APPROACH TO MONITOR PELAGIC *SARGASSUM* LANDINGS IN SOUTH FLORIDA

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Citizen science is becoming an effective approach to monitor phenomena in large geographical areas over long periods of time. The influx of pelagic *Sargassum* is a regional problem throughout the Atlantic, from Brazil to Florida. While satellite imagery can estimate *Sargassum* blooms on a regional level, it is difficult to have systematic in situ abundance observations. The impacts of *Sargassum* in the Caribbean vary between geographical locations. To test the use of citizen sciences techniques to monitor *Sargassum*, we piloted a study using two apps, “CitSci” and “Epicollect5.” In both apps used, the “*Sargassum* Watch” project was established. Observations included uploading photographs of the *Sargassum* landing and algae species, recording name of area, geographical coordinates, and date of observation, and reporting abundance using a category table (designed by UNAM). Between March 2018 and May 2019, a total of 216 *Sargassum* landing events were collected in South Florida. The category table was robust enough to distinguish “very little to no *Sargassum*” (47% of observations) to “low accumulation” (38% of observations), and “moderate accumulation (19% of observations). Using the citizen science apps effectively requires training and calibration of using the app, and active feedback between the managers and participants of the project to simplify the app. Regardless of the challenges, this citizen science program is an opportunity to expand the geographical range of *Sargassum* monitoring efforts at a regional level.

P26

ASSESSING INVERTEBRATE HABITAT PREFERENCE IN A SHALLOW TROPICAL COASTAL BAY

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Submerged aquatic vegetation are fundamental contributors to habitat complexity in shallow coastal systems. Biscayne Bay's shallow systems is characterized by seagrasses and red macroalgal mats, the dominant habitats available for invertebrate epifauna. The structural complexity of seagrasses differs from macroalgae: while seagrasses are flat and vertical, macroalgae form three-dimensional architecture. Previous studies suggest macrophyte architecture and environmental factors dictate habitat preference. This research tests if habitat preference among epifauna between seagrass and red algal mats exists in a shallow coastal area in Biscayne Bay. Macroalgal mats and seagrass were collected from Deering Bay in October and December 2017 and March 2018. Results showed that total epifaunal abundances were higher in red macroalgal habitat than seagrass. Species richness was also higher in red algal mats than in seagrass. However, habitat preference was taxa specific with some species selecting for seagrass and other for red algal mats ($X^2= 8271.2$, $p < 0.001$). Polychaetes preferred seagrass, while isopods and tanaids had site-specific preference. Rarer taxa such as caridean shrimp and starfish, showed no habitat preference. While habitat preference may occur among epifauna, other factors from seasonality or small-scale environmental variability can influence epifaunal distribution. The variability in habitat preference demonstrates that both seagrasses and macroalgae are important contributors to maintaining invertebrate diversity within the coastal community.

P27

CHARACTERIZATION OF ALGAL SEDIMENTATION, ADHESION, AND MORPHOLOGICAL TYPES SUCCESSION IN DIFFERENT SUBSTRATES

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Algae adhesion, colonization, and succession in hard substrates is complex, and can depend on a biotic variables, topography, and the impact of the surrounding community. The objective of this study was to determine the effect of substrate material on community structure of early colonization of algae cells. The experiment consisted of three different substrates: nylon mesh, expanded PVC mesh, and *Luffa cylindrica* fruits. All three substrates were lined up in 0.5 sq m structures designed to keep the mesh submerged at 10 cm. The structures were placed in a brackish lagoon in Southern Brazil, and sampling of the community was made for 696 h. Both phytoplanktonic and mesh algae communities were analyzed to the highest taxonomy level by count, biovolume and dry weight. Water was analyzed for nutrients, salinity, dissolved oxygen, pH, turbidity, conductivity, temperature, in vivo chlorophyll and phycocyanin, and extracted chlorophyll. *Luffa cylindrica* had higher dry biomass values, reaching 560% incremented compared to nylon by the end of the experiment, and showed a higher adhered:sedimented algae ratio. The phytoplankton data show that dinoflagellates inhabit the mesh system temporarily, but influence overall community structure. There was no significant relationship between nutrients change and the adhered community. From this study, we defined 6 morphological types to describe mesh algae succession, where single-celled diatoms, spherical algae, colonial diatoms, colonial algae, filamentous algae, and dinoflagellates are the big groups useful for describing the community.

P28

INVESTIGATING THE EFFECT OF SURFACE ENERGY ON ATTACHED CULTIVATION OF ALGAE

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Algae based products are used in a variety of industries including environmental remediation, nutraceuticals, personal care products, and biofuels. Most research to date has been focused on suspended cultivation of microalgae. Yet, algal cultivation on substrates has a promising potential as an effective strategy for boosting the efficiency of algal growth systems. Viewing algae as colloidal entities has the potential for tailoring the thermodynamics of growth substrates to enhance algal attachment and growth. The goal of this research is to investigate the effects of substrate surface energy on algal attachment particularly for filamentous algal species with specialized attachment mechanisms. The substrate surface energies were measured *via* sessile drop contact angle measurements with three probe fluids. Different types of algae were then cultivated in reactors containing substrates with different surface energies. The amount of attached biomass was compared, and the results were related to the substrate surface energies. Extended Derjaguin-Landau-Verwey-Overbeek (xDLVO) theory was used for describing the interaction energy between algae and substrate in early stages of attachment. This work helps improve fundamental scientific understanding of algal adhesion and growth with the ultimate goal of enabling the design of more efficient economically viable systems.

P29

***EISENIA ARBOREA*: USING BARCODING TECHNIQUES TO GAIN INSIGHTS INTO DEEP WATER KELP SPECIATION PATTERNS**

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Environmental gradients occur in both terrestrial and marine environments and can influence a taxa's phenotype. One of the main environmental parameters in marine systems is water flow or hydrodynamic pressure. Previous research examined deep water kelp *Eisenia arborea* populations along a flow gradient from shallow to deep water in the Southern California bight. *E. arborea* populations showed distinct morphology with respect to shallow and deep subtidal zones. Reciprocal transplant analyses showed that isolates retained their morphology, suggesting that these two populations were adapted to differential flow regimes and were possibly examples of incipient speciation. Preliminary phylogenetic analyses further suggested incipient speciation in these two populations, and this work builds on that research. Three gene regions (COI, LSU-Z fragment, and *rbcL* spacer), were used as barcoding loci. Both barcoding gap analyses and phylogenetic analyses evaluated gene regions. Maximum likelihood analyses found that the *rbcL* spacer gene region was the most informative barcoding gene region, and the LSU-Z fragment the least. Initial analyses also suggested that the two populations were different and showed some clustering by population. Moreover, the deep populations were more variable suggesting that they may form the founding population. Continued sequencing and further combined analyses of all three regions will hopefully further resolve speciation patterns and provide more insights into incipient speciation patterns.

P30

A STUDY IN OCHRE: GENETIC DIVERSITY OF *LAMINARIA HYPERBOREA* FORESTS ALONG THE IRISH COASTLINE

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Laminaria hyperborea is a subtidal ecosystem engineer along coastlines of Northern Europe. The distribution of this species has shifted over millennia, leaving regions of predicted high genetic diversity, climate refugia from the last glacial maximum (LGM), towards its southern distribution limit. In Ireland, *L. hyperborea* is an important foundation species, supporting diverse faunal assemblages and producing large quantities of organic carbon throughout the year. We investigated the genetic diversity of eight populations in Ireland, including sites near predicted climatic refugia, using nine microsatellite loci. Diversity was found to be highest in Lough Hyne, a special area of conservation (SAC), and populations demonstrate isolation by distance, with high connectivity between populations within counties. Expected heterozygosity was highest at Lough Hyne and decreased northward the lowest value at Bridges of Ross. Short-range dispersal of *L. hyperborea* propagules in the subtidal environment likely drive patterns of isolation by distance. Climatic refugia or SACs house the most diverse populations.

#P31

HIGH-THROUGHPUT SEQUENCING OF CYANOBACTERIAL COMMUNITIES IN BOREAL PLAIN LAKES

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Cyanobacteria are ubiquitous in freshwater ecosystems; however, this clade has the potential to form harmful algal blooms (HABs) and release cyanotoxins. Consequently, HABs can cause the degradation of wetland ecosystems and drinking source waters. With climate change comes increasing global temperatures that will increase the frequency of HABs. To investigate cyanobacterial community dynamics, this study examines the Boreal Plain of Alberta, a forested wetland, a region of the Boreal Forest — the largest terrestrial carbon sink. Previous publications have studied the hydro-, geo- and chemical features of the landscape; but there are no studies on the phytoplankton communities. Hence, 34 lakes were analyzed using 16S rRNA gene sequencing with an Illumina MiSeq during July to evaluate the microbial community structure. Amplicons were quality controlled using DADA2 to produce amplicon sequence variants (ASVs). The SILVA SSU rRNA database was used for classification. The surrounding surficial hydrology wetlands (n = 19), forestlands (n = 10), and mixed (n = 5) showed large differences in community diversity. The top 5 phyla throughout the set were Actinobacteria, Bacteroidetes, Proteobacteria, Cyanobacteria, and Verrucomicrobia. Of the samples, 94% contained ASVs classified as *Cyanobium gracile* PCC-6307. This picophytoplankton is small in size (0.5-2µm) and is related to *C. rubescens*, a potential microcystin producer. Based on the study, wetlands may increase the variability of community diversity and *Cyanobium* is more common than previously expected.

P32

NOVEL SPECIES OF *NEOLYNGBYA* FROM BENTHIC CYANOBACTERIAL MATS OF COASTAL SOUTH FLORIDA.

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South Florida has a subtropical to tropical climate with distinct wet and dry seasons that can alter the salinity of coastal waters. The extensive and diverse coastline of southern Florida favors the growth of benthic cyanobacterial mats (BCMs), with untapped cyanobacterial diversity. To elucidate the diversity of these cyanobacteria, BCMs were sampled and isolated into unialgal cultures. Cyanobacterial isolates were maintained in BG11 supplemented with artificial salts (35 g L⁻¹) and cultured at 25°C. Based on morphometric features, ecological characteristics, and

phylogenetic relationships, our research presents two putative novel species of *Neolyngbya* and one new combination. Future work is aimed at elucidating the diversity of secondary compounds present within these marine novel taxa.

#P33

THE EFFECTS OF ALGAECIDES AND HERBICIDES ON A *MICROCYSTIS* WINTER BLOOM IN LAKE OKEECHOBEE, FLORIDA (USA)

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Microcystis-dominated cyanobacterial harmful blooms (cyanoHABs) are a reoccurring problem in Lake Okeechobee (LO). As public awareness on their risks increases, there is a need for studies on both short and long-term management. To provide science-based best management practices or treatment options, we tested various concentrations and combinations of algaecides/herbicides. Bloom waters, dominated by *Microcystis wesenbergii*, with some *M. aeruginosa* and *Dolichospermum circinale*, were collected from LO in November/2018. The material was exposed to 15 different algaecides, herbicides, or combinations, at four concentrations each. Cell abundance and morphology, chlorophyll a, phycocyanin and microscopic analyses were undertaken at collection and 24 and 72 hours post-treatment. Microcystin (MC) concentrations were measured from the crude bloom, but determined too low for further analyses. The most efficacious chemicals for treating this bloom were sodium carbonate peroxyhydrate; copper (Cu) sulfate pentahydrate; Cu ethanolamine complex; and combinations of diquat dibromide with endothall, Cu gluconate/citrate and Cu ethanolamine. Other promising methods include combinations of flumioxazin with Cu gluconate/citrate and endothall with liquid H₂O₂. Some chemicals, including liquid H₂O₂ and endothall alone, were unable to deplete cyanobacterial abundance, thus considered an ineffective treatment option for *M. wesenbergii*-dominated blooms. Future work aims at treating toxic blooms and monitoring toxin degradation.

P34

MICROALGAL EXTRACTS REDUCE CELL VIABILITY AND IMPROVE ANTIBIOTIC SENSITIVITY IN MICROBIAL BIOFILMS

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The incidence of biofilm-associated microbial infections is rising, posing a significant health threat in hospital settings and supporting the development of resistance in nosocomial infections. The chemical and physical properties of biofilms restrict access of chemotherapeutic agents to film-forming, opportunistic pathogens like *Stenotrophomonas maltophilia* and *Candida albicans*. Microalgal extracts may contain polyphenols, hydroxy fatty acids, and antioxidants which could alter the solubility dynamics of such agents at the biofilm surface. In this study, diverse species of microalgae were extracted with two different solvent systems, hexanes/isopropanol (HIPA) and 2-methyltetrahydrofuran (2-MTHF), and screened for antimicrobial effects against established biofilms. For all species tested, the two extraction solvents demonstrated comparable effects on established biofilms and similar polyphenol and antioxidant components. Extracts from *Botryococcus braunii*, *Clorochromonas danica*, and *Nannochloropsis oculata* reduced cell viability of both *S. maltophilia* and *C. albicans* in established biofilms. Furthermore, extracts from *N. oculata* improved the sensitivity of *S. maltophilia* biofilms to ceftriaxone. Based on our findings, additional

research should focus on the organic components of *N. oculata*, *B. braunii*, *C. danica* that contribute to reduced microbial cell viability in established biofilms.

P35

LIGHT-CONTROLLED PH UPREGULATION IN TROPICAL MACROALGAE: A PROPOSED MECHANISM TO SUSTAIN CALCIFICATION UNDER OCEAN ACIDIFICATION

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Biotic control of calcified reef macroalgae thalli surface boundary layer chemistry may overcome low pH in bulk seawater to accommodate ocean acidification (OA). We examined surface boundary layer O₂ and pH dynamics in 5 calcifying macroalgae (*Halimeda*, *Udotea*, *Jania*, *Neogoniolithon*, CCA) from the Florida Reef Tract under ambient (8.1) and low (7.65) pH using microsensors (100 μm) at the thalli surface in a flow-through flume. The role of photosynthesis and photosynthesis-independent proton pumps in controlling boundary layer pH were examined using a photosystem II inhibitor (DCMU). All 5 calcifying macroalgae had a strong linear relationship between O₂ production and pH in the first 15-30 s of irradiance. Once a quasi-steady-state [O₂] was reached (300 s), boundary layer pH was greater (0.02-0.32) than the bulk seawater in the light at ambient pH, but was inhibited by DCMU. At low pH in the light, there was greater Δ pH (2-3 times) between the thalli surface and the bulk seawater compared to ambient. This enhanced Δ pH was arrested with DCMU. We postulate that the mechanism driving pH increase at the thalli surface is a HCO₃⁻/H⁺ symport or HCO₃⁻/OH⁻ antiport, evidenced by the immediate and rapid increase in pH upon illumination and carbonate modeling of expected Δ pH. Secondarily, CO₂ uptake was enhanced at low pH in species that facultatively used HCO₃⁻, potentially in an effort to conserve energy required for CCMs under greater CO₂ availability. We present conceptual models of these mechanisms relevant to OA effects on calcification in tropical macroalgae.

P36

ENSO EFFECTS NEW PRODUCTION AND EUKARYOTIC PHYTOPLANKTON IN THE GALAPAGOS ARCHIPELAGO

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The Galápagos Islands have garnered fame for their geomorphological and macrofaunal diversity. Perhaps less widely appreciated, but capturing the fascination of oceanographers, is that the islands rest at the convergence of many major currents which provide a mix of oligotrophic subtropical gyre and high-nitrate low chlorophyll (HNLC) water masses. Strong upwelling occurs on the western side of the Galápagos platform, but is also present in other locales due to island mass effect. During El Niño Southern Oscillation (ENSO) equatorial waters warm, winds weaken, and upwelling is not as prevalent. Annual cruises from 2014-16 suggest that ENSO affects the distribution of new production and the suspect phytoplankton groups contributing to it. Size fractionated nitrate uptake rates and chlorophyll-a concentrations showed that larger phytoplankton groups' nitrate uptake rates were a function of biomass while smaller groups were not. 2015 had the lowest nitrate concentrations, but still had high new production (f ratio), although from different locales compared to 2014 and 2016. Chlorophytes were dominant throughout the three years. There was a shift from *Syndiniales* sp. in 2015 to *Gyrodinium* sp. and *Oligotrichia* sp. in 2016. During

the ENSO pennate diatoms such as *Pseudo-nitzsca* sp. were more common, while centric diatoms prevailed in 2016. Despite differences in the communities, physiological data indicates that they may be functionally redundant. However, areas of new production vary spatially which could still impose ecological effects.

P37

MONITORING PROGRAM FOR PELAGIC *SARGASSUM* LANDINGS IN SOUTH FLORIDA

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Influxes of *Sargassum* are common events in the Caribbean, Gulf of Mexico and Florida, but since 2011 abundance of those landings have increased. This poses issues for tourism, fisheries and local economy while demanding scientists and managers to supply explanations and solutions. In order to address this problem, a monitoring program began in September 2018 to quantify frequency and abundance of *Sargassum* landings at Dania Beach, Florida. This includes identifying species and morphotypes, as well as the use of a transect/quadrat method to estimate abundance. We found an average abundance per month of 317.27 g/m² with no significant differences between September to February, with an increase in April. Species were identified as *S. natans* and *S. fluitans* while morphological results were consistent with previous identifications of Parr (1939) and Wrinn (2016) with *S. natans* I and *S. fluitans* III being dominant while *S. natans* VIII began to occur in January. Seasonal morphotype dominance can be expected to change as spring and summer approach. Inorganic carbon, estimated using the Loss on Ignition method, was similar between the different morphotypes with a 24:76 C_{org} to C_{ing} carbon ratio, meaning these landing contribute a high % of organic matter to beaches, with a relatively low % of possible sand contribution. Based on the average recorded abundance per month, 241.12 g/m² correspond to organic matter and only 76.14 g/m² contribute to sand formation for the studied period.

P38

DIVERSITY OF NEMALIALES (RHODOPHYTA) SPECIES FROM MESOPHOTIC ENVIRONMENTS IN THE HAWAIIAN ISLANDS

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Macroalgal communities worldwide are well-studied in shallow subtidal and intertidal environments; however, the biodiversity of mesophotic habitats is relatively poorly known due to the difficulty of accessing depths up to 150m. Recent developments in exploration techniques are allowing us to characterize the Hawaiian macroalgal flora from these mesophotic zones. In order to describe the biodiversity of the florideophycean order Nemaliales, an investigation will be conducted on approximately 100 specimens collected from mesophotic environments, which were previously identified as members of the order based on morphology and DNA sequence data for plastidial (*psaA/ rbcL/ UPA*) and mitochondrial (COI) markers. Previous studies of the biodiversity of mesophotic macroalgae of the Hawaiian Archipelago have revealed several new records for Hawai'i and undescribed species. The use of molecular techniques in combination with morphological data will allow us to more fully catalog the composition of algae in the Hawaiian archipelago, and to better understand the community as a whole, including investigating invasive species and studying biogeographic patterns. Analyses of preliminary data using UPA and *rbcL* revealed a phylogeny with well-supported clades, including representatives for three of the six families of the Nemaliales, with three specimens highlighted as genetically distinct from species described for shallow and mesophotic waters in Hawaiian Islands, one belonging to the genus *Scinaia* and the other two to *Dichotomaria*.

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ALTERATIONS TO THE MICRO-GEO-ENVIRONMENT AND ITS IMPACT ON ALGAL EXOSKELETONS: A PERSPECTIVE IN COCCOLITHOPHORES

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Coccolithophores are unicellular, eukaryotic marine algae that possess a distinctive ability to self-assemble intricate protective exoskeletons composed of biogenic calcite, acquired from their surrounding environment. At the nano-scale, their exoskeleton is composed of overlapping layers of coccoliths, forming the coccosphere. While its exact function is unknown, it is not essential for physiological growth. Although calcite has been reported as the dominating mineral, studies have shown coccoliths can contain strontium, barium, boron and zinc. Therefore, we assessed the ability of silicate to displace calcite in exoskeletons of *Pleurochrysis carterae* and *Emiliana huxleyi* to assess their potential use in biomaterials. Silicate was chosen as calcium silicates are the main binding agent in portland cement-based composites. To evaluate their ability to uptake and incorporate silicate through existing metabolic pathways, doping studies were performed under various silicate (0.02mM to saturation) and calcium concentrations (1.25 - 42mM) and ratios (0.1 - 124X). Mineralogical characterization and microstructural properties were discerned using scanning electron microscopy with energy dispersive X-Ray spectroscopy and X-Ray diffraction analyses. The impact of altered micro-geo-environments on growth and physiology was also assessed. Exposures having moderate silicate and low calcium grew the best having double the biomass than the control. The results of this work can be used to assess the potential manipulation of algal exoskeletons to provide novel green building alternatives.

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UNRAVELLING SPATIAL PATTERNS OF ALGAL ARRANGEMENT IN GIANT CLAMS

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Giant clams house several species of symbiotic dinoflagellates (Family: Symbiodiniaceae) that enable them to live within shallow, low nutrient coral reef habitats. The dinoflagellate provides photosynthetically-fixed carbon to the clam in return for a stable environment and waste byproducts from the clam. Giant clams have enhanced this symbiosis by housing the dinoflagellate in an outer mantle that is exposed to incoming irradiance. Within the outer mantle, the giant clam utilizes the iridocyte cell to filter and refract light into the dinoflagellate while also arranging the algae in a particular manner to efficiently absorb the filtered and refracted photons. The objective of this study is to determine if each species utilizes a unique spatial arrangement of algae for photosynthesis or if that arrangement is associated with the environment the clam lives in. To compare the arrangement of algae across different species, tissue samples from the outer mantle of five different species of giant clams (Genus: *Tridacna*) were collected in the Republic of Palau. *T. derasa* tissue samples were also collected across inner and outer reef habitats to determine if the arrangement of algae in the mantle tissue is correlated with the environment the clam resides in. I used micro-computed tomography to analyze the three-dimensional arrangement of algae within the outer mantle tissues.

Preliminary results suggest each species has a unique geometric arrangement of dinoflagellates that remains consistent across markedly different coral reef habitats.

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REVISION OF THE GENUS *SIRODOTIA* (BATRACHOSPERMALES, RHODOPHYTA).

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This study evaluated the species level taxonomy and phylogenetic relationships among species in the freshwater rhodophyte genus *Sirodotia* using DNA sequences (*rbcL* and COI-5P) including samples from Australia, Brazil, Costa Rica, Finland, India, Malaysia, Mexico, New Zealand, South Africa and USA. Analyses of *rbcL* and COI-5P sequences revealed that the genus forms a well-supported clade within the order Batrachospermales. Two major clades were distinguished within the genus: one with *S. suecica* only from Australasia, Europe, North America and South Africa; the other with *Sirodotia* sp.1, *Sirodotia* sp.2, *Sirodotia* sp.3 from Brazil, *Sirodotia* sp.4 from India and *S. huillensis* from Mexico and USA. Analyses of COI-5P sequences also showed the genus with two well-supported groups: a smaller clade representing sequences of *S. huillensis*; and a second clade with several smaller clades containing five species – *S. suecica*, *Sirodotia* sp. 1, *Sirodotia* sp.2, *Sirodotia* sp. 3 and *Sirodotia* sp.4. Interspecific variation among the species of the second group was high (2.3-3.9% for *rbcL* and 6.2-8.9% for COI-5P). We found few morphological characters to distinguish species. However, the cryptic species did show a clear geographic pattern. Molecular evidence indicated that the sample from India exhibited high molecular divergence compared to the closest species (*Sirodotia delicatula* from Malaysia).

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NEW SPECIES OF *GALENE* AND *HOWELLA* GEN. NOV. (HALYMENIACEAE, RHODOPHYTA) FROM THE MESOPHOTIC ZONE OFF BERMUDA

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The mesophotic zone off the coast of Bermuda has been explored for macroalgae beginning with the R/V *Seahawk* cruises of the 1980s and most recently on the Nekton XL Catlin cruise of the R/V *Baseline Explorer* in 2016. In this paper, we unveil two new members of the Halymeniaceae discovered on these missions based upon a combined phylogenetic analysis of mitochondrial (COI-5P), chloroplast (*rbcL*) and nuclear genes (LSU), as well as morphological and anatomical characteristics. *Howella gorgoniarum* gen. et sp. nov. that conspicuously grows on the base of soft corals, represents one of three species in the genus. Two other species from Australia are added to the new genus based upon molecular phylogenetic placement. First collected offshore of Bermuda in 1960 and

misidentified as *Halymenia hancockii*, *Galene leptoclados* sp. nov. represents the first species in its genus collected outside of New Zealand. Both new taxa are distinguished from congeners morphologically as well as genetically.

P43

THE DIVERSITY AND RESILIENCE OF KELP ECOSYSTEMS IN IRELAND

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Our basic understanding of kelp ecosystems worldwide suggests they are changing, undergoing shifts in distribution, phase shifts with herbivores or ephemeral algae, or completely disappearing in response to various climate pressures. The northeast Atlantic is a unique habitat buffeted by an energetic climate system throughout the year and provides a rich seascape for marine communities. European kelp forests are dominated by stipitate Laminariales, specifically *Laminaria hyperborea* from the Mer d'Irroise northwards. We are only just beginning to understand the complex dynamics of these diverse and productive Irish kelp ecosystems at a time in which they are likely undergoing great change. In order to better understand the diversity and resilience within the Irish populations of *L. hyperborea* this project aims to describe: i) the historical to present day distribution of subtidal kelp forests along Ireland's coastline, ii) the allelic diversity in populations from the south east of Ireland (hypothesized glacial refugia) to the north (Co. Donegal – Belfast), iii) the presence of kelp propagules in the benthic micro-communities ('spore banks'), and iv) new monitoring tools for continued mapping or reporting for kelp forest communities and phase shifts. These data are important from an academic perspective but are also critical in order to inform commercial interests, such as wild harvesting and kelp farming.

P44

FOUR NEW TO SCIENCE FILAMENTOUS CYANOBACTERIA ISOLATED FROM LAGUNA MADRE, TEXAS BASED ON TOTAL EVIDENCE APPROACH INCLUDING BIOCHEMISTRY

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The Laguna Madre with its Mexican part – Tamaulipas is the largest hypersaline system in the world. During morphological observation of the microbial mats collected from the sand flats of the Laguna Madre, we identified 26 filamentous cyanobacteria. These taxa belonged to the following orders: Spirulinales, Oscillatoriales, and Synechococcales with about 60 percent from total cyanobacterial species richness. That was in overall agreement with MiSeq analysis in which *Coleofasciculus chthonoplastes* and *Lyngbya aestuarii* were identified as the dominant taxa. Here we focused on 4 cultured filamentous species. Utilization of the 16S rRNA and short protein coding gene phylogenies suggested these four taxa to be new cryptic genera akin to *Lyngbya aestuarii*, *Oxynema*, *Kamptonema*, and *Halomicronema*. Considering the cryptic origins of numerous cyanobacterial taxa and the polyphyletic nature of Oscillatoriales, we emphasize the importance of thorough 16S phylogenies coupled with protein coding gene analysis, with supporting information about the ecology, ultrastructure, and biochemistry. Ecosystem of Laguna Madre has a unique cyanobacterial diversity compared to other hypersaline lagoons.

P45

SEASONAL VERTICAL DISTRIBUTION OF PHYTOPLANKTON IN A SUBTROPICAL DYSTROPHIC LAKE

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Physical, chemical, and competitive processes can influence the vertical distribution of phytoplankton in freshwater lakes. In DOC-rich waters, the photic zone may be limited to just a few meters, often above the thermocline where deep chlorophyll maxima typically occur. In these low-nutrient, high-OC environments, mixotrophs may be the dominant functional group. Mixotrophic algae, which combine heterotrophy and autotrophy, are able to sustain their metabolic functions under light, nutrient, or prey (bacteria, dissolved or particulate organic carbon) limitation, outcompeting strict auto and heterotrophs in stressful conditions. In subtropical dystrophic Lake Annie, mixotrophs may be serving as organizers of phytoplankton assemblages spatially and temporally. The proposed study aims to determine the influence of changing DOC and bacteria concentrations on phytoplankton species diversity, richness, and mixotrophy across vertical depths and seasons. Patterns of seasonal vertical phytoplankton distribution will be used alongside physiochemical measurements and long-term data to elucidate the potential driving mechanism(s) of mixotrophy in this subtropical lake. Preliminary results suggest diversity is greatest in the hypolimnion during stratification, while an opposite trend is observed during lake turnover. Preliminary results also suggest that species richness and diversity are greatest with higher DOC concentrations, likely due to increased resource availability for mixotrophic species.

P46

EXPLORING THE FRESHWATER RHODOPHYTA DIVERSITY OF AFRICA

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Historical literature, records from select herbaria and recent field collections were utilized to create a checklist of macroscopic freshwater rhodophytes from the African continent. To date, we have found records for taxa in the orders Acrochaetales, Batrachospermales, Ceramiales, Hildenbrandiales and Thoreaales. Within the Batrachospermales, 11 of the 15 genera are present in the flora. For the other orders, a few species of one or two genera have been recorded. 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 in Africa, whereas *Hildenbrandia angolensis* has been reported from numerous locations on other continents. Freshwater red algae have been collected from twelve countries, but the majority of records are from South Africa. Sequence data from previous research and this study for nine specimens have confirmed species of *Kumanoa*, *Sheathia*, *Sirodotia* and *Torularia*. *Torularia atra* and *Sirodotia suecica* are cosmopolitan species based on similar sequence data from numerous continents. We have also identified three new species as well as a form taxon. Our results indicate at least 18 species present in this flora based on morphological and DNA sequence data. This continent remains undersampled and future collecting efforts would undoubtedly uncover more species.

P47

RE-EVALUATION OF THE *SHEATHIA ARCUATA* SPECIES COMPLEX (BATRACHOSPERMALES, RHODOPHYTA)

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Populations of *Sheathia arcuata* have been reported from geographically widespread locations. Although the populations exhibit morphological similarity, substantial sequence divergence in the *rbcL* gene has been observed. Morphological delineation of species is based on the characteristics of the gametophyte. More recent studies of species in *Sheathia* and other genera of the Batrachospermales have delineated species based on DNA sequence divergence in the *rbcL* coupled with COI, distinct geographic ranges and unique morphological characters, when present. The current study was conducted to re-evaluate this species complex using all of these types of data. All *rbcL* sequences identified as *Sheathia arcuata* or closely related species were gathered from GenBank and new *rbcL* and COI sequences generated as well. Phylogenetic analyses resolved at least five divergent clades with most being from geographically distinct regions. Morphology of the gametophyte specimens representing the clades is quite similar. For at least one clade, all specimens were the chlamydomonad sporophyte and therefore without comparative morphological data. New species will be circumscribed based on morphology when available, sequence data and geography.

P48

A COMPARISON OF PERIPHYTON DIVERSITY USING ILLUMINA SEQUENCING

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Benthic communities provide ecosystem services essential to creating and maintaining a healthy aquatic habitat. These assemblages coordinate freshwater biogeochemical cycles, form the foundation of the aquatic food web, and influence diversity exhibited by the stream ecosystem. Shifts in population composition potentially exert bottom up control over the services they provide. As Hawaii's streams face growing pressures from industrialization and agriculture, tourism and invasive species, it becomes increasingly important to catalogue and monitor stream principal communities. This observational study, focused on elucidating Hawaii's freshwater benthic diversity, was located in three streams monitored by the Division of Aquatic Resources (DAR) and included benthic sampling from Hawaii's dry and wet seasons between 2015-2016. Environmental DNA (from all members of the microbial community) was extracted for each sample and submitted for high-throughput sequencing. Shannon H' indices were derived from the relative abundance of OTUs. Correlation of relative diversity between seasonal transects was tested for all streams. Additionally, comparisons were made between streams to test for significant differences in diversity based upon stream character. Results to be presented at the conference.

P49

MORPHOLOGICAL AND MOLECULAR ASSESSMENT OF *HALIMEDA* (BRYOPSIDALES, CHLOROPHYTA) IN CARRIE BOW CAY, BELIZE

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Halimeda is a green algal genus that has historically been classified by morphological characteristics, which has caused inaccurate naming of species. This problem has been exacerbated due to cryptic species and phenotypic plasticity that occurs in this genus. This study examines the diversity of *Halimeda* around the Carrie Bow Cay Field Station in Belize. A morphological identification was assigned to each sample by measuring segments, recording the

nodal siphon pattern, and the predominant segment shape. Molecular identification was inferred for each sample using *tufA*, and ITS. The molecular and morphological data revealed that there were seven different species of *Halimeda* collected in the vicinity of the study site. The diminutive species *H. hummii* represents a possible new record for the Belize Barrier Reef and broader Meso-American Barrier Reef System. This study also highlights plasticity within the species of *H. incrassata*.

P50

HONOR BY ASSOCIATION, LEVERAGING CO-EXPRESSION NETWORKS FOR GENE DISCOVERY IN SPECIALIZED METABOLIC PATHWAYS

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Specialized metabolites serve myriad biological functions that allow organisms to interact with and manage their environment (e.g., resist abiotic stress, combat negative ecological interactions and promote beneficial ones). These metabolites are synthesized in response to dynamic ecological pressures, and as a consequence, the pathways involved in metabolite biosynthesis are often fast-evolving, lineage-specific, and remain uncharacterized at the genetic level. This hampers our ability to understand metabolic gene innovation at the level of individual pathways. To address this challenge, we developed the mutual ranks to modules workflow, a method for identifying small, overlapping modules of co-expressed genes in global co-expression networks. These modules serve as the basis for high-throughput prediction of specialized metabolic pathways. Using the model plant *Arabidopsis*, modules accurately recovered the enzymatic genes of functionally characterized specialized pathways as well as genes involved in pathway regulation and metabolite transport. Importantly, a co-expression network approach can straightforwardly be applied to any species, model and non-model, so long as the transcriptome can be sampled under a range of ecologically relevant conditions. The utility of this approach is illustrated by ongoing work in our lab to characterize various pathways for the production of specialized metabolites, from plant allelochemicals to algal phycotoxins.

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INSIGHTS INTO ST JOHN ISLAND'S (USVI) RICH BENTHIC MACROALGAL FLORA (CHLOROPHYTA, PHAEOPHYTA, RHODOPHYTA) AND TRENDS IN CARIBBEAN BIODIVERSITY

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The Eastern Caribbean Sea contains an enormous amount of marine habitat and unknown, but rich biodiversity especially in terms of its marine flora. To spite this rich biodiversity and a long history of exploration, these floras remain among the most poorly characterized in the western hemisphere. This is especially true for USVI (St. John, St. Thomas, St Croix and Water Island), which have not been thoroughly characterized for over a hundred years. Moreover, St. John Island has over 80% of the island designated as national park and its marine habitats in marine protected areas (MPAs) and represents the perfect system for further study. Our project has begun the long-term process of characterizing this poorly known, but rich benthic marine algal flora with a particular emphasis on St. John Island. Select sampling sites were surveyed annually from 2014 to 2017. A species occurrence and herbarium database was created for St. John from 2014 to 2017 from the benthic field survey data. St. John's flora was then compared to other Eastern Caribbean floras to gauge species richness across floras and to ascertain any trends in biodiversity. St. John has one of the richest floras in the Eastern Caribbean with 52 red, 43 brown and 61 green algal species but biodiversity seems to be declining across the region. Implications of these results will be discussed

along with future plans for addressing questions concerning marine biodiversity and biogeography and the implementation of NGS tools.

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DIPLURA KOREANA SP. NOV. (ISHIGEALES, PHAEOPHYCEAE) FROM KOREA

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Diplura is a crustose brown algal genus that is widely distributed in warm and cold marine waters. Since it was erected by Hollenberg (1969), this genus has been composed of two species, *Diplura simplex* J. Tanaka & Chihara from Japan and *D. simulans* Hollenberg from California. *Diplura* samples were collected along the coastal line of Korea from 2017 to 2018, and morphological and molecular studies about them were performed. Our *Diplura* samples are distinguished from *D. simplex* by having branched vegetative filaments and some branched plurangial reproductive filaments whereas from *D. simulans* by tightly adjoined vegetative filaments and some branched plurangial reproductive filaments. Phylogenetic analyses based on *rbcL* gene also revealed that our samples nested within *Diplura* and in a distinct clade from congeners. In this study, we propose this to be a new species *Diplura koreana* sp. nov. based on morphological and molecular data.

P53

VIRAL EDNA SURVEYS FROM AQUATIC HABITATS SHOW A DIVERSE CLASS OF SELFISH GENETIC ELEMENTS HAVE INVADDED THE GENOMES OF ALGAE INFECTING PHYCODNAVIRUSES.

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Phycodnaviruses are an enigmatic clade of “giant” viruses with large double-stranded DNA genomes that are abundant and ubiquitous in (fresh and marine) aquatic habitats, and known to infect algal species. Like islands, lakes and streams act as isolated habitats in a terrestrial landscape for aquatic viruses, where both internal and external ecological factors drive patterns in biodiversity. The aim of this study is to characterize the biodiversity of phycodnaviruses from diverse freshwater habitats to understand their temporal and seasonal variation and diversity. Using environmental DNA (eDNA), a two step PCR approach was developed and used to amplify and sequence the DNA polymerase (*polB*) gene, a commonly used gene for phycodnavirus systematics, from freshwater habitats. These habitats include urban, rural, peninsula, and mountain lakes and streams that vary spatially and limnologically. During the survey of phycodnavirus biodiversity a consistent amplification of amplicons larger than the predicted size of the *polB* target product was detected. Sequencing of these larger amplicons revealed them to be a diverse set of inteins, unique selfish genetic elements that are capable of splicing themselves out of proteins while facilitating the fusion of the two remaining protein fragments. Our eDNA PCR surveys show that phycodnaviruses, especially those that contain inteins show spatial and temporal variation and underscore the importance of sampling strategy when conducting eDNA surveys.