

75th Annual Meeting of the Psychological Society of America

July 13-22, 2021
Virtual via Whova

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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, Maggie Amsler, or visit the website: www.psaalgae.org

ORGANIZERS FOR THE 2021 PSA ANNUAL MEETING:

Schonna R. Manning, University of Texas at Austin
Amy Carlile, University of New Haven

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Presidential Message

Welcome to the 75th Annual Meeting and our 2nd Annual Virtual Meeting of the Phycological Society of America! While we are not able to all be together physically again this year, using what we learned from last year and having more time to prepare the current program director (PD) Schonna Manning with the aid of our previous PD Amy Carlile have put together an amazing program for us all. This program will have all of the traditional interactions that our live meetings have had, from talks and posters, to plenaries and symposia, from workshops to our business meeting. We will even be having a virtual auction hosted by the Chair of Board of Trustees Morgan Vis! This meeting will have everything except the actual food. And by everything, I mean the return of the Bold Award and the Lewin Award as well!

With well over 600 attendees this will be the largest PSA annual meeting ever! I believe this is because we all enjoy algae so much and the cost (free) had nothing to do with this record attendance. Towards the future we will be using all that we have and will learn about virtual meetings to extend the reach of our future meetings to allow for greater attendance and participation, so stay tuned for more information.

Enjoy this (last) all virtual meeting, and looking forward to our meetings in reality, with a splash of virtual for taste.

Eric W. Linton
PSA President 2021



PSA Organizing Committee Message

While we all wish we could meet in person, we hope that you enjoy the virtual meeting through Whova. Be sure to create an account/login to access the meeting content. We have an amazing program with >120 contributed talks, 60 posters, and 25 lightning talks. Please use the Whova platform to attend sessions, connect with colleagues, and continue your scientific discussions. Should you miss a talk (or two!), all presentations will be available for viewing through Whova up to two weeks after the meeting adjourns.

Thank you for your participation to help make PSA2021 the largest PSA meeting ever! - Schonna & Amy





PSA Meeting Code of Conduct



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

Expected Behavior

- Treat all participants with respect and consideration; value the diversity of views and opinions.
- Communicate openly and respectfully, critiquing ideas and not individuals.
- Do not engage in or tolerate personal attacks directed toward other participants. .
- Be aware of your surroundings and of your fellow participants' well-being. Alert the PSA contacts listed below if you notice a dangerous situation, unacceptable behavior, 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 and discrimination will not be tolerated.
- Physical or verbal abuse of and microaggressions towards 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 or nonverbal actions related to gender, gender identity and expression, sexual orientation, disability, physical appearance, body size, race, religion, national origin, and other intersectional identities, 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 asked 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 and to revoke membership in the society.

Reporting Unacceptable Behavior

- If you are the victim of unacceptable behavior or you have witnessed any such behavior, please immediately notify the designated PSA contacts for 2021: e-mail to diversity@psaalgae.org; or to Eric Linton, PSA President (executive@psaalgae.org), or to Schonna Manning, Program Director (schonna.manning@utexas.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.

Meet the PSA IDEA Working Group!



IDEA* WORKING GROUP

* INCLUSIVITY | DIVERSITY | EQUITY | ACCESS

	RANAH CHAVOSHI		ROBIN KODNER		GISELE MULLER- PARKER
	BRIDGETTE CLARKSTON		PATRICK MARTONE	<p>Contact us! diversity@psaalgae.org</p>	
	KATY DAVIS		SOPHIE MCCOY		

**Phycological
Society
of
America**

PSA2021 PROGRAM

MEETING HIGHLIGHTS

Presidential Plenary and Symposium

To many, the cyanobacteria represent tiny, annoying filaments that contaminate our cultures and seem to bloom at inopportune times in our freshwaters. Yet recent research has opened up exciting new vistas into the nature of cyanobacteria. Far from merely being nuisances, cyanobacteria are integral to numerous ecosystems. Lynn J. Rothschild will deliver the plenary and the PSA Presidential Symposium shall illuminate such intriguing questions as what constitutes a cyanobacterial “species” in dryland soils (Nicole Pietrasiak), how do we best articulate the biodiversity of this ancient lineage (Jeff Johansen), and lastly an intriguing case of potentially new, deleterious forms to worry about (Susan Wilde).

Co-Editors Symposium

Meet our new co-editors at this symposium, in honor of the late Robert G. Sheath, former editor of the *Journal of Phycology*. Melinda Coleman, Sonya Dyhrman, Thomas Mock, Christopher Lane, and Andrew Allen will each tell us about their research and interests.

IDEA Symposium

This inaugural symposium celebrates diversity and the efforts of phycologists and marine scientists to foster equity and inclusion in the science community. The IDEA (Inclusivity, Diversity, Equity, Access) Symposium includes three invited speakers followed by a moderated Q&A session. Ligia Collado-Vides, Florida International University, Camille Gaynus, University of Pennsylvania, and Austin Shelton, University of Guam, will talk about their science in the context of diversity, their career paths, and their current efforts to support diversity in science.

Lang Lecture

Stacy Krueger-Hadfield, PSA’s second Lang Fellow, will discuss research and insights made possible by the Lang Fellowship.

Bold Award

The Bold Award was established in 1973 to honor Harold C. Bold, former president of the Phycological Society and has been awarded at PSA annual meetings since 1974. The Award is given for the outstanding graduate student paper(s) presented at the Annual Meeting as determined by the Bold Award Committee. Come see what these hard-working students have been up to!

Lewin Poster Award

The Lewin Award was established in 2009 by colleagues of Ralph A. Lewin, former president of The Society and a distinguished teacher and researcher at The University of California at San Diego, Scripps Institution of Oceanography. All posters can be viewed in the Exhibitor center on Whova.

PLUS, Lightning Talks, Poster Sessions, the PSA Endowment Auction, Special Sessions, Workshops, and more!!

PROGRAM SCHEDULE (times are listed in Eastern Daylight Time, UTC-4)

TUESDAY, JULY 13, 2021

10:45 Welcome to the 75th Annual Meeting of the Phycological Society of America (virtual)!

11:00-13:00 **PRESIDENTIAL PLENARY AND SYMPOSIUM**

Moderators: Eric Linton and Dale Casamatta

Presidential Plenary



11:00 FROM EARTH TO ET: THE USE OF SYNTHETIC BIOLOGY FOR NASA'S MISSIONS

Lynn J. Rothschild, NASA Ames Research Center/Brown University,
lynnjrothschild@gmail.com



11:50 DRYLAND SOILS – A TREASURE CHEST OF HIDDEN DIVERSITY

Nicole Pietrasiak, Plant and Environmental Sciences Department, New Mexico State University, USA, npietras@nmsu.edu



12:10 RECOGNIZING CYANOBACTERIAL DIVERSITY IN THE MODERN ERA

Jeffrey R. Johansen, John Carroll University, johansen@jcu.edu



12:30 INVESTIGATING THE TOXIC INVASION OF HYDRILLA/AETOKTHONOS HYDRILLICOLA IN FRESHWATER FOODWEBS

Susan B. Wilde, University of Georgia, swilde@uga.edu; Phillips, T., orcaluvr@uga.edu, Gerrin, W., wgerrin@uga.edu; Neidermeyer, T., Martin-Luther-Universität Halle-Wittenberg, timo.niedermeyer@pharmazie.uni-halle.de; Breinlinger, S., Martin-Luther-Universität Halle-Wittenberg, Martin-Luther-Universität Halle-Wittenberg, s.breinlinger@posteo.de

12:50-13:00 ~ Panel Q&A ~

13:00-13:30 *Break and Interact*

13:30-14:30 SESSION A

SESSION A TRACK 1 Moderator: Dail Laughinghouse IV

13:30 EXPANDING THE DISTRIBUTION OF OCULATELLA (OCULATELLACEAE, CYANOBACTERIA): NEW DISCOVERIES FROM NIGERIA, CHINA AND NEW MEXICO

Akagha, M.U., John Carroll University, USA, makagha22@jcu.edu; Johansen, J.R., John Carroll University, USA, johansen@jcu.edu, Pietrasiak, N.P., New Mexico State University, USA, npietras@nmsu.edu, Wells, S.L., John Carroll University, USA, slwells22@jcu.edu, Wang, J., Taiyuan Normal University, China, nostoc@126.com

13:40 A WINDOW TO THE PAST: CYANOBACTERIAL DIVERSITY AND BIOGEOGRAPHY IN HERBARIA SPECIMENS

Wilmotte, A., BCCM/ULC cyanobacteria collection, InBios-Centre for Protein Engineering, University of Liege, Belgium, awilmotte@uliege.be; Pessi, I.S., Arctic Microbial Ecology Group & HELSUS, University of Helsinki, Finland, igor.pessi@helsinki.fi; Velazquez D., Department of Biology, Universidad Autonoma de Madrid, Spain, david.velazquez@uam.es; Durieu B., InBios a Centre for Protein Engineering, University of Liege, Belgium, benoit.durieu@uliege.be; Lara Y., Early Life Traces and Evolution, UR Astrobiology, University of Liege, Belgium, ylara@uliege.be; Laughinghouse H.D., Agronomy Department, Ft. Lauderdale Research and Education Center, University of Florida - IFAS, Florida, USA, hlaughinghouse@ufl.edu

13:50 ANALYZING THE FULL GENOMIC COMPLIMENT OF RIBOSOMAL RNA OPERONS, FOR TAXONOMIC DISAMBIGUATION OF THE CYANOBACTERIAL GENUS, BRASILONEMA

Villanueva, C. D., Cleveland State University, Department of Biological, Geological, & Ecological Sciences, Cleveland, OH 44115 U.S.A, c.d.villanueva@vikes.csuohio.edu; Krautová, M., Department of Biology and Ecology, University of Hradec Králové, Hradec Králové, Czech Republic; Johansen, J. R., Department of Biology, John Carroll University, University Heights, OH 44118 U.S.A., johansen@jcu.edu

14:00 A NEW SPECIES OF TIMAVIELLA (OCULATELLACEAE, CYANOBACTERIA) FROM CANYONLANDS NATIONAL PARK

Palmer, E.G., John Carroll University, USA, epalmer21@jcu.edu; Johansen, J.R., John Carroll University, USA, johansen@jcu.edu, Selgjekaj, S., New Mexico State University, USA, sselgjekaj21@jcu.edu; Pietrasiak, N., New Mexico State University, USA, npietras@nmsu.edu

14:10 MOLECULAR ANALYSIS OF DESERT STRAINS IN THE GENUS TRICHOCOLEUS (SYNECHOCOCCALES, CYANOBACTERIA)

Szinte, A. L., John Carroll University, OH, U.S.A. aszinte22@jcu.edu; Johansen, J. R., John Carroll University, OH, U.S.A., johansen@jcu.edu

14:20 Panel Q&A

SESSION A TRACK 2

Moderator: Roksana Majewska

13:30 BEYOND E. HUXLEYI: CELL SIZE, ELEMENTAL CONTENT AND ALLOMETRY OF A DIVERSE RANGE OF COCCOLITHOPHORE SPECIES

Villiot, N., The Lyell Centre for Earth and Marine Science and Technology, Heriot-Watt University, United Kingdom, nv53@hw.ac.uk; Poulton, A. J., The Lyell Centre for Earth and Marine Science and Technology, Heriot-Watt University, United Kingdom, a.poulton@hw.ac.uk, Butcher, E. T., University of Southampton, United Kingdom, elizabeth@eosecology.co.nz, Daniels, L. R., University of Southampton, Lucie.Daniels@soton.ac.uk, United Kingdom, Coggins, A., University of Southampton, United Kingdom, acoggins74@gmail.com

13:40 RE-DISCOVERY OF THE THIRD MATING SYSTEM OF “VOLVOX AFRICANUS“ FROM CULTURES ORIGINATING FROM THE HOMETOWN OF DINOSAURS IN THAILAND*

Nozaki H., The University of Tokyo & National Institute for Environmental Studies, Japan, nozaki@bs.s.u-tokyo.ac.jp; Mahakham, W., Khon Kaen University, Thailand, mwuthi@kku.ac.th; Heman, W., Kalasin University, Thailand, wirawan.kk@gmail.com; Matsuzaki, R., National Institute for Environmental Studies & University of Tsukuba, Japan, matsuzaki.ryo@nies.go.jp; Kawachi, M., National Institute for Environmental Studies, Japan, kawachi.masanobu@nies.go.jp

13:50 RESISTANCE THROUGH SEX: INSIGHTS INTO THE CONJUGATION PROCESS AND ZYGOSPORE STRUCTURE IN FIELD SAMPLED MOUGEOTIA SP. (ZYGNETOPHYCEAE)

Permann, C., University of Innsbruck, Austria, charlotte.permann@uibk.ac.at; Herburger, K., University of Copenhagen, Denmark, klaus.herburger@plen.ku.dk; Niedermeier, M., Max Planck Institute of Colloids and Interfaces, Germany, Martin.Niedermeier@mpikg.mpg.de; Felhofer, M., University of Natural Resources and Life Sciences Vienna (BOKU), Austria, martin.felhofer@boku.ac.at; Gierlinger, N., University of Natural Resources and Life Sciences Vienna (BOKU), Austria, burgi.gierlinger@boku.ac.at; Holzinger, A., University of Innsbruck, Austria, Andreas.Holzinger@uibk.ac.at

14:00 MECHANICS AND EVOLUTION OF CELL SHEET FOLDING – EMBRYONIC INVERSION IN VOLVOX

Hoehn S.S.M.H., University of Cambridge, UK, s.hoehn@damtp.cam.ac.uk; Haas P.A., Max Planck Institute for Molecular Cell Biology and Genetics, DE, haas@pks.mpg.de

14:10 CHLOROPLAST mRNAs ARE 3' POLYURIDYLATED IN THE GREEN ALGA PITHOPHORA ROETTLERI (CLADOPHORALES)

Meade, M.J., Department of Natural Sciences, University of Virginia's College at Wise, mj6mv@uvawise.edu, Proulx, G.C.R., Department of Natural Sciences, University of Virginia's College at Wise, gcp5a@uvawise.edu, Manoylov, K.M., Department of Biological and Environmental Sciences, Georgia College and State University, kalina.manoylov@gcsu.edu, Cahoon, A. B., Department of Natural Sciences, University of Virginia's College at Wise, abc6c@uvawise.edu

14:20 Panel Q&A

SESSION A TRACK 3

Moderator: Juliet Brodie

13:30 PAST CLIMATE-DRIVEN RANGE SHIFTS STRUCTURING INTRASPECIFIC BIODIVERSITY LEVELS OF THE GIANT KELP (MACROCYSTIS PYRIFERA) AT GLOBAL SCALES

Assis, J., CCMAR, CIMAR, Universidade do Algarve, Gambelas, Faro, Portugal, jorgemfa@gmail.com; Faugeron, S., Pontificia Universidad Catolica de Chile, Chile, sfaugeron@bio.puc.cl; Alberto, F., University of Wisconsin Milwaukee, USA, albertof@uwm.edu; Macaya E., Universidad de Concepción, Chile, emacaya@oceanografia.udec.cl; Zuccarello, J., School of Biological Sciences, Victoria University of Wellington, New Zealand, Joe.Zuccarello@vuw.ac.nz; Serrão, E. A., CCMAR, CIMAR, Universidade do Algarve, Gambelas, Faro, Portugal

13:40 UNDERSTOREY CHANGES COMPOSITION AFTER TEMPERATE KELP FOREST COLLAPSE BUT KEEPS RICHNESS AND DIVERSITY

Piñeiro-Corbeira, C., Universidad de A Coruña, A Coruña, Spain, c.pcorbeira@udc.es; Barrientos, S., BioCost Research Group, Facultad de Ciencias and Centro de Investigaciones Científicas Avanzadas (CICA), Universidad de A Coruña, A Coruña, Spain, sara.barrientos@udc.es; Isabella Provera, BioCost

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13:50 GLOBAL SPECIES RICHNESS PATTERNS OF MARINE FORESTS OF LARGE BROWN MACROALGAE

Fragkopoulou, E., University of the Algarve, Portugal, eli_frag@hotmail.com; Serrão, E.A., University of the Algarve, Portugal, eserrao@ualg.pt; De Clerck, O., Ghent University, Belgium, odclerck@gmail.com; Costello, M.J., Nord Universitet, Norway, mark.j.costello@nord.no; Araújo, M.B., National Museum of Natural Sciences, Spain, University of Évora, Portugal, mba@uevora.pt; Duarte, C.M., Aarhus University, Denmark, King Abdullah University of Science and Technology (KAUST), Saudi Arabia, carlos.duarte@kaust.edu.sa; Krause-Jensen, D., Aarhus University, Denmark dkj@bios.au.dk; Assis, J., University of the Algarve, Portugal, jorgemfa@gmail.com

14:00 DIVERSITY OF EUCHEUMATOID-ASSOCIATED EPIPHYTIC FILAMENTOUS RED ALGAE (EFA) IN MALAYSIA

Poong, S-W., Institute of Ocean and Earth Sciences, University of Malaya, Malaysia, szewan@um.edu.my; Lim, P.E., Institute of Ocean and Earth Sciences, University of Malaya, Malaysia, phaikem@um.edu.my; Brakel, J., Scottish Association for Marine Science, United Kingdom, Janina.Brakel@sams.ac.uk; Ross, S., Centre for Environment, Fisheries and Aquaculture Science, United Kingdom, stuart.ross@cefas.co.uk; Gachon, C. M. M., Unité Molécules de Communication et Adaptation des Micro-organismes, Muséum National d'Histoire Naturelle, France, claire.gachon@mnhn.fr; Brodie, J., Natural History Museum, United Kingdom, j.brodie@nhm.ac.uk

14:10 CHARACTERIZING PSEUDOCRYPTIC DIVERSITY IN HAWAIIAN MESOPHOTIC RED BLADES OF THE GENUS CROISSETEA

Cabrera, F.P., University of Hawai'i, USA, feresa@hawaii.edu; Huisman, J.M. Western Australian Herbarium, AUS, john.huisman@dbca.wa.gov.au; Spalding, H.L., College of Charleston, USA, spaldinghl@cofc.edu; Kosaki, R.K., NOAA Papahānaumokuākea Marine National Monument, USA, randall.kosaki@noaa.gov; Smith, C.M., University of Hawai'i, USA, celia@hawaii.edu; Sherwood, A.R., University of Hawai'i, USA, asherwoo@hawaii.edu

14:20 Panel Q&A

14:30-15:30 SESSION B

SESSION B TRACK 1

Moderator: Ira Levine

14:30 A NEW CRUSTOSE SPECIES OF PHYMATOLITHON (HAPALIDIALES, CORALLINOPHYCIDAE) FROM THE MEDITERRANEAN SEA (ABU QIR, EGYPT)?

Kittle III, R.P., University of Louisiana at Lafayette, USA, c000269538@louisiana.edu; Richards, J.L., University of Louisiana at Lafayette, USA, joer207@gmail.com; Nguyen, A., University of Louisiana at Lafayette, USA, a.nguyen210@gmail.com; Gabriel, D.L., Research Center in Biodiversity and Genetic Resources, University of the Azores, Portugal, danielalgabriel@gmail.com; Sauvage, T., Instituto de Biociências, Universidade Federal do Rio Grande do Sul, Brazil, tomsauv@gmail.com; Schmidt,

W.E., University of Louisiana at Lafayette, USA, william.schmidt@louisiana.edu; Fredericq, S., University of Louisiana at Lafayette, USA, slf9209@louisiana.edu

14:40 MOLECULAR SYSTEMATICS OF HAWAIIAN GRACILARIALES (RHODOPHYTA) BASED ON RBCL DNA SEQUENCE ANALYSES

Gurgel, C.F.D., Federal University of Santa Catarina, Brazil, f.gurgel@ufsc.br; Terada R., Kagoshima University, Japan, terada@fish.kagoshima-u.ac.jp; McDermid K.J., University of Hawaii at Hilo, USA, mcdermid@hawaii.edu; Fredericq S., University of Louisiana, USA, slf9209@louisiana.edu

14:50 NEW DEEPWATER SPECIES OF RED ALGAE GROWING IN RHODOLITH BEDS IN THE NW GULF OF MEXICO

Fredericq, S. University of Louisiana at Lafayette, USA, sfredericq@yahoo.com; Arakaki, N., Instituto del Mar del Perú, Perú, narakakim@gmail.com; Ehrenhaus, C., University of Louisiana at Lafayette, USA, Irallia@hotmail.com; Norris, J.N., National Museum Natural History, USA, norrisj@si.edu; Richards, J.L., University of Louisiana at Lafayette, USA, joer207@gmail.com; Gabriel, D., University of the Azores, Portugal, danielalgabriel@gmail.com; Sauvage, T., Universidade Federal do Rio Grande do Sul, Brazil, tomsauv@gmail.com; Gurgel, C.F.D., Universidade Federal de Santa Catarina, Brazil, f.gurgel@ufsc.br; Kittle, R., University of Louisiana at Lafayette, USA, ronaldkittleull@gmail.com; Kravesky-Self, S., University of Louisiana at Lafayette, USA, sherry.kravesky@louisiana.edu; Schmidt, W.E., University of Louisiana at Lafayette, USA, william.schmidt@louisiana.edu

15:00 MOLECULAR AND MORPHOLOGICAL ANALYSES REVEAL NEW TAXA ADDITIONS TO THE TRIBE STREBLOCLADIEAE (RHODOMELACEAE, RHODOPHYTA)

Bustamante, D.E., Universidad Nacional Toribio Rodríguez de Mendoza, Peru, daniilo.bustamante@untrm.edu.pe; Won, B.Y., Chosun University, Korea, giving_won@hanmail.net; Wynne, M., University of Michigan, USA, mwynne@umich.edu; Cho, T.O., Chosun University, Korea, tocho@chosu.ac.kr

15:10 NEW PEYSSONNELIOID ALGAE SPECIES FROM HAWAI'I'S MESOPHOTIC CORAL ECOSYSTEMS

Sherwood, A. R., University of Hawai'i, USA, asherwoo@hawaii.edu; Alvarado, E., University of Hawai'i, USA, erikaalv@hawaii.edu; Cabrera, F.P., University of Hawai'i, USA, feresa@hawaii.edu; Kosaki, R.K., NOAA Papahānaumokuākea Marine National Monument, USA, randall.kosaki@noaa.gov; Paiano, M.O., University of Hawai'i, USA, mpaiano@hawaii.edu; Smith, C.M., University of Hawai'i, USA, celia@hawaii.edu; Spalding, H.L., College of Charleston, USA, spaldinghl@cofc.edu; Wade, R.M., University of Wisconsin-Milwaukee, USA, wader@uwm.edu

15:20 Panel Q&A

SESSION B TRACK 2

Moderator: Trisha Spanbauer

14:30 TEMPERATE KELP FOREST COLLAPSE BY HERBIVORY: A DEMOGRAPHIC STUDY

Barrientos, S., BioCost Research Group, Facultad de Ciencias and Centro de Investigaciones Científicas Avanzadas (CICA), Universidad de A Coruña, A Coruña, Spain, sara.barrientos@udc.es; Barreiro, R., BioCost Research Group, Facultad de Ciencias and Centro de Investigaciones Científicas Avanzadas (CICA), Universidad de A Coruña, Spain, rodolfo.barreiro@udc.es; Piñeiro-Corbeira, C., BioCost Research Group, Facultad de Ciencias and Centro de Investigaciones Científicas Avanzadas (CICA), Universidad de A Coruña, Spain, c.pcorbeira@udc.es

14:40 A COMPARISON OF REPRODUCTIVE TIMING OF MACROCYSTIS PYRIFERA AND INVASIVE SARGASSUM HORNERI ON CATALINA ISLAND

Bishop, A.M., Moss Landing Marine Labs California State University & Cheadle Center for Biodiversity & Ecological Restoration University of California Santa Barbara, a_bishop@ucsb.edu

14:50 RESISTANCE AND EARLY RECOVERY OF DURVILLAEA INCURVATA DOMINATED - COMMUNITIES TO A PULSE DISTURBANCE IN A CHILEAN SOUTHERN ROCKY SHORE

Fica-Rojas, E., Universidad Austral de Chile, Chile, eliiseo.sp@gmail.com; López, D., Universidad Austral de Chile, Chile, danyelalopez@gmail.com; Pérez-Matus, A., Pontificia Universidad Católica de Chile, Chile, aperez@bio.puc.cl; Valdivia, N. A., Universidad Austral de Chile & Centro FONDAF de Investigación de Dinámicas de Ecosistemas Marinas de Altas Latitudes (IDEAL), Chile, nelson.valdivia@uach.cl

15:00 HELLO DARKNESS: RED ALGAL PATCH DYNAMICS ON TEMPERATE ROCKY REEFS

McHugh, T.A., San Diego State University, USA, Current Institution: The Nature Conservancy, USA; M. Spector, San Diego State University, USA, Current Institution: NOAA Channel Islands National Marine Sanctuary, USA, pike.spector@noaa.gov; M.S. Edwards, San Diego State University, USA

15:10 A COMPARISON OF PHYSIOLOGICAL RESPONSES BETWEEN ATTACHED AND FLOATING POPULATIONS OF BLOOM FORMING SARGASSUM HORNERI UNDER NUTRIENT AND LIGHT STRESSES

Bao, M.L., Department of Marine Science, Incheon National University, Korea mlin0527@163.com; Park, J.S., Research Institute of Basic Sciences, Incheon National University, Korea, dazzlepark@hanmail.net; Wu, H.L., Jiangsu Institute of Marine Resources Development, Jiangsu Ocean University, China, hgwuhailong@163.com; Yarish, C., Department of Ecology and Evolutionary Biology, University of Connecticut, USA, charles.yarish@uconn.edu; Kim, J.K., Department of Marine Science, Incheon National University, Korea, jang.kim@inu.ac.kr

15:20 Panel Q&A

SESSION B TRACK 3

Moderator: Katherine Perri

14:30 MITIGATING HARMFUL CYANOBACTERIAL BLOOMS IN A HOTTER, HYDROLOGICALLY MORE EXTREME WORLD

Paerl, H.W., University of North Carolina at Chapel Hill, USA, hpaerl@email.unc.edu; Havens, K.E., Florida Sea Grant and University of Florida Institute of Food and Agricultural Sciences, USA (deceased); Hall, N.S., University of North Carolina at Chapel Hill, USA, nshall@email.unc.edu; Otten, T.G., Bend Genetics, LLC, USA, ottentim@bendgenetics.com; Hai, X., Nanjing Institute of Geography and Limnology, Chinese Academy of Sciences, China, hxu@niglas.ac.cn; Zhu, G., Nanjing Institute of Geography and Limnology, Chinese Academy of Sciences, China, gwzhu@niglas.ac.cn; Qin, B., Nanjing Institute of Geography and Limnology, Chinese Academy of Sciences, China, qinbq@niglas.ac.cn

14:40 HARMFUL ALGAL BLOOM DYNAMICS IN THE LAKE OKEECHOBEE SYSTEM: PRELIMINARY FINDINGS FROM MONTHLY FIELD MONITORING AND EXPERIMENTAL MESOCOSMS

Mazzei, V., U.S. Geological Survey, Caribbean-Florida Water Science Center, USA, vmazzei@usgs.gov; Karwacki, E., U.S. Geological Survey, Caribbean-Florida Water Science Center, USA, ekarwacki@contractor.usgs.gov; Loftin, K.A., U.S. Geological Survey, Kansas Water Science Center, USA, kloftin@usgs.gov; Lopez, J.V., Nova Southeastern University, USA, joslo@nova.edu; Krausfeldt,

L.E., Nova Southeastern University, USA, lkrausfe@nova.edu; Rosen, B.H., Florida Gulf Coast University, USA, brosen@fgcu.edu; Urakawa, H., Florida Gulf Coast University, USA, hurakawa@fgcu.edu

14:50 REAL-TIME MONITORING TO ADDRESS HARMFUL ALGAL BLOOMS IN THE INDIAN RIVER LAGOON, FLORIDA

Hanisak, M. D. dhanisak@fau.edu; Davis, K. S., Harbor Branch Oceanographic Institute at Florida Atlantic University, Fort Pierce, FL, USA

15:00 n/a

15:10 METABARCODING REVEALS HIGH GENETIC DIVERSITY OF HARMFUL ALGAE ON THE COAST OF TEXAS (GULF OF MEXICO): A CASE STUDY

Campbell, L., Texas A&M University, USA, lisacampbell@tamu.edu; Gaonkar, C.C, Texas A&M University, USA, chetan.gaonkar@exchange.tamu.edu

15:20 Panel Q&A

15:30-16:00 *Break and Interact*

16:00-17:30 LIGHTNING TALKS Moderator: Stacy Kueger-Hadfield

16:00 A TALE OF ALGAE IN TOMALES BAY

Angela Korabik, University of California, Davis, arkorabik@ucdavis.edu

16:03 HEAVY METAL BIOMONITORING IN COASTAL WATERS WITH BROWN MACROALGAE TRANSPLANTS

Anton Vasquez, University Santiago de Compostela, antonvazquez.arias@usc.es

16:06 ORGANELLAR MRNA PROCESSING IN NON-MODEL ALGAL SPECIES

Bruce Cahoon, University of Virginia, Wise, abc6c@uvawise.edu

16:09 EFFECTS OF APPLICATION TECHNIQUE AND BINDER USAGE ON THE DEVELOPMENT OF DIRECTLY SEEDED SUGAR KELP (SACCHARINA LATISSIMA) SPOROPHYTES

Crystal Ng, The University of Connecticut, crystal.ng@uconn.edu

16:12 UNCOVERING DIVERSITY IN THE MESOPHOTIC ZONE OF HAWAI'I: SPECIES NEW TO SCIENCE IN THE GENERA HALOPELTIS AND LEPTOFAUCHEA (RHODYMENIALES, RHODOPHYTA)

Erika Alvarado, University of Hawai'i, erikaalv@hawaii.edu

16:15 INFERENCE OF TRANSCRIPTIONAL REGULATORS REVEALS GENOME-WIDE REGULATORY RELATIONSHIPS IN SYMBIODINACEAEN DINOFLAGELLATES

Felipe Porto, The University of Connecticut, felipe.porto@uconn.edu

16:18 PHYLOGEOGRAPHY OF AMANSIA GLOMERATA (CERAMIALES, RHODOPHYTA) IN THE HAWAIIAN ISLANDS

James Fumo, University of Hawai'i, jfumo@hawaii.edu

16:21 A DNA BARCODE APPROACH TO CYSTOSEIRA S.L. (PHAEOPHYCEAE) DIVERSITY REVEALS CRYPTIC DIVERSITY, TAXONOMIC CONFLICT AND NOVEL BIOGEOGRAPHICAL INSIGHTS

Joao Neiva, jmneiva@gmail.com

16:24 GREEN ALGAE FROM WHITE SANDS NATIONAL PARK

Karolina Fucikova, Assumption University, k.fucikova@assumption.edu

16:27 FINE SCALE POPULATION STRUCTURE IN LAMINARIA HYPERBOREA ECOSYSTEMS ACROSS IRELAND

Kathryn Schoenrock, NUI Galway, kathryn.schoenrock@nuigalway.ie

16:30 BULL KELP (NEREOCYSTIS LUETKEANA) AND WIRE WEED (SARGASSUM MUTICUM) IN THE SALISH SEA

Katie Dobkowski, Friday Harbor Laboratory, kdobkows@gmail.com

16:33 CHANGES IN CRYPTOPHYTE PBP SPECTRA UNDER VARYING LIGHT QUALITY

Kristiaan Merritt, University of South Carolina, kfm1@email.sc.edu

16:39 CYANOBACTERIA ARE OPTIMAL CANDIDATES FOR MARTIAN ALGAE PRODUCTION

Mate Ravasz, Algacraft, mate@algacraft.com

16:42 KELP-ASSOCIATED MICROBIOTA ARE STRUCTURED BY HOST ANATOMY

Matt Lemay, Hakai Institute, matt.lemay@hakai.org

16:45 GRACILARIALES: A CHLOROPLAST GENOME COMPARISON OF SHALLOW AND DEEP SPECIES FROM HAWAII

Monica Paiano, University of Hawai'i, mpaiano@hawaii.edu

16:51 COMPARISONS OF MICROBIOMES AMONG FRESHWATER RED ALGAE (BATRACHOSPERMALES, RHODOPHYTA) REVEAL CORE TAXA

Roseanna Crowell, Ohio University, rc907218@ohio.edu

16:54 FRESHWATER RED ALGAE AS ECO-EVOLUTIONARY MODELS

Sarah Shainker, University of Alabama, Birmingham, sjs2@uab.edu

16:57 PHYTOPLANKTON DIVERSITY AND FUNCTIONAL TRAITS UNDER EXTREME CLIMATE EVENTS SIMULATED BY A PELAGIC MESOCOSM EXPERIMENT

Serena Rasconi, Thonon les Bains, France, serena.rasconi@inrae.fr

17:00 DEVELOPMENT OF AN ASSAY FOR IDENTIFYING ENDOLITHIC EUKARYOTIC CELLS FOUND IN "RHODOLITH-FORMING" CORALLINE ALGAE

Sherry Kravesky, University of Louisiana, Lafayette, sherry.kravesky@louisiana.edu

17:03 THE MICROBIAL COMMUNITY OF SACCHARINA LATISSIMA AND CLIMATE CHANGE

Siobhan Shenk, University of British Columbia, sschenk@student.ubc.ca

17:12 BUBBLE FARMING(C) FOR SUSTAINABLE ALGAL CULTURE

Vandana Vinayak, Dr Hari Singh Gour Central University, kapilvinayak@gmail.com

17:30

Conclude

WEDNESDAY, JULY 14, 2021

11:00-14:00 **METABARCODING WORKSHOP**

Instructors: Erin Borbee and Elaine Shen

An Introduction To Metabarcoding Data Analysis Using QIIME2

Metabarcoding is a powerful tool that has enabled us to evaluate communities and elucidate biodiversity that has long been underestimated by culture-based and/or visual surveys in many taxonomic groups. In this workshop, we will cover experimental design considerations as well as the bioinformatic steps involved in analyzing these data. We will start with background on experimental design and the bioinformatic workflow and then will move into an interactive coding portion with example data using QIIME2. Topics will cover: Sampling design and mock communities, Introduction to QIIME2 (file types, formats, metadata), Demultiplexing and quality control, Denoising and merging paired-end data, Measuring alpha and beta diversity, and Importing and exporting data. Preparing for the workshop: We will be running QIIME2 using a Jupyter Notebook, which will provide an online command-line interface similar to that of Terminal on MacOS. Therefore, we recommend: A basic understanding of BASH (a great and short free tutorial: <https://swcarpentry.github.io/shell-novice/> ; QIIME2's cheat sheet: <https://docs.google.com/document/d/10riUwsZ9wYELEShZ21gdmHgDIZPRoiwvNPDh6szR46s/edit> ; and (optional recommendation) a second screen or monitor to be able to view the Zoom call while running your own code. Note: We are borrowing suggestions from official QIIME2 workshops, which can be found on <https://workshops.qiime2.org/>.

14:30-16:00 **SCIENCE COMMUNICATION**

Moderator: Rick McCourt

The Curious World of Seaweed Meets an Ocean Garden: Art and Algae Come Into the Classroom

Speaker: Josie Iselin, Loving Blind Productions, josieiselin@lovingblind.com; discussion with Bryan Wysor., Roger Williams University, bwysor@rwu.edu

Josie Iselin will give a presentation chronicling her journey as an artist into the science of seaweed culminating in her newest book *The Curious World Seaweed*. Then she and Brian Wysor will have a discussion on how the art of algae has been a proven pathway to undergraduate learning of phycology. Brian will share how his use of *An Ocean Garden* by Iselin in his Intro to Phycology class for undergraduates has been an icebreaker for many students and Iselin will share her experiences with elementary, high school and undergraduate classes using art workshops as a method for bringing ecological concepts and basic seaweed taxonomy to a broad range of students. Wysor and Iselin have a proven rapport and it will be a wide-ranging, open and fun discussion about alternative ways for bringing the marine science of seaweeds into the classroom.

THURSDAY, JULY 15, 2021

11:00-13:36 **BOLD SESSION** Moderator: Matt P. Ashworth

11:00 PROTIST COMMUNITY STRUCTURE ACROSS INDONESIA AND ITS FUTURE IMPLICATIONS FOR MARINE PROTECTED AREA DESIGN

Borbee, E.M., Department of Biological Sciences, The University of Rhode Island, USA,
eborbee@uri.edu; Humphries, A.T., Department of Fisheries, Animal, and Veterinary Sciences, The University of Rhode Island, USA, humphries@uri.edu ; Madduppa, H., Department of Marine Science and Technology, Institut Pertanian Bogor, Indonesia, hawis@apps.ipb.ac.id ; Lane, C.E., Department of Biological Sciences, The University of Rhode Island, USA, clane@uri.edu

11:12 THE ROLE OF HOST-ASSOCIATED MICROBIOMES IN PHOTOSYNTHETIC FUNCTIONING WITHIN THE HABITAT FORMING MACROALGAE, *HORMOSIRA BANKSII*

McGrath, A. H., University of Sydney, Coastal Marine Ecosystems Group, NSW Australia, alexander.mcgrath@sydney.edu.au ; Wood, G. Minderoo Foundation, WA Australia, gwood@minderoo.org ; Steinberg, P. University of Sydney, Marine Coastal Ecosystems Group, NSW Australia p.steinberg@unsw.edu.au ; Marzinelli, E. M. University of Sydney, Marine Coastal Ecosystems Group, NSW Australia, e.marzinelli@sydney.edu.au

11:24 PREDICTIVE MODELLING ASSESSMENT OF SUITABLE HABITATS FOR STARRY STONEWORT (*NITELLOPSIS OBTUSA*) IN THE UPPER MIDWEST AND NORTHEAST (USA)

Neuman, E. K., Annis Water Resources Institute, Grand Valley State University, Muskegon, MI, neumanem@mail.gvsu.edu; Woznicki, S. A., Annis Water Resources Institute, Grand Valley State University, Muskegon, MI, woznicse@gvsu.edu; Karol, K. G., Lewis B. and Dorothy Cullman Program for Molecular Systematics, New York Botanical Garden, Bronx, NY, kkarol@nybg.org; McNair, J. N., Annis Water Resources Institute, Grand Valley State University, Muskegon, MI, mcnairja@gvsu.edu; Hamsher, S. E., Annis Water Resources Institute, Grand Valley State University, Muskegon, MI, Department of Biology, Grand Valley State University, Allendale, MI, hamshers@gvsu.edu

11:36 ON THE DIVERSITY OF *DICTYOTA* J.V. LAMOUREUX IN BRAZIL

Lopes-Filho, E.A.P., Museu Nacional, Universidade Federal do Rio de Janeiro, Brazil, lopesf.erick@gmail.com; Salgueiro, F., Universidade Federal do Estado do Rio de Janeiro, Brazil, fabiano.salgueiro@unirio.br; De-Paula, J.C., Universidade Federal do Estado do Rio de Janeiro, Brazil, , joel.paula@unirio.br

11:48 MICROBIOTA-MACROALGAL RELATIONSHIPS IN THE HAWAIIAN ARCHIPELAGO ARE INFLUENCED BY PHYLA AND MORPHOLOGICAL COMPLEXITY

Kuba, G. M., College of Charleston, Charleston SC, kubag@g.cofc.edu; Spalding, H. L., College of Charleston, Charleston SC, spaldinghl@cofc.edu; Hill-Spanik, K. M., Grice Marine Lab, College of Charleston, Charleston SC, hillkm1@cofc.edu, Fullerton, H., College of Charleston, Charleston SC, fullertonhe@cofc.edu

12:00 LABORATORY INDUCED EVOLUTION OF THERMAL TOLERANCE DIFFERS IN GENOTYPES OF THE SYMBIOTIC DINOFLAGELLATE *BREVIOLUM MINUTUM*

Bateman, T.G, tbateman@udel.edu; Lortie, M.; Warner, M.E. School of Marine Science and Policy, University of Delaware, USA

12:12 PHOTOPROTECTION AS A POSSIBLE TARGET OF THE EX1-DEPENDENT $^1\text{O}_2$ STRESS SIGNALING IN *CHLAMYDOMONAS REINHARDTII*

Khorshidi, H., University of Saskatchewan, Canada, hanie.khorshidi@usask.ca; Miskiewicz, E., University of Saskatchewan, Canada, ewa.m@usask.ca; Wilson, K. E., University of Saskatchewan, Canada, ken.wilson@usask.ca

~ INTERMISSION ~ 12:24-12:36

12:36 MICROBIOME CHANGES IN A STRANDING SIMULATION OF THE HOLOPELAGIC MACROALGAE *SARGASSUM NATANS* AND *SARGASSUM FLUITANS*

Mendonça, I. R. W., Institute of Biosciences, University of Sao Paulo, Brazil, inara.mendonca@usp.br; Theirlynck, T., Royal Netherlands Institute for Sea Research, The Netherlands; Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, The Netherlands, tom.theirlynck@nioz.nl; Zettler, E., Royal Netherlands Institute for Sea Research, The Netherlands, erik.zettler@nioz.nl; Amaral-Zettler, L., Royal Netherlands Institute for Sea Research, The Netherlands; Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, The Netherlands, linda.amaral-zettler@nioz.nl; Oliveira, M. C., Institute of Biosciences, University of Sao Paulo, Brazil, mcdolive@ib.usp.br

12:48 HOW DOES YOUR COCCOLITHOPHORE GROW? EXCRETION AND UTILISATION OF DOM AND DON BY CULTURED *EMILIANA HUXLEYI*

William McMinn, Lyell Centre for Earth and Marine Science and Technology, Heriot-Watt University, wrm3@hw.ac.uk

13:00 GOING WITH THE FLOW: PHYTOPLANKTON MORTALITY AND COMMUNITY DYNAMICS

Simmons, L.J., University of Wisconsin-Milwaukee, United States, ljk3@uwm.edu; Berges, J.A., University of Wisconsin-Milwaukee, United States, berges@uwm.edu

13:12 AN ANALYTICAL APPROACH TO MONITORING SURFACE CHEMISTRY OF SMALL-SCALE *SKELETONEMA MARINOI* ALGAL BLOOMS

Rogers, M. M., The Ohio State University, United States, rogers.1064@buckeyemail.osu.edu; Neal, J. F., The Ohio State University, United States neal.496@buckeyemail.osu.edu; Saha, A., The Ohio State University, United States saha.121@buckeyemail.osu.edu; Algarni, A. S., The Ohio State University, United States algarni.5@buckeyemail.osu.edu; Hill, T. C. J., Colorado State University, United States, thomas.hill@colostate.edu; Allen, H. C.; The Ohio State University, United States, allen@chemistry.ohio-state.edu

13:24 THE CLONING AND ENGINEERING OF DIATOM MITOCHONDRIAL GENOMES IN YEAST AND BACTERIA

Cochrane, R. R., University of Western Ontario (UWO), Canada, rcochra3@uwo.ca; Brumwell, S. L., UWO, Canada, sbrumwe2@uwo.ca; Shrestha, A., UWO, Canada, ashrest7@uwo.ca; Giguere, D. J., UWO, Canada, dgiguere@uwo.ca; Soltysiak, M. P. M., UWO, Canada, msoltys4@uwo.ca; Hamadache, S., UWO, Canada, shamadac@uwo.ca; Wang, J., UWO, jwan625@uwo.ca; Tholl, S. Q., UWO, Canada, stholl@uwo.ca; Janakirama, P., Designer Microbes Inc., Canada, preetam.janakirama@gmail.com; Gloor, G. G., UWO, Canada, ggloor@uwo.ca; Edgell, D. R., UWO, Canada, dedgell@uwo.ca; Karas, B. J., UWO, Canada, bkaras@uwo.ca

13:36 EVOLUTION OF SPAWNING CAULIFLOWER CORALS CORRESPOND TO THE SPECIATION OF MUTUALISTIC MICROALGAE

Turnham, K. E., Penn State University, University Park, PA 16802, ket7@psu.edu; Drew C. Wham, Penn State University, University Park, PA 16802; Eugenia Sampayo, The University of Queensland, St. Lucia,

QLD4072, Australia; Todd C. LaJeunesse, Penn State University, University Park, PA 16802.
tcl3@psu.edu.

13:48 THREE SEX PHENOTYPES IN A HAPLOID ALGAL SPECIES GIVE INSIGHTS INTO THE EVOLUTIONARY TRANSITION TO A SELF-COMPATIBLE MATING SYSTEM

Takahashi, Kohei,¹ Hiroko Kawai-Toyooka,^{1,2} Ryo Ootsuki,^{3,4} Takashi Hamaji,⁵ Yuki Tsuchikane,⁴ ;
Hiroyuki Sekimoto,⁴ Tetsuya Higashiyama,^{1,6,7} Hisayoshi Nozaki^{1,8}

¹Department of Biological Sciences, Graduate School of Science, The University of Tokyo, Japan

²Faculty of Bioscience and Applied Chemistry, Hosei University, Japan

³Department of Natural Sciences, Faculty of Arts and Sciences, Komazawa University, Japan

⁴Department of Chemical and Biological Sciences, Faculty of Science, Japan Women's University, Japan

⁵Research and Development Initiative, Chuo University, Japan

⁶Institute of Transformative Bio-Molecules, Nagoya University, Japan

⁷Division of Biological Science, Graduate School of Science, Nagoya University, Japan

⁸Center for Environmental Biology and Ecosystem Studies, National Institute for Environmental Studies, Japan

14:00-14:20 *Break and Interact*

14:20-15:30 SESSION C

SESSION C TRACK 1

Moderator: Thomas Dempster

14:20 TYPE SPECIMEN SEQUENCING AND DNA-BASED SPECIES DELIMITATION RESOLVE THE COSMOPOLITAN CORALLINA BERTEROI AND OCCURRENCE OF C. CHAMBERLAINE IN CHILE

Calderon, M. S., Universidad de Magallanes, Chile, marthacalderonrios@gmail.com; Bustamante, D.E., Universidad Nacional Toribio Rodríguez de Mendoza de Amazonas, Peru, danilo.bustamante@untrm.edu.pe; Gabrielson, P.W., University of North Carolina, USA, drseaweed@hotmail.com; Martone P.T., University of British Columbia, Canada, patrick.martone@botany.ubc.ca; Huber S., University of British Columbia, Canada, saladsoren@gmail.com; Mansilla, A., Universidad de Magallanes, Chile, andres.mansilla@umag.cl

14:30 SUNGMINIACEAE FAM. NOV. (RALFSIALES, PHAEOPHYCEAE), SUNGMINIA GEN. NOV. AND THREE NEW SUNGMINIA SPECIES FROM KOREA BASED ON MOLECULAR AND MORPHOLOGICAL ANALYSES

Oteng'o, A. O., Department of Life Science, Chosun University, Gwangju, 61452, Korea, aotinga@gmail.com; Won, B. Y., Department of Life Science, Chosun University, Gwangju, 61452, Korea, givingwon10@gmail.com; Cho, T. O., Department of Life Science, Chosun University, Gwangju, 61452, Korea, tocho@chosun.ac.kr

14:40 WHOLE GENOME SEQUENCING OF THE KELP GENUS ALARIA (PHAEOPHYCEAE) REVEALS FORGOTTEN LINEAGES AND HYBRIDIZATION AMONG SPECIES

Bringloe, T.T., School of BioSciences, University of Melbourne, Australia, trevor.bringloe@unimelb.edu.au; Zaparenkov, D., School of BioSciences, University of Melbourne, Australia; Starko, S., Department of Biology, University of Victoria, Canada; Verbruggen, H., School of BioSciences, University of Melbourne, Australia

14:50 METABARCODING OF AUTOTROPHIC EUGLENIDS BASED ON V2 18S RDNA MARKER, CURATED REFERENCE DATABASE AND OPTIMIZED PROTOCOL OF DNA ISOLATION

Łukomska-Kowalczyk, M., University of Warsaw, Poland, majalukomska@biol.uw.edu.pl; Gumińska, N., University of Warsaw, Poland; Chaber, K., University of Warsaw, Poland; Zakryś, B., University of Warsaw, Poland

15:00 ON DETECTION, IDENTIFICATION, AND DELIMITATION OF PLANKTONIC DIATOM SPECIES IN METABARCODE DATA, EXAMPLES FROM CHAETOCEROS AND BACTERIASTRUM

Kooistra, W. H. C. F., Stazione Zoologica Anton Dohrn, Italy, kooistra@szn.it; De Luca, D., University of Naples Federico II, Italy, danielle.deluca088@gmail.com; Piredda, R., University of Bari Aldo Moro, Italy, roberta.piredda@uniba.it; Sarno, D., Stazione Zoologica Anton Dohrn, Italy, diana.sarno@szn.it

15:10 IDENTIFICATION OF LATITUDINAL AND TISSUE-SPECIFIC AMPLICON SEQUENCE VARIANTS OF BACTERIA IN HOST MICROBIOMES OF THE BROWN ALGA FUCUS VESICULOSUS (PHAEOPHYCEAE)

Morrison, H.G., Marine Biological Laboratory, Woods Hole, USA, morrison@mbi.edu; Capistrant-Fossa, K.A., University of Maine, USA, kyle.capistrantfossa@utexas.edu; Engelen, A.H., University of Algarve, Portugal, aengelen@ualg.pt; Ester A. Serrão, Universidade do Algarve, Portugal, eserrao@ualg.pt; Brawley, S.H., University of Maine, USA, brawley@maine.edu

15:20 Panel Q&A

SESSION C TRACK 2

Moderator: Ondine Frauenglass

14:20 TOWARDS A SYNTHETIC ALGAL CHLOROPLAST: A STREAMLINED PLATFORM FOR CREATING DESIGNER CHLOROPLAST GENOMES IN PHAEODACTYLUM TRICORNUTUM

Walker, E. J. L., Department of Biochemistry at Western University, Canada, ewalke72@uwo.ca; Davis, J. G., Department of Biochemistry at Western University, Canada, jdavi33@uwo.ca; Pampuch, M., Department of Biochemistry at Western University, Canada, mpampuch@uwo.ca; Cochrane, R. R., Department of Biochemistry at Western University, Canada, rcochra3@uwo.ca; Gloor, G. B., Department of Biochemistry at Western University, Canada, ggloor@uwo.ca; Karas, B. J., Department of Biochemistry at Western University, Canada, bkaras@uwo.ca

14:30 SYNTHETIC PROMOTERS FOR CONTROL OF GENE EXPRESSION IN THE MODEL DIATOM PHAEODACTYLUM TRICORNUTUM

Kassaw T., Colorado State University, United States, tessema.kassaw@colostate.edu; Peers G., Colorado State University, United States, graham.peers@colostate.edu

14:40 UNRAVELLING FUCOXANTHIN BIOSYNTHESIS IN DIATOMS

Bai, Y., Colorado State University, USA, yu.bai@colostate.edu; Cantrell, M., Colorado State University, USA, michaelbcantrell@gmail.com; Dautermann, O., Johannes Gutenberg-Universität, Germany, dautermann@berkeley.edu; Ware, M., Colorado State University, USA, Maxwell.Ware@colostate.edu; Lohr, M., Johannes Gutenberg-Universität, Germany, lohr@uni-mainz.de; Peers, G., Colorado State University, USA, Graham.Peers@colostate.edu

14:50 MOLECULAR ANALYSES FOR THE SNOW-INHABITING MICROORGANISM, CHIONASTER NIVALIS

Matsuzaki, R., University of Tsukuba & National Institute for Environmental Studies, Japan, matsuzaki.ryo@nies.go.jp; Takashima, Y., University of Tsukuba, Japan, takashima.yusuke.gu@u.tsukuba.ac.jp; Suzuki, I., University of Tsukuba, Japan, iwanes6803@biol.tsukuba.ac.jp; Kawachi, M., National Institute for Environmental Studies, Japan, kawachi.masanobu@nies.go.jp; Nozaki, H., The University of Tokyo & National Institute for Environmental Studies, Japan, nozaki@bs.s.u-tokyo.ac.jp; Nohara, S., National Institute for Environmental Studies, Japan, snohara@nies.go.jp; Degawa, Y., University of Tsukuba, Japan, degawa@sugadaira.tsukuba.ac.jp

15:00 THE ANTARCTIC CHLAMYDOMONAS SP. UWO241 HAS A REDUCED REPERTOIRE OF PHOTORECEPTOR GENES AND AN ABERRANT PHOTOTACTIC RESPONSES

Cvetkovska, M., University of Ottawa, Canada, mcvetkov@uottawa.ca; Wilkins, K., University of Ottawa, Canada, kwilk022@uottawa.ca; Poirier, M., University of Ottawa, Canada, mpoir121@uottawa.ca; Fugard, K., University of Ottawa, Canada, kfuga057@uottawa.ca

15:10 GRATELOUPIA LANCEOLA (HALYMENIACEAE, RHODOPHYTA) IS THE CORRECT NAME OF THE NON-NATIVE SPECIES IN ALGIERS COAST KNOWN AS G. LANCEOLATA?

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15:20 Panel Q&A

SESSION C TRACK 3

Moderator: I-Shuo Huang

14:20 NEW PARTS FROM OLD: EVOLUTION OF THE CRYPTOPHYTE PHYCOBILIPROTEIN ANTENNA

Green, B.R., Univ. British Columbia, Canada, brgreen@mail.ubc.ca; Rathbone, H.W., UNSW, Australia, h.rathbone@unsw.edu.au; Michie, K.A., UNSW Australia, k.michie@unsw.edu.au; Landsberg, J.J., Univ. Queensland, Australia, m.landsberg@uq.edu.au; Curmi, P.M.G., UNSW, Australia, p.curmi@unsw.edu.au

14:30 INSIGHTS INTO THE EVOLUTION OF A PRIMARY ENDOSYMBIOSIS THROUGH ANALYSIS OF THE PAULINELLA GENOME

Stephens, T. G., Rutgers University, United States of America, ts942@sebs.rutgers.edu; Calatrava, V., Carnegie Institution for Science, United States of America, vcalatrava@carnegiescience.edu; Gabr, A., Rutgers University, United States of America, arwa.gabr@rutgers.edu; Grossman, A. R., Carnegie Institution for Science, United States of America, arthurg@stanford.edu; Bhattacharya, D., Rutgers University, United States of America, dbhattac@rutgers.edu

14:40 THE TETRADESMUS (SCENEDESMUS) OBLIQUUS PAN-GENOME

Hayes, R.D. DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, USA, rdhayes@lbl.gov; Calhoun, S.E., DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, USA, secalhoun@lbl.gov; Kamel, B.S., DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, USA, bskamel@lbl.gov; Peredo, E.L., Marine Biological Laboratory, Woods Hole, USA, elperedo@mbl.edu; Cardon, Z., Marine Biological Laboratory, Woods Hole, USA, zcardon@mbl.edu;

Umen, J., Donald Danforth Plant Science Center, USA, jumen@danforthcenter.org; Polle, J., Brooklyn College of CUNY, USA, jpolle@brooklyn.cuny.edu; Starkenburg, S., Los Alamos National Laboratory, USA, shawns@lanl.gov; Grigoriev, I.V., DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, USA, ivgrigoriev@lbl.gov

14:50 EVALUATION OF THE CHLOROPLAST 16S GENE AS A DNA BARCODE MARKER ACROSS MAJOR ALGAL GROUPS

Verbruggen, H., University of Melbourne, Australia, heroen@unimelb.edu.au

15:00 THE PATCHWORK PLASTID PROTEOMES OF FUCOXANTHIN DINOFLAGELLATES

Novak-Vanclova, A.M.G., Institut de Biologie de l'École Normale Supérieure, France, novak@biologie.ens.fr; Fuhai Liu, placeholder, placeholder@placeholder.xy, Richard G. Dorrell, Institut de Biologie de l'École Normale Supérieure, France, dorrell@biologie.ens.fr

15:10 BRILLIANT AND BRIGHT: THERE'S MORE TO STRUCTURAL COLOUR IN THE SEaweEDS THAN MEETS THE EYE

Brodie, J., Natural History Museum, London, UK, j.brodie@nhm.ac.uk; Maria Murace, M., University of Cambridge, UK, mm2518@cam.ac.uk; Arnould-Pétré, M., Natural History Museum, London, UK, m.arnould-petre@nhm.ac.uk; Vignolini, S., University of Cambridge, UK, sv319@cam.ac.uk

15:20 Panel Q&A

15:30-16:00 *Break and Interact*

16:00-17:30 POSTER SESSION I Moderator: Jeff Morris (* *Lewin Competition*)

P2 PHYLOGEOGRAPHIC ANALYSIS OF ALSIDIUM TRIQUETRUM AND A. SEAFORTHII FROM THE MEXICAN ATLANTIC

Palma-Ortiz, C. A., Departamento de Hidrobiología, Universidad Autónoma Metropolitana-Iztapalapa, México, foxh.solid@gmail.com; Núñez-Resendiz, M. L., Departamento de Hidrobiología, Universidad Autónoma Metropolitana-Iztapalapa, México, mlnr@ciencias.unam.mx; Dreckmann, K. M., Departamento de Hidrobiología, Universidad Autónoma Metropolitana-Iztapalapa, México, tuna@xanum.uam.mx; Senties, A., Departamento de Hidrobiología, Universidad Autónoma Metropolitana-Iztapalapa, México, asg@xanum.uam.mx.

P3 EVALUATION OF TRAIT DRIFT AND EVOLUTION OF FIELD-ADAPTED NANNOCHLOROPSIS CULTURE IN OUTDOOR OPEN RACEWAY PONDS

Jebali, A., New Mexico Consortium, USA, ajebeli@newmexicoconsortium.org; Echenique, I., University of California San Diego, USA; Balleza, M. Cyanotech, USA; Martinez, H., New Mexico Consortium, USA; Nalley, J. Qualitas Health, USA; O'Kelly, C., Cyanotech corporation, USA; Shurin, J. University of California San Diego, USA; Corcoran, A. New Mexico Consortium, USA.

P4 EFFECT OF HERBIVORY AND NUTRIENTS ON INTERACTIONS AMONG COMMON CORAL REEF ALGAE OF FLORIDA KEYS

A. Duran, L. Cromie, L. A. Palma, D. E. Burkepile, L. Collado-Vides and A. Concepcion

P5 A SURVEY OF SILICATE UTILIZATION BY DIVERSE FRESHWATER ALGAL TAXA

Driskill A. M., Dept Biological Sciences, University of Wisconsin-Milwaukee, driskill@uwm.edu; Thorngate-Rein ND; Berges, J. A., Dept Biological Sciences, University of Wisconsin-Milwaukee,

berges@uwm.edu; Young, E. B., Dept Biological Sciences, University of Wisconsin-Milwaukee
ebyoung@uwm.edu

P6 HOW UTILIZING AN IMLS GRANT FOR DIGITIZATION OF THE UCSB HERBARIUM'S SEAWEED COLLECTION PROVIDES VITAL DATA TO BETTER UNDERSTAND THE CHANGING MARINE ENVIRONMENT

Bishop, A.M., Cheadle Center for Biodiversity & Ecological Restoration University of California Santa Barbara, a_bishop@ucsb.edu; Wahlert, G.A., Cheadle Center for Biodiversity & Ecological Restoration University of California Santa Barbara, wahlert@cber.ucsb.edu; Seltmann, K.C., Cheadle Center for Biodiversity & Ecological Restoration University of California, Santa Barbara, seltmann@ucsb.edu

P7 BCCM/ULC: A PUBLIC CULTURE COLLECTION AS RESERVOIR OF CYANOBACTERIAL DIVERSITY AND TAXONOMIC REFERENCE STRAINS

Ahn, A. C., BCCM/ULC Cyanobacteria collection - University of Liège, Belgium, acahn@uliege.be; Beets, K., BCCM/ULC Cyanobacteria collection - University of Liège, Belgium, kbeets@uliege.be; Berthold, D., Fort Lauderdale Research and Education Center, USA, dberthold@ufl.edu; Laughinghouse, H. D., Fort Lauderdale Research and Education Center, USA, hlaughinghouse@ufl.edu; Wilmotte, A., BCCM/ULC Cyanobacteria collection - University of Liège, Belgium.

P8 CULTIVATION OF SNOW ALGAE SPECIES IN OPEN RACEWAY PONDS FOR BIO JET FUEL PRODUCTION IN A BIOREFINERY CONCEPT

Yilmaz, A., Institute of Environmental Sciences, Bogazici University, Turkey, arca.yilmaz@boun.edu.tr; Polat, B., Department of Chemical Engineering, Bogazici University, Turkey, benaypolat@gmail.com; Kahveci, H., Department of Molecular Biology, Genetics and Bioengineering, Sabanci University, Turkey, hazarkahveci@sabanciuniv.edu; Haznedaroglu, B. Z., Institute of Environmental Sciences, Bogazici University, Turkey, berat.haznedaroglu@boun.edu.tr

P9 TECHNO-ECONOMIC ASSESSMENT OF SUSTAINABLE AVIATION FUEL PRODUCED IN AN INTEGRATED ALGAL BIOREFINERY

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P10 MICROALGAL EXTRACTS INCREASE FLUCONAZOLE SENSITIVITY IN *CANDIDA ALBICANS* BIOFILMS

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P11 ARE METALS REALLY INSIDE THE CELLS OF BROWN ALGAE?

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P12* DISTRIBUTION AND DIVERSITY OF ABUNDANT MACROALGAL ASSEMBLAGES IN COASTAL SOUTH CAROLINA: LOOKING IN ALL THE RIGHT PLACES

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P13 MACROALGAL COVER CORRELATED WITH ANNUAL SEA ICE COVER ALONG A LATITUDINAL GRADIENT ON THE CENTRAL WESTERN ANTARCTIC PENINSULA

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P14* *ASPARAGOPSIS TAXIFORMIS* AND *A. ARMATA* (RHODOPHYTA, BONNEMASSONIACEAE) TWO PRODUCTIVE SPECIES OF ANTI-METHANOGENIC MOLECULES FOR APPLICATIONS IN CATTLE FARMS

D. Spagnuolo¹, dspagnuolo@unime.it, R. Min², M. Morabito¹, A. Manghisi¹, B., L. Castleberry², C. Lockard², H. M. Waldrip², D. B. Parker², D. N. Miller³, A. Akbay⁴, and D. Brauer², G. Genovese¹.

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P15 A REINFORCEMENT LEARNING APPROACH TO MODELING PLANKTON SWIMMING BEHAVIOR – A TEST CASE WITH *KARENIA BREVIS*

Henrichs, D. W., Texas A&M University – College Station, dhenrichs@tamu.edu

P16* LOW-COST PRODUCTION OF HIGH-PURITY C-PHYCOCYANIN FROM *DESERTIFILUM THARENSE*

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P17 MOLECULAR CHARACTERIZATION OF ALGAL LIPIDS FOR BIO-JET FUEL PRODUCTION

Borhan, E., emren.borhan17@gmail.com, Polat, B. Bogazici University Institute of Environmental Sciences, Istanbul, Turkey

P18 EXAMINING THE IMPACT OF ALGAE ON MICROBIAL COMMUNITIES IN WASTEWATER

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P19* PREDATION AND MICROBIAL LANDSCAPE DYNAMICS IN CYANOBACTERIAL MAT METACOMMUNITIES

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P20* INFERENCE OF TRANSCRIPTIONAL REGULATORS REVEALS GENOME-WIDE REGULATORY RELATIONSHIPS IN SYMBIODINACEAN DINOFLAGELLATES

Porto, F. W., UCONN Department of Marine Sciences, USA, felipe.porto@uconn.edu; Lin, S. UCONN Department of Marine Sciences, USA, State Key Laboratory of Marine Environmental Science and Marine Biodiversity and Global Change Research Center, China, senjie.lin@uconn.edu

P21* THE ROLE AND REGULATION OF HEAT SHOCK PROTEINS IN THE ANTARCTIC ALGA *CHLAMYDOMONAS* SP. UWO241

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P22* SEASONAL SPECIES DIVERSITY OF SEAWEEDS IN THE INTERTIDAL ZONE OF WANDO-GUN, KOREA

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P23* COMPARING QUANTITATIVE METHODS FOR ANALYZING SEDIMENT DNA RECORDS OF CYANOBACTERIA IN EXPERIMENTAL AND REFERENCE LAKES

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P24 VARIATION IN THE COVERAGE AND MORPHOLOGY OF SEAGRASSES IN A REEF LAGOON OF THE MEXICAN CARIBBEAN DUE TO POSSIBLE EFFECTS OF *SARGASSUM* DRIFT

Ortegón-Aznar, I., Departamento de Biología Marina, Campus de Ciencias Biológicas y agropecuarias, Universidad Autónoma de Yucatán, oaznar@correo.uady.mx; Alvarez-Rocha, M., Departamento de Biología Marina, Campus de Ciencias Biológicas y agropecuarias, Universidad Autónoma de Yucatán, alrocha98@gmail.com

P25 *SARGASSUM* MITIGATION LOCATIONS IN BARBADOS

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P26 SPATIAL DIVERSITY OF SEAWEEDS FROM ELEPHANT AND VEGA ISLANDS, ANTARCTICA: NEW RECORDS AND CONNECTIVITY FACING CLIMATE CHANGES

Mello, J. P. S.¹, Osaki, V. S.², Rosa, L.H.³. & F. Pellizzari.

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³Departamento de Microbiologia, Universidade Federal de Minas Gerais (UFMG) Brasil

P27 MORPHOLOGICAL AND MOLECULAR SYSTEMATICS OF THE TAXONOMICALLY CONFUSED FRESHWATER DINOFLAGELLATE HEMIDINIUM, BASED ON THE FIRST OBTAINED NORTH AMERICAN ISOLATES

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P28 SHORT-TERM PHYSIOLOGICAL RESPONSES OF THE KELP ECKLONIA ARBOREA DURING *IN SITU* BIOASSAYS AT DIFFERENT DEPTHS

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P29 COMMUNITY METABARCODING OF THE EUSTIGMATOPHYCEAE (AND BEYOND) TARGETING THE *RBCL* LOCUS

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P48 LOST IN THE TROPICS: *CHONDRUS* SP. NOV. (RHODOPHYTA) ON EAST HAWAII ISLAND

Kittle III, R. P., University of Louisiana at Lafayette, USA, C00269538@louisiana.edu; Veillet,

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P30 SULFATED POLYSACCHARIDE PRODUCTION, COMPOSITION, AND BIOLOGICAL ACTIVITY FROM FOUR STRAINS OF THE MARINE RHODOPHYTE PORPHYRIDIUM (*NÄGELI*)

Perri, K.A., Texas A&M University, USA, kaperry@tamu.edu; Havlak, K.K., Montana State University,

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P31 LAGUNA SALADA AS A POTENTIAL RESERVOIR FOR THE BROWN TIDE ORGANISM, *AUREOUMBRA LAGUNENSIS*, IN A SOUTH TEXAS ESTUARY

Hayes, K.C., Texas A&M University–Corpus Christi, Kenneth.hayes@atmucc.edu

17:30

Conclude

TUESDAY, JULY 20, 2021

10:45 OPENING REMARKS

11:00-13:30 CO-EDITOR SYMPOSIUM
Moderators: Mike Graham and Kirsten Muller



11:00 FUTURE-PROOFING KELP FORESTS
Melinda A. Coleman, New South Wales Department of Primary Industries, Australia.
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**11:20 ALGAL PARTNERSHIPS, INTERACTIONS AND INTERDEPENDENCIES:
TRACKING PATTERNS AND THEIR SENSITIVITY TO A CHANGING
ENVIRONMENT**
Sonya Dyhrman, Department of Earth and Environmental Science, Columbia University;
Lamont-Doherty Earth Observatory, Columbia University, sdyhrman@ldeo.columbia.edu



**11:40 FROM POLE TO POLE – DIVERSITY AND ADAPTIVE EVOLUTION OF
EUKARYOTIC PHYTOPLANKTON TO CONDITIONS OF GLOBAL CHANGE**
Thomas Mock, University of East Anglia, t.mock@uea.ac.uk



12:00 ARE RED ALGAL PARASITES ACTUALLY TRANSMISSIBLE CANCERS?
Christopher E. Lane, clane@uri.edu; Jillian Freese, University of Rhode Island, RI, USA



**12:20 EVOLUTION AND METABOLIC CONFIGURATION OF NITROGEN AND
IRON METABOLISM IN MARINE DIATOMS**
Andrew E. Allen, Scripps Institution of Oceanography, University of California, San
Diego & J. Craig Venter Institute, aallen@ucsd.edu

12:40-13:00 Panel Q&A

13:00-13:30 *Break and Interact*

13:30-14:30 SESSION D

SESSION D TRACK 1

Moderator: Darren Henrichs

13:30 COMPARATIVE GENOMICS OF SYMBIODINIACEAE AND SYMBIOSIS AS A DRIVER OF DIVERSIFICATION

González-Pech, R.A., University of South Florida, USA, raulgonzalez@usf.edu; Chan, C.X., The University of Queensland, Australia, c.chan1@uq.edu.au; Parkinson, J.E., University of South Florida, USA

13:40 CRUSTAPHYTUM? SP. NOV., A NEW MAGNIFICENT AND EXPANSIVE SPECIES OF CRUSTOSE CORALLINE ALGAE FROM THE FLOWER GARDEN BANKS NATIONAL MARINE SANCTUARY

Richards, J.L., University of Louisiana at Lafayette, U.S.A., joer207@gmail.com; Kittle III, R.P., University of Louisiana at Lafayette, U.S.A., C00269538@louisiana.edu; Abshire, J.R., University of Louisiana at Lafayette, U.S.A., jaida2122000@gmail.com; Mire, C.T., University of Louisiana at Lafayette, U.S.A., carolinetmire@gmail.com; Kravesky-Self, S., University of Louisiana at Lafayette, U.S.A., sherry.kravesky@louisiana.edu; Schmidt, W.E. University of Louisiana at Lafayette, U.S.A., william.schmidt@louisiana.edu; Fredericq, S. University of Louisiana at Lafayette, U.S.A., sfredericq@yahoo.com

13:50 FUNCTIONAL STRUCTURE OF A HYPEREUTROPHIC TROPICAL BAY IN RIO DE JANEIRO, BRAZIL

Coração, A.C.S., Institute of Biosciences, Federal University of the State of Rio de Janeiro, Brazil, amandac.t@hotmail.com; Paiva, P.C., Federal University of Rio de Janeiro, Brazil, paulo.paiva@gmail.com; Lopes-Filho, E.A.P., National Museum, Federal University of Rio de Janeiro, Brazil, lopesf.erick@gmail.com; De-Paula, J. C., Federal University of the State of Rio de Janeiro, Brazil, joel.paula@unirio.br

14:00 DECIPHERING CORAL REEF ECOLOGICAL PUZZLE USING PROPER ALGAL TAXONOMIC RESOLUTION

Duran, A., Florida International University, alduran@fiu.edu

14:10 DIATOMS AND DINOFLAGELLATES DIVERSITY INHABITING A COASTAL UPWELLING SYSTEM: A METABARCODING APPROACH

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14:20 Panel Q&A

SESSION D TRACK 2

Moderator: Kate Rolheiser

13:30 IN A NUTSHELL – A LOOK AT THE PHYLOGENETICS OF GENUS STROMBOMONAS (EUGLENOPHYTA)

Fells, A., University of Warsaw, Poland, a.fells@uw.edu.pl; Łukomska-Kowalczyk, M., University of Warsaw, Poland, majalukomska@biol.uw.edu.pl; Chaber, K., University of Warsaw, Poland, k.chaber2@uw.edu.pl; Zakryś, B., University of Warsaw, Poland, zakrys@biol.uw.edu.pl

13:40 AN EFFECTIVE APPROACH TO THE STUDY OF EUGLENIDS

Chaber, K., k.chaber2@uw.edu.pl, A. Fells, University of Warsaw, Poland, a.fells@uw.edu.pl; M. Łukomska-Kowalczyk, University of Warsaw, Poland, majalukomska@biol.uw.edu.pl; B. Zakryś, University of Warsaw, Poland, zakrys@biol.uw.edu.pl

13:50 MITOCHONDRIAL MRNA PROCESSING IN THE CHLOROPHYTE ALGA PEDIASTRUM DUPLEX AND THE STREPTOPHYTE ALGA CHARA VULGARIS REVEALS AN EVOLUTIONARY BRANCH

Proulx, G., University of Virginia's College At Wise, gcp5a@uvawise.edu

14:00 n/a

14:10 PHYLOTRANSCRIPTOMICS INDICATES MULTIPLE INDEPENDENT ORIGINS OF MULTICELLULARITY AND CELLULAR DIFFERENTIATION IN THE VOLVOCINE ALGAE

Lindsey, C.R., Georgia Institute of Technology, USA, clindsey8@gatech.edu; Rosenzweig, F., Georgia Institute of Technology, USA, frank.rosenzweig@biology.gatech.edu; Herron, M., Georgia Institute of Technology, USA, xprinceps@gmail.com

14:20 Panel Q&A

SESSION D TRACK 3

Moderator: Stephen Gomez

13:30 DIFFERENTIAL PHYSIOLOGICAL RESPONSES OF ULVA RIGIDA TO WASTEWATER RELATED TOXIC COMPOUNDS

Viana, I. G., Instituto Español de Oceanografía, Centro Oceanográfico de A Coruña, Galicia, Spain, ines.viana@ieo.es; Beiras, R., Departamento de Ecoloxía e Bioloxía Animal, Universidade de Vigo, 36310, Vigo, Galicia, Spain, rbeiras@uvigo.es

13:40 MOLECULAR STRATEGIES FOR ENHANCING PHOTOSYNTHETIC EFFICIENCY IN GREEN ALGAE

Sayre, R.T., Senior Research Scientist, New Mexico Consortium, Los Alamos, NM, 87544, USA, richardtsayre@gmail.com

13:50 HEAVY METAL REMOVAL FROM INDUSTRIAL WASTEWATER BY MICROALGAE

Sakarya, F.K., Institute of Environmental Sciences, Bogazici University, Turkey, koray.sakarya@boun.edu.tr, Haznedaroğlu, B. Z., Institute of Environmental Sciences, Bogazici University, Turkey, berat.haznedaroglu@boun.edu.tr

14:00 ALGAE-BASED DAIRY MANURE WASTEWATER TREATMENT INTEGRATED WITH ANIMAL FEED PRODUCTION

Ozcelik, D., Bogazici University, Turkey, duygozcelik@gmail.com; Haznedaroglu, B. Z., Bogazici University, Turkey, berat.haznedaroglu@boun.edu.tr

14:10 USE OF ALGAE IN A NOVEL WASTEWATER TREATMENT SYSTEM

Ceballos C., Northeastern Illinois University, c-ceballos1@neiu.edu, Belloso, E.N., Northeastern Illinois University, USA, e-belloso@neiu.edu; Millenia, J., Northeastern Illinois University, USA, m-jimenez20@neiu.edu; Slate, J.E., Northeastern Illinois University, USA, j-slate@neiu.edu; Kumar, K., Metropolitan Water Reclamation District of Greater Chicago, USA, kumark@mwr.org; Gross, M.A., Gross-Wen Technologies, Inc., USA, info@gross-wen.com; Wen, Z., Gross-Wen Technologies, Inc., USA info@gross-wen.com

14:20 Panel Q&A

14:30-15:30 SESSION E

SESSION E TRACK 1

Moderator: Sabrina Heiser

14:30 THE POTENTIAL IMPACT OF CLIMATE WARMING ON THE FRESHWATER ALGAL FLORA OF ARCTIC LAKES: EVIDENCE FROM THE EOCENE

Siver, P.A., pasiv@conncoll.edu; Lott, A.M., aliz@conncoll.edu. Department of Botany, Connecticut College, New London, CT. U.S.A.

14:40 TERRESTRIALIZATION OF ZYGENEMATOPHYCEAE: HOW ADAPTATION TO STRESSFUL ENVIRONMENTS SHAPED THEIR TRANSITION TO LAND

Holzinger, A., Department of Botany, University of Innsbruck, Austria, Andreas.Holzinger@uibk.ac.at; Rippin, M., Clinical Genomics Uppsala, Uppsala University, Sweden; martin.rippin@scilifelab.uu.se; Arc, E., Department of Botany, University of Innsbruck, Austria, Erwann.Arc@uibk.ac.at; Kranner, I., Department of Botany, University of Innsbruck, Austria, Ilse.Kranner@uibk.ac.at; Becker, B.; Botanical Institute, Cologne University, Germany, Department of Botany, b.becker@uni-koeln.de

14:50 n/a

15:00 EELGRASS-ASSOCIATED MESOGRAZERS LIMIT THE DISTRIBUTION OF ULVA SPP. VIA TOP-DOWN CONTROL OF ITS EARLY LIFE STAGES

Vila Duplá, M. Moss Landing Marine Laboratories, USA, vildup@ugr.es

15:10 THE GENUS ACHNANTHES (BACILLARIOPHYCEAE) AS A MODEL TO INVESTIGATE THE NATURE OF PUTATIVELY OBLIGATE EPIZOIC DIATOMS

Ashworth, M.P., UTEX Culture Collection of Algae, University of Texas, Austin, USA, mashworth@utexas.edu; Frankovich, T.A., Florida Bay Interagency Science Center, Florida International University, USA, tfrankov@fiu.edu; Majewska, R., Unit for Environmental Sciences and Management, North-West University, South Africa, roksana.majewska@nwu.ac.za; Lam, D.W., University of Alabama, USA, dwlam@ua.edu; Manning, S.R., UTEX Culture Collection of Algae, University of Texas, Austin, USA, schonna.manning@utexas.edu

15:20 Panel Q&A

SESSION E TRACK 2

Moderator: Tim Bateman

14:30 ADAPTATIONS OF MICROCYSTIS FLOS-AQUAE TO THE PRESENCE OF PSEUDOKIRCHNERIELLA SUBCAPITATA AND UV-B EXPOSURE CORRELATE WITH CHANGES IN THE METABOLITES PROFILE OF THE CYANOBACTERIUM

Chia, M., Department of Botany, Ahmadu Bello University, Zaria, Nigeria, chia28us@yahoo.com

14:40 DEPENDENCE OF BIOCHEMICAL COMPOSITION AND BIOMASS PRODUCTION OF CLADOPHORA SP ON NUTRIENTS AND LIGHT INTENSITY IN PROLONGED LABORATORY ENRICHMENT

Cuhel, R.L., University of Wisconsin-Milwaukee, USA, rcuhel@alum.mit.edu; Sanchez-Estrada, C., University of Wisconsin-Milwaukee, USA; Aguilar, C., University of Wisconsin-Milwaukee, USA, aguilar@uwm.edu

14:50 INORGANIC NUTRIENT METABOLISM OF DIATOM ENRICHMENTS FROM THE LAURENTIAN GREAT LAKE MICHIGAN: GROWTH THROUGH THE NIGHT PHASE WITH ADEQUATE DAYTIME LIGHT

Aguilar, C., School of Freshwater Sciences, University of Wisconsin-Milwaukee, USA, aguilar@uwm.edu; Jordan, E., University of Wisconsin-Milwaukee, USA; Soderling, M., Wisconsin Department of Natural Resources, USA; Cuhel, R.L. School of Freshwater Sciences, University of Wisconsin-Milwaukee, USA, rcuhel@uwm.edu

15:00 DECIPHERING PHOTOSYNTHETIC CARBON PARTITIONING AND ITS REGULATION IN RESPONSE TO VERY-LOW AND HIGH CO₂ IN MICROCHLOROPSIS GADITANA NIES 2587 BY QUALITATIVE PROTEOMICS

Jutur, P. P., International Centre for Genetic Engineering and Biotechnology, India, jppavan@icgeb.res.in; KAREYA, M. S., International Centre for Genetic Engineering and Biotechnology, India, kareyamukul9@gmail.com; MARIAM, I., International Centre for Genetic Engineering and Biotechnology, India, [iqqramariam27@gmail.com](mailto:iqramariam27@gmail.com); NESAMMA, A. A., International Centre for Genetic Engineering and Biotechnology, India, asha22@gmail.com

15:10 RELYING ON LIGHT IN A LIGHT-LIMITED ENVIRONMENT: CHLOROPHYLL BIOSYNTHESIS IN THE ANTARCTIC PSYCHROPHILE CHLAMYDOMONAS SP. UWO241
Poirier, M., University of Ottawa, Canada, mpoir121@uottawa.ca; Cvetkovska, M., University of Ottawa, Canada, mcvetkov@uottawa.ca

15:200 Panel Q&A

SESSION E TRACK 3

Moderator: Tahmineh Rouzbahani

14:30 n/a

14:40 EFFECTS OF LIGHT INTENSITY, PHOTOPERIOD AND NITRATE LEVELS ON FATTY ACIDS BIOMASS OF GREEN ALGAE SCENEDESMUS DIMORPHUS

Ramezanpour, Z., Applied Aquatic Ecological Association of the International Sturgeon Research Institute (A.R.E.E.O.), zohreh66@gmail.com, Imanpour, J., Biologist in Guilan Univ., javidiman@gmail.com, Ghassemi, S. student of Guilan Univ., saede63ghasemi@gmail.com, Ghanbari-Pirbasti, F., Chemist in Clean Nature Explorer Company, fatemeghanbari@yahoo.com

14:50 CAN THE GREEN MICROALGAE HELP IN REDUCING WATER SCARCITY IN JORDAN?
Mais A. S., Al-Balqa Applied University, Jordan, M.Swies@bau.edu.jo; Arnot, T. C., University of Bath, United Kingdom, T.C.Arnot@bath.ac.uk; Rod J., University of Bath, UK

15:00 KINETIC AND THERMODYNAMICS INVESTIGATION OF THE PYROLYSIS OF FRESHWATER MACROALGAE, SPIROGYRA CRASA

Badshah S.L., Department of Chemistry, Islamia College University Peshawar, Peshawar, 25120, Pakistan. shahbiochemist@gmail.com; Shah, Z., Department of Botany, Islamia College University Peshawar, Pakistan, zaish808@yahoo.com; Iqbal A., Department of Botany, Islamia College University Peshawar, Pakistan, arshad.iqbal@icp.edu.pk; Alves J.L.F., Department of Chemical Engineering and Food Engineering, Federal University of Santa Catarina, Brazil, zeluiz_alves@hotmail.com; Da Silva

J.C.G., Department of Chemical Engineering and Food Engineering, Federal University of Santa Catarina, Brazil, jean.constantino@cear.ufpb.br

15:10 MULTI-OMICS INVESTIGATION OF ABIOTIC STRESS RESPONSES IN ALGAL BIOFUEL STRAINS

Calhoun, S., US Department of Energy Joint Genome Institute, Lawrence Berkeley National Laboratory, USA, secalhoun@lbl.gov; Bell, T.A.S., University of Montana, USA; Dahlin, L., National Bioenergy Center, National Renewable Energy Laboratory, USA; Kruse, C., Los Alamos National Laboratory, USA; Kamel, B., US Department of Energy Joint Genome Institute, Lawrence Berkeley National Laboratory, USA; Louie, K., US Department of Energy Joint Genome Institute, Lawrence Berkeley National Laboratory, USA; Treen, D., US Department of Energy Joint Genome Institute, Lawrence Berkeley National Laboratory, USA; Bowen, B., US Department of Energy Joint Genome Institute, Lawrence Berkeley National Laboratory, USA; Northen, T.R., US Department of Energy Joint Genome Institute, Lawrence Berkeley National Laboratory, USA; Huesemann, M., Pacific Northwest National Laboratory, USA; Guarnieri, M.T., National Bioenergy Center, National Renewable Energy Laboratory, USA; Starckenburg, S.R., Los Alamos National Laboratory, USA; Grigoriev, I.V., US Department of Energy Joint Genome Institute, Lawrence Berkeley National Laboratory, USA

15:20 Panel Q&A

15:30-16:00 *Break and Interact*

16:00-17:30 Poster Session II Moderator: Karolina Fucikova (**Lewin Competition*)

P32 EARLY SUMMER PHYTOPLANKTON COMPOSITION IN A TEMPERATE LAKE ALTERED BY BODY WASH MICROPLASTICS IN A MESOCOSM EXPERIMENT

Yokota, K., State University of New York College at Oneonta, United States of America; Kiyoko.Yokota@oneonta.edu; Mehroose, M., Nova Southeastern University, United States of America, mm4907@mynsu.nova.edu

P33 GOING WITH THE FLOW: PHYTOPLANKTON MORTALITY AND COMMUNITY DYNAMICS

Simmons, L.J., University of Wisconsin-Milwaukee, United States, ljk3@uwm.edu; Berges, J.A., University of Wisconsin-Milwaukee, United States, berges@uwm.edu

P34 ESTIMATING PHYTOPLANKTON CARBON BIOMASS USING DNA

Zhou, L., Marine Science Department, University of Connecticut, U.S.A., lingjie.zhou@uconn.edu; Lin, S., Marine Science Department, University of Connecticut, U.S.A., senjie.lin@uconn.edu

P35 POTENTIALLY HARMFUL ALGAL BLOOMS IN A TROPICAL ESTUARINE GRADIENT—(BAHIA- BRAZIL)

Conceição, L. P., Programa de Pós-Graduação em Botânica-Universidade Estadual de Feira de Santana, lorena.pedreira@yahoo.com.br; Nunes, C. C. S., Programa de Pós-Graduação em Botânica-Universidade Estadual de Feira de Santana, caiobio08@gmail.com; Affe, H. M. J., Faculdade de Oceanografia – FAOC, Universidade do Estado do Rio de Janeiro, Sub-rede Oceanos, Rede Clima, Instituto Nacional de Pesquisas Espaciais - INPE, helenmaffe@gmail.com; Nunes, J. M. C., Laboratório de Algas Marinhas-LAMAR, Instituto de Biologia-UFBA, jmcnunes2000@gmail.com

- P36** COMPETITIVES INTERACTIONS IN MARINE MACROALGAE: A REVIEW
Napolitani, M. A., Unidade Multiusuário de Análises Ambientais, Instituto de Biologia, Universidade Federal do Rio de Janeiro, napolitania@gmail.com; Martins, N.T., Laboratório de Algas Marinhas, Instituto de Biociências, Universidade de São Paulo; Oliveira, V. P., Unidade Multiusuário de Análises Ambientais, Instituto de Biologia, Universidade Federal do Rio de Janeiro
- P37** PROTECTING THEIR HOME: EELGRASS MESOGRAZERS' TOP-DOWN CONTROL OF EARLY LIFE STAGES OF ULVA SPP.
Vila Duplá, M. Moss Landing Marine Laboratories, USA, vildup@ugr.es
- P38** INHIBITION OF DRUG-RESISTANT BACTERIA BY SULFATED POLYSACCHARIDES FROM PORPHYRIDIUM PURPUREUM (RHODOPHYTA)
Saad, M.G., Washington State University, Pullman, WA, marwa.aly@wsu.edu; Manning, S.R., University of Texas at Austin, Austin, TX, schonna.manning@utexas.edu; Dong, W.J., Washington State University, Pullman, WA, dongwenji@wsu.edu
- P39** RISK ASSESSMENT OF THE ANTIBIOTIC AMOXICILLIN ON TOXIN PRODUCING AND NON - TOXIN PRODUCING STRAINS OF MICROCYSTIS
Gana, Y. A., Department of Zoology, Ahmadu Bello University, Zaria, Nigeria; Chia, M. A., Department of Botany, Ahmadu Bello University, Zaria, Nigeria, chia28us@yahoo.com, amchia@abu.edu.ng; Sha'aba, R. I., Department of Biology, Ahmadu Bello University, Zaria, Nigeria ; Gauje, B., Department of Biology, Ahmadu Bello University, Zaria, Nigeria ; Gadzama, I. M. K., Department of Biology, Ahmadu Bello University, Zaria, Nigeria ; Sonnie Joshua Oniye, S. J., Department of Zoology, Ahmadu Bello University, Zaria, Nigeria
- P40** NEW GREEN CHEMISTRY: A BIOTECHNOLOGICAL APPROACH TO PRODUCE GLYCOLATE IN CHLAMYDOMONAS REINHARDTII
Rössler, S., University of Leipzig, Germany, sonja.roessler@uni-leipzig.de; Wagner, H., University of Leipzig, Germany, hwagner@uni-leipzig.de; Schad, A., University of Leipzig, Germany, antonia.schad@uni-leipzig.de; Wilhelm, C., University of Leipzig, Germany, cwillhelm@rz.uni-leipzig.de
- P41** BIOCRUST COMMUNITY COMPOSITION AND IMPLICATIONS FOR CARBON FLUX UNDER TIMED LIGHT INCUBATION
Hoellrich, M. R.¹, Darrouzet-Nardi, A.², Santiago, L.³, Pietrasiak, N.¹ New Mexico State University¹, University of Texas at El Paso², University of California Riverside³
- P42** A DNA BARCODE APPROACH OF COLPOMENIA (ECTOCARPALES, PHAEOPHYCEAE) SPECIES FROM SOUTH AND SOUTHEASTERN AUSTRALIA
Martins, N.T., Laboratory of Marine Macroalgae, University of São Paulo, Brazil, tavaresmartins.nuno@gmail.com; Gurgel C., F., D., Department of Botany, Federal University of Santa Catarina, Brazil; Spokes T., S., Department of Environment and Water, State Herbarium of South Australia, Australia; Cassano, V., Laboratory of Marine Macroalgae, University of São Paulo, Brazil
- P43** MORPHOLOGICAL AND ECOLOGICAL CHARACTERIZATION OF THREE NEW SYMMETRIC BIRAPHID (NAVICULOID) DIATOM SPECIES FROM STREAMS OF THE ISLAND OF CYPRUS
Cantonati, M., MUSE - Museo delle Scienze, Limnology and Phycology Section, Italy, marco.cantonati@muse.it; Bilous, O., Institute of Hydrobiology of NAS of Ukraine, Ukraine; bilous_olena@ukr.net; Saber, A.A., Museo delle Scienze, Limnology and Phycology Section, Italy, Botany Department, Faculty of Science, Ain Shams University, Egypt; abdullah_elattar@sci.asu.edu.eg

P44 CULTURE OF RED ALGAE CHONDRACANTHUS CHAMISSOI IN PERU

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P45 DEFINING OPTIMUM: GROWTH CONDITIONS AFFECT HEAT STRESS RESISTANCE IN THE ANTARCTIC EXTREMOPHILE CHLAMYDOMONAS SP. UWO241

Osmers, P., University of Ottawa, Canada, posme102@uottawa.ca; Cvetkovska, M., University of Ottawa, Canada, mcvetkov@uottawa.ca

P46 EXTRATERRESTRIAL CYANOBACTERIA AND DIATOMS IN THE ORGUEIL (CI1) AND MURCHISON (CM2) CARBONACEOUS CHONDRITES

Hoover, R. B., United States Space & Rocket Center, USA, RichardBHoover@Icloud.Com; Rozanov, A.Yu., Borissiak Paleontological Institute, Russia, aroza@Paleo.ru

P47 TEMPORAL TRENDS OF HEAVY METAL CONCENTRATIONS IN BROWN MACROALGAE FROM COASTAL ENVIRONMENTS

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P48 LOST IN THE TROPICS: CHONDRUS SP. NOV. (RHODOPHYTA) ON EAST HAWAII ISLAND

Kittle III, R. P., University of Louisiana at Lafayette, USA, C00269538@louisiana.edu; Veillet, A., University of Idaho at Moscow, USA, aveillet@uidaho.edu; Schmidt, W.E., University of Louisiana at Lafayette, USA, william.schmidt@louisiana.edu; Fredericq, S., University of Louisiana at Lafayette, USA, slf9209@louisiana.edu; McDermid, K.J., University of Hawaii at Hilo, USA, mcdermid@hawaii.edu

P49 THE CLONING AND ENGINEERING OF DIATOM MITOCHONDRIAL GENOMES IN YEAST AND BACTERIA

Cochrane, R. R., University of Western Ontario (UWO), Canada, rcochra3@uwo.ca; Brumwell, S. L., UWO, Canada, sbrumwe2@uwo.ca; Soltysiak, M. P. M., UWO, Canada, msoltys4@uwo.ca; Shrestha, A., UWO, Canada, ashrest7@uwo.ca; Giguere, D. J., UWO, Canada, dgiguer@uwo.ca; Hamadache, S., UWO, Canada, shamadac@uwo.ca; Wang, J., UWO, jwan625@uwo.ca; Tholl, S. Q., UWO, Canada, stholl@uwo.ca; Janakirama, P., Designer Microbes Inc., Canada, preetam.janakirama@gmail.com; Gloor, G. G., UWO, Canada, ggloor@uwo.ca; Edgell, D. R., UWO, Canada, dedgell@uwo.ca; Karas, B. J., UWO, Canada, bkaras@uwo.ca

P50 COMPETITIVE INTERACTIONS AS A MECHANISM FOR CHEMICAL DIVERSITY MAINTENANCE IN NODULARIA SPUMIGENA

Sandra Lage^{1,2}, Hanna Mazur-Marzec² and Elena Gorokhova¹ ¹Department of Environmental Science, Stockholm University, Stockholm, Sweden. ²Division of Marine Biotechnology, Institute of

Oceanography, University of Gdańsk, Gdynia, Poland

P51 WORLDWIDE LITERATURE SURVEY OF MARINE MACROPHYTIC HABITATS AND EPIFAUNAL ASSEMBLAGES: TRENDS AND GAPS IN RESEARCH

Hosoki, S., Institute of Environment, Department of Biology, Florida International University, Miami, Florida, USA, shoso001@fiu.edu; Iporac, L.A.R., Institute of Environment, Department of Biology, Florida International University, Miami, Florida, USA, lipor001@fiu.edu; Collado-Vides, L., Institute of Environment, Department of Biology, Florida International University, Miami, Florida, USA, colladol@fiu.edu

P52 THE ROLE OF MACROALGAL MICROBIOMES IN THE CYCLING OF MERCURY THROUGH COASTAL ECOSYSTEMS

Penn, S.C. Moss Landing Marine Laboratories, United States, spenn@mlml.calstate.edu

P54 GROWTH-ENHANCING EFFECT OF AMPEP IN NEOPYROPIA YEZOENSIS

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P55 EFFECT OF HERBIVORY ON MORPHOLOGY OF CRUSTOSE ALGAE

Sonia D. Rodriguez, Ligia Collado-Vides, Alain Duran

P56 EFFECT OF DESICCATION ON GROWTH, PIGMENT AND BIOCHEMICAL RESPONSES IN AGAROPHYTON VERMICULOPHYLLUM

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P57 CYANOBACTERIAL AKINETE DISTRIBUTION, VIABILITY, AND CYANOTOXIN RECORDS IN SEDIMENT ARCHIVES FROM THE NORTHERN BALTIC SEA

S.M. Wood^{1,2}, A. Kremp², H. Savela^{1,#}, S. Akter³, V-P Vartti⁴, S. Saarni⁵, S. Suikkanen^{1,*}

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⁴ STUK Radiation and Nuclear Safety Authority, Helsinki, Finland

⁵ Department of Geography and Geology, University of Turku, Finland

P58 ENDOPLURA JEJUENSIS SP. NOV. AND E. KOREANA SP. NOV. (RALFSIALES, PHAEOPHYCEAE) FROM KOREA BASED ON MOLECULAR AND MORPHOLOGICAL ANALYSES

Oteng'o, A. O., Department of Life Science, Chosun University, Gwangju, 61452, Korea, aotinga@gmail.com; Won, B. Y., Department of Life Science, Chosun University, Gwangju, 61452, Korea, givingwon10@gmail.com; Cho, T. O., Department of Life Science, Chosun University, Gwangju, 61452, Korea, tocho@chosun.ac.kr

P59 THE INTRIGANT OCCURRENCE OF MANY GAS VESICLES IN BENTHIC MARINE CYANOBACTERIA

Caires, T. A., Universidade Estadual de Feira de Santana, Brazil, taiaracaires@gmail.com

P60 20 YEAR VARIATION IN CARBON AND NITROGEN RATIOS IN KELP POPULATIONS ACROSS THE PACIFIC RIM WITH A SPECIAL FOCUS ON CALIFORNIA

Winqvist, T. A. San Diego State University, Twinquist9732@sdsu.edu; Edwards, M, San Diego State University, Medwards@sdsu.edu

P61 GROWTH OF CHLORELLA KESSLERI UNDER HIGH NITRATE CONDITIONS

Rani, V., University of Szeged, Hungary, Biological Research Centre, Hungary, vaishalirk29@gmail.com; Maróti, G., Biological Research Centre, Hungary

P62 EFFECTS OF LEAD (Pb) EXPOSURE ON THE GROWTH, PIGMENT CONTENTS AND OXIDATIVE STRESSES IN THE RED ALGA, AGAROPHYTON VERMICULOPHYLLUM

Kim, Y. W., Department of Marine Science, Incheon National University, Incheon 22012, Korea, ywoo700@naver.com; Park, J. S., Research Institution of Basic Sciences, Incheon National University, Incheon 22012, Korea, dazzlepark@hanmail.net; Kim J. K., Department of Marine Science, Incheon National University, Incheon 22012, Korea, jang.kim@inu.ac.kr

17:30 PSA Endowment Auction

18:00 Conclude

WEDNESDAY, JULY 21, 2021

11:00-13:00 NSF WEBINAR

NSF RESEARCH AND TRAINING OPPORTUNITIES FOR THE PHYCOLOGY COMMUNITY

Herron, M., National Science Foundation, mherron@nsf.gov

Join NSF Program Officers to learn about new and ongoing NSF funding opportunities of relevance to phycologists at all career stages. This session will cover how NSF funds research, the grant proposal process, and funding opportunities through Biology core programs and current special solicitations. Overviews of Research Experiences for Undergraduates (REU) opportunities, the Graduate Research Fellowship Program (GRFP), Postdoctoral Research Fellowships in Biology (PRFB), the Faculty Early Career Development Program (CAREER), and the Mid-Career Advancement (MCA) program will be provided. A question-and-answer session will follow the overview of the funding and training opportunities and tips on proposal preparation.

13:30-14:30 ALGAE IN EDUCATION Moderator: Marissa Nalley

13:30 ALGAE FOUNDATION'S ALGAE TECHNOLOGY EDUCATIONAL CONSORTIUM (ATEC) AND ALGAE ACADEMY (AA) SERVING 100,000 STUDENTS AND BIOECONOMY TRAINEES

Levine, I.A., Algae Foundation and University of Southern Maine, Lewiston, ME, ilevine@maine.edu; Cannis, T., Algae Foundation and Global Algae Innovations, Inc., USA, tcannis@thealgae.foundation.org

13:40 ALGAE ACADEMY: EDUCATING STUDENTS ON THE POWER OF ALGAE

Cannis, T, The Algae Foundation, USA, tcannis@thealgaeoundation.org; Ira Levine, Algae Foundation, United State, ilevine@thealgaeoundation.org; Jakob Nalley, The Algae Foundation, USA, jnalley6@gmail.com; Marissa Nalley, The Algae Foundation, USA, mnalley@thealgaeoundation.org; and Jesse Traller, The Algae Foundation, USA, jessetraller@globalgae.com

13:50 ATEC - ALGAE WORKFORCE TRAINING FOR THE 21ST CENTURY

Gómez, S. M., Santa Fe Community College, USA, stephen.gomez@sfcc.edu; Frauenglass, M. O., ondine.frauenglass@sfcc.edu; Santa Fe Community College, Santa Fe, New Mexico, US

14:00 ALGAE IN THE DARK – USING ALGAE GROWN HETEROTROPHICALLY AS A TEACHING TOOL

DeKloe, J., Solano College, Vacaville, CA, James.DeKloe@solano.edu

14:10 REDESIGNING OF UPPER DIVISION UNDERGRADUATE BIOCHEMISTRY LABORATORY COURSE WITH FOCUS ON ALGAL BIOTECHNOLOGY

Maitra, K., California State University - Fresno, Fresno, CA, kmaitra@mail.fresnostate.edu

14:20 Panel Q&A

15:00-16:00 PSA Business Meeting

THURSDAY, JULY 22, 2021

11:00 LANG LECTURE Moderator: Patrick Martone

WHAT'S PLOIDY GOT TO DO WITH IT?

Stacy Krueger-Hadfeld, University of Alabama, Birmingham, sakh@uab.edu

11:30-13:00 IDEA SYMPOSIUM Moderators: IDEA Working Group



11:30 REFLECTIONS ON DIVERSITY AND INCLUSIVENESS: A PERSPECTIVE FROM A PHYCOLOGIST

Ligia Collado-Vides, Florida International University, Miami, Florida, colladol@fiu.edu



11:50 SCIENCE WILL ONLY BENEFIT FROM DIVERSITY

Camille Gaynus, University of Pennsylvania, Philadelphia, Pennsylvania, cgaynus@gmail.com



12:10 ISLANDERS IN MARINE SCIENCE AND SUSTAINABILITY
Austin Shelton

12:30 Panel Discussion

13:00-13:30 IDEA Breakout Discussion

13:00-13:30 *Break and Interact*

13:30-14:30 SESSION E

SESSION E TRACK 1

Moderator: Ron Kittle

13:30 n/a

13:40 PHOTOSYNTHETIC RESPONSE TO A WINTER HEATWAVE IN LEADING AND TRAILING EDGE POPULATIONS OF AN INTERTIDAL RED ALGAE

Kolzenburg, R., University of Portsmouth, UK, regina.kolzenburg@gmail.com; Ragazzola, F., University of Portsmouth, UK, federica.ragazzola@port.ac.uk; Tamburello, L., Ischia Marine Centre, Stazione Zoologica Anton Dohrn, Italy, laura.tamburello@szn.it; McQuaid, C., Rhodes University, South Africa, c.mcquaid@ru.ac.za; Zardi, G.I., University of Algarve, Portugal and Rhodes University, South Africa, zardi73@yahoo.it; Nicastro, K. R., University of Algarve, Portugal, katynicastro@gmail.com

14:50 EFFECT OF ELEVATED CO₂ AND TEMPERATURE ON THE GROWTH, PHOTOSYNTHETIC PIGMENTS AND NUTRIENT UPTAKE OF GRATELOUPIA FILICINA

Hwang, J.H., Incheon National University, Korea, jeonghwa0055@naver.com; Song, H.I., Incheon National University, Korea, hyen0120@naver.com; Park, J.S., Incheon National University, Korea, dazzlepark@hanmail.net; Kim, J.K., Incheon National University, IKorea, jang.kim@inu.ac.kr

14:00 WHO CARES MORE ABOUT CHEMICAL DEFENCES IN THE RED SEAWEED PLOCAMIUM SP. – THE SEAWEED OR ITS ONLY GRAZER?

Heiser, S., University of Alabama at Birmingham, USA, heiser@uab.edu; Amsler, C.D., University of Alabama at Birmingham, USA, amsler@uab.edu; Brothers, C.J., Walla Walla University, USA, cecilia.brothers@wallawalla.edu; Shilling, A.J., University of South Florida, USA, andrewjshilling@yahoo.com; Davis, C.B., University of Alabama at Birmingham, USA, cbdavis5@uab.edu; Hutchens, L., University of Alabama at Birmingham, USA, lb47@uab.edu; Amsler, M.O., University of Alabama at Birmingham, USA, mamsler@uab.edu; McClintock, J.B., University of Alabama at Birmingham, US, mcclinto@uab.edu; Baker, B.J., University of South Florida, USA, bjbaker@usf.edu

14:10 EFFECTS OF IRRADIANCE, NUTRIENT ENRICHMENT, AND CO₂ ON PHOTOSYNTHETIC EFFICIENCY OF HAWAIIAN CHONDRUS SP. NOV. AND HALYMENIA HAWAIIANA (RHODOPHYTA)

Whetstone, C.R. University of Hawaii at Hilo, USA, clararw@hawaii.edu; McDermid, K.J., University of Hawaii at Hilo, USA, mcdermid@hawaii.edu

14:20 Panel Q&A

SESSION E TRACK 2

Moderator: Maggie Amsler

13:30 TEMPORAL DYNAMICS AND FUNCTIONAL REDUNDANCY IN THE MICROBIOME OF A MACROALGAL FOUNDATION SPECIES

Davis, K. University of British Columbia, kmdavis@zoology.ubc.ca

13:40 TISSUE SPECIFICITY AND CROSS-ATLANTIC, NORTH TO SOUTH LATITUDINAL DIFFERENTIATION OF HOST MICROBIOMES OF THE BROWN ALGA FUCUS VESICULOSUS (PHAEOPHYCEAE)

[Engelen, A.H.](mailto:aengelen@ualg.pt), CCMAR, University of Algarve, Portugal, aengelen@ualg.pt; Capistrant-Fossa, K.A., University of Maine, USA, kyle.capistrantfossa@utexas.edu; Morrison, H.G., Marine Biological Laboratory, Woods Hole, USA, hmorrison1981@gmail.com; Quigley, C.T.C., University of Maine, USA, charlotte.quigley@maine.edu; Morozov, A., Marine Biological Laboratory, Woods Hole, USA, amorozov@mbi.edu; Serrão, E.A., Universidade do Algarve, Portugal, eserrao@ualg.pt; Brodie, J., Natural History Museum, UK, j.brodie@nhm.ac.uk; Gachon, C.M.M., Scottish Association for Marine Science, UK, claire.gachon@sams.ac.uk; Badis, Y., Scottish Association for Marine Science, UK, yacine.badis@sams.ac.uk; Johnson, L.E., Université Laval, Canada, ladd.johnson@bio.ulaval.ca; Hoarau, G., Nord University, Norway, galice.g.hoarau@nord.no; Abreu, M.H., ALGApplus, Portugal, htabreu@algapplus.pt; Tester, P.A., Ocean Tester LLC, USA, ocean.tester@gmail.com; Stearns, L.A., University of Kansas, USA, stearns@ku.edu; Brawley, S.H., University of Maine, USA, brawley@maine.edu

14:50 CO-CULTURE REMODELS THE TRANSCRIPTOMES OF PROCHLOROCOCCUS, SYNECHOCOCCUS AND 'HELPER' BACTERIUM ALTEROMONAS DURING HIGH CO₂ GROWTH

[Barreto Filho, M.M.](mailto:barretof@uab.edu), University of Alabama at Birmingham Department of Biology, USA, barretof@uab.edu; Walker, M., University of Alabama at Birmingham Department of Biology, USA, sfidemw@uab.edu; Morris, J.J., University of Alabama at Birmingham Department of Biology, USA, evolve@uab.edu

14:00 YOU ARE THE PLASTID YOU STEAL: PREY SPECIES INGESTED IMPACTS PHYSIOLOGICAL AND TRANSCRIPTIONAL RESPONSE IN THE CILIATE MESODINIUM CHAMAELEON

[Paight, C.](mailto:cpaight@ucsb.edu) University of California Santa Barbara, USA, cpaight@ucsb.edu; Johnson, M.D. Woods Hole Oceanographic Institution, USA mattjohnson@whoi.edu; Lasek-Nesselquist, E. Wadsworth Center, USA, elasekness@gmail.com; Moeller, H.V. University of California Santa Barbara, USA, hvmoeller@ucsb.edu

14:10 SEEKING SEAWEED SILICON: LOCALIZING SI IN DIVERSE ALGAE

[Young, E. B.](mailto:ebyoung@uwm.edu), Dept Biological Sciences, University of Wisconsin-Milwaukee ebyoung@uwm.edu; Driskill A. M., Dept Biological Sciences, University of Wisconsin-Milwaukee, driskill@uwm.edu; Berges, J. A., Dept Biological Sciences, University of Wisconsin-Milwaukee, berges@uwm.edu

14:20 Panel Q&A

SESSION E TRACK 3

Moderator: Marina Frontasveya

13:30 HERITABILITY OF INCREASED BIOMASS IN THE GIANT KELP *MACROCYSTIS PYRIFERA* SUPPORTS THE DEVELOPMENT OF ITS GENOMIC BREEDING PROGRAM

Wade, R. M., University of Wisconsin-Milwaukee, USA, wader@uwm.edu; Yorke, C. E., University of California-Santa Barbara, USA, ceyorke@ucsb.edu; Montecinos, G. J., University of Wisconsin-Milwaukee, USA, gjmontec@uwm.edu; Miller, R. J., University of California-Santa Barbara, USA, rjmiller@ucsb.edu; Reed, D. C., University of California-Santa Barbara, USA, danreed@ucsb.edu; Nuzhdin, S. V., University of Southern California, snuzhdin@usc.edu; Alberto, F. A., University of Wisconsin-Milwaukee, USA, albertof@uwm.edu

13:40 PROTOPLAST ISOLATION AND REGENERATION FROM THE POTENTIAL ECONOMIC BROWN ALGA *PETALONIA FASCIA* (ECTOCARPALES, PHAEOPHYCEAE)

Avila-Peltroche, J., Chosun University, Korea, jose_avila22@hotmail.com; Won, B.Y., Chosun University, Korea; Cho, T.O., Chosun University, Korea

14:50 ANTIOXIDANT PROPERTIES AND MINERAL COMPOSITION OF RED SEAWEED *GRACILARIA VERRUCOSA*

Yılmaz, M., Çanakkale Onsekiz Mart University, School of Graduate Studies, melisyilmaz@comu.edu.tr; Ak, İ., Çanakkale Onsekiz Mart University, Faculty of Marine Science and Technology, ilknurak@gmail.com; Türker, G., Çanakkale Onsekiz Mart University, Faculty of Applied Science, gulenturker@hotmail.com

14:00 CONTRASTING RESULTS OF NATURAL AND FARMED POPULATIONS OF THE RED ALGA AGAROPHYTON CHILENSE AGAINST TEMPERATURE VARIATION

Usandizaga, S., Centro-Imar, Universidad de los Lagos, Puerto Montt, Chile, susandizaga@gmail.com; Camus, C., Centro-Imar, Universidad de los Lagos, Puerto Montt, Chile, carolina.camus@ulagos.cl; Guillemín, M-L., Universidad Austral de Chile, Facultad de Ciencias Valdivia, Chile, marielaureguillemin@gmail.com; Buschmann, A. H., Centro-Imar, Universidad de los Lagos, Puerto Montt, Chile, abuschma@ulagos.cl

14:10 EFFECT OF KELPAK® ON THE GROWTH AND THERMAL TOLERANCE OF *NEOPYROPIA YEZOENSIS*

Song, H.I., Department of Marine Science, Incheon National University, Incheon 22012, Korea, hyen0120@naver.com; Han, S., Department of Marine Science, Incheon National University, Incheon 22012, Korea, soh0428@naver.com; Park, J.S., Research Institution of Basic Sciences, Incheon National University, Incheon 22012, Korea, dazzlepark@hanmail.net; Kim, J.K., Department of Marine Science, Incheon National University, Incheon 22012, Korea, jang.kim@inu.ac.kr

14:20 Panel Q&A

14:30- 15:30 SESSION G

SESSION G TRACK 1

Moderator: Mickey Rogers

14:30 ASSESSING CHANGES IN COASTAL ECOSYSTEM ENGINEERS AND ASSOCIATED COMMUNITIES IN NARRAGANSETT BAY

Green-Gavrielidis, L., Salve Regina University, USA, l.greengavrielidis@salve.edu; Pantoni, G., University of Rhode Island, USA, gpant26@my.uri.edu; Hobbs, N.V., University of Rhode Island, USA, nvshobbs@uri.edu; Taylor, D., Roger Williams University, USA, dtaylor@rwu.edu; Cicchetti, G., Environmental Protection Agency, USA, cicchetti.giancarlo@epa.gov; Thornber, C., University of Rhode Island, USA, thornber@uri.edu

14:40 EFFECTS OF A MACROALGAL FOUNDATION SPECIES ON ABIOTIC HETEROGENEITY AND THE BETA DIVERSITY OF INTERTIDAL COMMUNITIES

Catalán, A.M., Instituto de Ciencias Marinas y Limnológicas, Universidad Austral de Chile, Chile, a.catalansegovia@gmail.com; López, D., Instituto de Ciencias Marinas y Limnológicas and Instituto de Ciencias Ambientales y Evolutivas, Universidad Austral de Chile, Chile, danyelalopez@gmail.com; Fica-Rojas, E., Instituto de Ciencias Ambientales y Evolutivas, Universidad Austral de Chile, Chile, eliiseo.sp@gmail.com; Broitman, B., Universidad Adolfo Ibáñez, Chile, bernardo.broitman@uai.cl; Valdívía, N., Instituto de Ciencias Marinas y Limnológicas, Universidad Austral de Chile, and Centro FONDAF de Investigación de Dinámicas de Ecosistemas Marinos de Altas Latitudes (IDEAL), Chile, nelson.valdivia@uach.cl; Scrosati, R.A., St. Francis Xavier University, Canada, rscrosat@stfx.ca

15:50 n/a

15:00 IDENTIFICATION OF ENVIRONMENTAL DRIVERS OF MICROBIOME STRUCTURE FROM THE BROWN ALGA FUCUS VESICULOSUS (PHAEOPHYCEAE)

Capistrant-Fossa, K.A., School of Marine Sciences, University of Maine, Orono, USA, kyle.capistrantfossa@utexas.edu; Morrison, H.G., Josephine Bay Paul Center, Marine Biological Laboratory, Woods Hole, USA, hmorrison1981@gmail.com; Engelen, A.H., CCMAR, University of Algarve, Faro, Portugal, aengelen@ualg.pt; Ester A. Serrão, Centro de Ciências do Mar, Universidade do Algarve, Faro, Portugal, eserrao@ualg.pt; Ladd E. Johnson, Département de biologie, Université Laval, Québec, Canada, ladd.johnson@bio.ulaval.ca; Patricia A. Tester, Ocean Tester LLC, Beaufort, NC, USA, ocean.testler@gmail.com; Brawley, S.H., School of Marine Sciences, University of Maine, Orono, USA, brawley@maine.edu

15:10 TROPHIC REGULATION OF ALGAL SIZE STRUCTURE

Rober, A.R., Department of Biology, Ball State University, Muncie, IN 47306, USA, arrober@bsu.edu; McCann, K.S., Department of Integrative Biology, University of Guelph, Guelph, Ontario N1G2W1, Canada, ksmccann@uoguelph.ca; Turetsky, M.R., Institute of Arctic and Alpine Research and Ecology and Evolutionary Biology Department, University of Colorado Boulder, Boulder, CO 80309, USA, merritt.turetsky@colorado.edu; Wyatt, K.H., Department of Biology, Ball State University, Muncie, IN 47306, USA, khwyatt@bsu.edu

15:20 Panel Q&A

SESSION G TRACK 2

Moderator: David Berthold

14:30 POLYPHASIC INVESTIGATIONS OF THE RARE HETEROCYTOUS CYANOBACTERIAL GENUS CAMPTYLONEMOPSIS FROM HAWAII AND INDIA

Singh, P., Banaras Hindu University, India, sps.bhu@gmail.com; Johansen, J.R., John Carroll University, USA, johansen@jcu.edu

14:40 TROPICAL CYANOBACTERIAL DIVERSITY ALONG A TROPHIC GRADIENT IN THE NEW RIVER, BELIZE

Lefler, F.W., University of Florida, USA, flefler@ufl.edu; Barbosa, M., University of Florida, USA, mbarbosa@ufl.edu; Berthold, D.E., University of Florida, USA, dberthold@ufl.edu; Zimba, P. V., Texas A&M University- Corpus Christi, USA, paul.zimba@tamucc.edu; Laughinghouse IV, H.D., University of Florida, USA, hlaughinghouse@ufl.edu

14:50 PRELIMINARY ASSESSMENT OF MICROBIAL COMMUNITY STRUCTURE OF WIND-TIDAL FLATS IN THE LAGUNA MADRE, TEXAS, USA

I.-Shuo Huang, Virginia Institute of Marine Science, USA, iwhuang@vims.edu; Lee J. Pinnell, Texas A&M University-College Station, USA, ljpinnell@cvm.tamu.edu; Jeffrey W. Turner, Texas A&M University-Corpus Christi, USA, Jeffrey.turner@tamucc.edu; Hussain Abdulla, Texas A&M University-Corpus Christi, USA, Hussain.abdulla@tamucc.edu; Lauren Boyd, Central Michigan University, USA, laurenmboyd15@gmail.com; Eric W. Linton, Central Michigan University, USA, linto1ew@cmich.edu; Paul V. Zimba, Texas A&M University-Corpus Christi, USA, pvzimbal@gmail.com

15:00 PHOTOSYNTHETIC PROTISTAN DIVERSITY ALONG A SPATIAL GRADIENT IN THE NEW RIVER, BELIZE

Barbosa, M., University of Florida, USA, mbarbosa@ufl.edu; Lefler, F., University of Florida, USA, flefler@ufl.edu; Berthold, D.E., University of Florida, USA, dberthold@ufl.edu; Laughinghouse IV, H.D., University of Florida, USA, hlaughinghouse@ufl.edu

15:10 n/a

15:20 Panel Q&A

SESSION G TRACK 3

Moderator: Alok Arun

14:30 HIGHLY TOXIC STRAIN OF PRYMENSIUM PARVUM IS AN ALLODIPLOID HYBRID
Auber, R.P., Purdue University, USA, rauber@purdue.edu; Pendleton, A.L., Purdue University, USA, pendlea@purdue.edu; Fallon, T.R., Scripps Institution of Oceanography, UC San Diego, USA, tfallon@ucsd.edu; Moore, B.S., Scripps Institution of Oceanography, UC San Diego, USA, bsmoore@ucsd.edu; Driscoll, W.W., Penn State Harrisburg, USA, wwd17@psu.edu; Wisecaver, J.H., Purdue University, USA, jwisecav@purdue.edu

14:40 PAN-ARCTICA : HORIZONTAL GENE TRANSFERS DEFINE THE CONVERGENT EVOLUTION OF DISTANTLY RELATED ALGAE FROM THE SAME OCEAN

Dorrell, R.G, Institut de Biologie de l'Ecole Normale Supérieure (IBENS), France dorrell@bio.ens.psl.eu; Kuo, A., Joint Genomes Institute, USA, akuo@lbl.gov ; Füssy, Z., Charles University, Czechia, zoltan.fussy@gmail.com; Richardson, E., University of Alberta, Canada, ehrichar@ualberta.ca; Salamov, A., Joint Genomes Institute, USA, aasalamov@lbl.gov; Zarevski, N., IBENS, France, niko.zarevski@gmail.com; Ibarbalz, F.M., University of Buenos Aires, Argentina, fedeibarbalz@gmail.com; Pierella Karlusich, J.J., IBENS, France, pierella@bio.ens.psl.eu; Stecca Steindorff, A., Joint Genomes Institute, USA, assteindorff@lbl.gov; Grigoriev, I., Joint Genomes Institute, USA, ivgrigoriev@lbl.gov; Lovejoy, C., Université Laval, Canada, Connie.Lovejoy@bio.ulaval.ca

14:50 ALL MIXED UP: RECONCILING DIVERGENT EVOLUTIONARY RESPONSES OF MIXOTROPHS TO CLIMATE CHANGE

Moeller, H. V., University of California, Santa Barbara, USA, hvmoeller@ucsb.edu; Lepori-Bui, M., University of California, Santa Barbara, USA, mleporibui@ucsb.edu; Gonzalez, L., Cold Regions

Research and Environmental Laboratory, USA, lgonzalez93292@gmail.com; Proulx, S. R., University of California, Santa Barbara, USA, sproul@ucsb.edu

15:00 PHYCOCOSM: SEQUENCING THE ALGAL TREE OF LIFE

Kuo, A., US Department of Energy Joint Genome Institute (JGI). akuo@lbl.gov; Hayes, R., JGI, rdhayes@lbl.gov; Calhoun, S., JGI, secalthoun@lbl.gov; Kamel, B., JGI, bskamel@lbl.gov; Salamov, A., JGI, asalamov@lbl.gov; Grigoriev, I., JGI, ivgrigoriev@lbl.gov

15:10 EXTRATERRESTRIAL AND INTRATERRESTRIAL CYANOBACTERIA, DIATOMS AND OTHER MICROALGAE: TOWARD A NEW PARADIGM CONCERNING THE ORIGIN AND DISTRIBUTION OF BIOSPHERES

Hoover, R. B., United States Space & Rocket Center, United States of America, RichardBHoover@Icloud.com; Rozanov, A. Yu., Borissiak Paleontological Institute, PIN/RAS, Moscow, Russian Federation, aroza@paleo.ru; Wickramasinghe, N. C., Centre for Astrobiology, University of Ruhuna, Matara, Sri Lanka, ncwick@gmail.com; Wallis, D. H., University of Buckingham, Buckingham, UK, dhwallis@fields-hq.com; Frontasyeva, M. V., Joint Institute for Nuclear Research, Dubna, Russian Federation, marina@nf.jinr.ru

15:20 Panel Q&A

15:30-16:00 *Break and Interact*

16:00-17:00 PSA Awards Ceremony

17:00 Adjourn Meeting

PSA2021 ABSTRACTS



Presidential Plenary

Lynn J. Rothschild, NASA Ames Research Center/Brown University, lynnjrothschild@gmail.com

FROM EARTH TO ET: THE USE OF SYNTHETIC BIOLOGY FOR NASA'S MISSIONS

Lynn Rothschild, a research scientist at NASA Ames and Adjunct Professor at Brown University, is passionate about the origin and evolution of life on Earth and elsewhere, while at the same time pioneering the use of synthetic biology to enable space exploration. A life-long protistologist by love and training, her research has focused on how life, particularly microbes, has evolved in the context of the physical environment, both here and potentially elsewhere. Rothschild has brought her imagination and creativity to the burgeoning field of synthetic biology, articulating a vision for the future of synthetic biology as an enabling technology for NASA's missions, including human space exploration and astrobiology. Since 2011 she has served as the faculty advisor of the award-winning Stanford-Brown iGEM (international Genetically Engineered Machine Competition) team, which has pioneered the use of synthetic biology to accomplish NASA's missions, particularly focusing on the human settlement of Mars, and such innovative technologies as biomining (patent pending), mycotecture, BioWires, making a biodegradable UAS (drone) and an Astropharmacy. Her lab is testing these plans in space on in the PowerCell synthetic biology secondary payload on a DLR satellite, EuCROPIS, launched in December 2018. A past-president of the Society of Protozoologists, she is a fellow of the Linnean Society of London, The California Academy of Sciences and the Explorer's Club. In 2015, she was awarded the Isaac Asimov Award from the American Humanist Association, and was the recipient of the Horace Mann Award from Brown University, and has been a NASA Innovative Advanced Concepts (NIAC) fellow four times, most recently in 2021. She frequently appears on documentaries, TV and radio, and lectures worldwide, including Windsor Castle, Comi Con, TechFestival and the Vatican, and most recently debated de-extinction for an Intelligence Squared USA debate. Her interest in building a cell combines her expertise in evolutionary biology, extremophiles, history and philosophy of science, synthetic biology and the search for life in the universe. Lynn was formerly Professor (Adjunct) at Stanford where she taught "Astrobiology and Space Exploration" for a decade.

Presidential Symposium (in order of presentation)

Nicole Pietrasiak, Plant and Environmental Sciences Department, New Mexico State University, USA, npietras@nmsu.edu

DRYLAND SOILS – A TREASURE CHEST OF HIDDEN DIVERSITY

Drylands cover vast extents of earth's continents. They are home to unique biodiversity adapted to withstand the extreme environmental conditions of this biome. Among the marvelous organisms that thrive here, cyanobacteria are important components in dryland soils crucial for dryland ecosystem health and soil quality. Despite their importance, and in stark contrast to aquatic habitats, we only have little knowledge of the cyanobacterial species that live there, how they evolved, and how widely they are distributed. While molecular soil biodiversity surveys rapidly reveal interesting and unique taxa in cyanobacteria and other microbial groups, we often are limited in our ability to associate cyanobacterial sequence data to known taxa. Moreover, we face a bottleneck of taxonomic manpower to describe this diversity while natural history and taxonomy degree programs and funding support are in global decline. My talk will present a review of recent advances in dryland soil cyanobacterial diversity in an effort to raise awareness about this enigmatic group. I will highlight recently discovered and described new taxa including the genera *Spirirestis*, *Mojavia*, *Roholtiella*, *Desikacharya*, *Macrochaete*, *Kastovskya*,

Myxacorys, *Chroakolemma*, and *Trichotorquatus*. With my talk I hope to inspire the current and next generations to join me in the discovery and exploration of our charismatically beautiful dryland cyanobacteria. Only by describing cyanobacterial diversity we can inventory, monitor, and conserve these keystone organisms. This is an urgent priority in our rapidly changing world, especially when drylands are expected to expand while suffering increasing damage due to wind and water erosions of their soils.

Jeffrey R. Johansen, John Carroll University, johansen@jcu.edu

RECOGNIZING CYANOBACTERIAL DIVERSITY IN THE MODERN ERA

Cyanobacteria, the most morphologically diverse prokaryotic lineage, has a long history of classification based on morphology and ecology. Numbers of taxa have waxed and waned over the years based on varying taxonomic concepts. However, we are now twenty years in to a period of intensive taxonomic activity in which many species, genera, families and orders are being described or recognized. This advance has occurred do to the advent of easily obtainable DNA sequence data, which has demonstrated that the cyanobacteria are deeply diverse based upon molecular criteria. The 16S rRNA gene has been used extensively for recognition of genera, and analysis of the associated 16S-23S ITS region has been especially effective at discrimination of cryptic and pseudocryptic species. More than 60 new genera have been described in the last 20 years, and we anticipate that this is just a start. However, difficulties currently face the cyanobacterial taxonomist. How do we integrate the 150 years of taxonomic progress into the new classification system? How will the increasing availability of whole genome sequencing impact the polyphasic approach to taxonomy? Will the ICN and ICNP codes be modified to accommodate description of taxa based on sequence data alone? Are we facing a future in which extensive revision and validation of nomenclaturally invalid taxa will be required? These questions likely face phycologists studying eukaryotic microalgae as well, and solving these issues for cyanobacteria will contribute to the general conversation on taxonomy of all algal phyla.

Susan B. Wilde, University of Georgia, swilde@uga.edu; Phillips, T., orcaluvr@uga.edu, Gerrin, W., wgerrin@uga.edu; Neidermeyer, T., Martin-Luther-Universität Halle-Wittenberg, timo.niederemeyer@pharmazie.uni-halle.de; Breinlinger, S., Martin-Luther-Universität Halle-Wittenberg, Martin-Luther-Universität Halle-Wittenberg , s.breinlinger@posteo.de

INVESTIGATING THE TOXIC INVASION OF HYDRILLA/AETOKTHONOS HYDRILLICOLA IN FRESHWATER FOODWEBS

Cyanobacterial harmful algal blooms are common in inland freshwater ecosystems, and while most of the attention has focused on the risks of toxic planktonic cyanobacteria, epiphytic and benthic cyanoHABs also present a threat to wildlife and human health. Vacuolar myelinopathy (VM) has been documented in Bald eagles across the southeastern United States since its discovery in DeGray Lake, Arkansas in 1994. We have field and laboratory evidence that VM is induced by aetokthonotoxin (AETX), a novel neurotoxin produced by the cyanobacterium *Aetokthonos hydrillicola* (*A. hydrillicola*) growing on highly invasive aquatic plants. We have completed the identification, of the compound as a lipid-soluble pentabrominated bisindole alkaloid. AETX is ingested directly by plant eating aquatic species (coots, waterfowl, snails, tadpoles, grass carp, sunfish) and indirectly through food chain transfer via consumption of toxic prey (eagles, owl, hawks, salamander, water snakes, bass). We recently quantified AETX in wild prey that people consume --coot tissues and filets of five fish species from Clark's Hill/J. Strom Thurmond Reservoir. We have documented hydrilla/*A. hydrillicola* and the novel AETX in 25 locations including large hydropower/water supply reservoirs, county water source reservoirs, suburban recreational lakes, and farm ponds. Epiphytic cyanobacteria present a novel risk of unknown capacity to

impact species and community dynamics through the introduction of novel toxins with potentially far-reaching effects across taxa and trophic levels within aquatic communities.

Co-Editor Symposium (in order of presentation)

Melinda A. Coleman, New South Wales Department of Primary Industries, Australia.
Melinda.coleman@dpi.nsw.gov.au

FUTURE-PROOFING KELP FORESTS

Climate change is causing widespread habitat deterioration and destruction and presents one of the biggest threats to species and global ecological function. Underwater kelp forests underpin fisheries and vast economic values on temperate coasts but are declining due to climate change. There is an urgent need to develop novel and proactive solutions to combat, reverse and prevent this habitat loss. I will discuss how genomic data is providing the evidence we need to assess vulnerability of kelp forests and “future-proof” management under climate change.

Sonya Dyhrman, Department of Earth and Environmental Science, Columbia University; Lamont-Doherty Earth Observatory, Columbia University, sdyhrman@ldeo.columbia.edu

ALGAL PARTNERSHIPS, INTERACTIONS AND INTERDEPENDENCIES: TRACKING PATTERNS AND THEIR SENSITIVITY TO A CHANGING ENVIRONMENT

Events of the last year have made me think about community resilience in new ways, both for human society and for algal communities and the ecosystems they support. While we have known for many years that there are myriad complex interactions ranging from allelopathy to symbiosis influencing the physiological ecology of eukaryotic algae and cyanobacteria, studying the details of these interactions has posed many methodological challenges. New cultured isolates of key symbioses, larger databases, novel bioinformatics methods to support ‘omic studies, and new abilities to track metabolites, among other exciting approaches, are now expanding our ability to resolve algal partnerships, interactions and interdependencies in new ways. For example, we now know that heterotrophic epibionts can influence rates of nitrogen fixation in the genus *Trichodesmium* in addition to physiochemical variables like light and temperature. This complicates modelling efforts focused on predicting nitrogen fixation rates now and in the future. Which of these small-scale interactions are the most critical for driving larger ecosystem processes? Are these processes sensitive to climate-driven changes in aquatic systems and potential shifts in the distribution of community members? Moving beyond previous methodological constraints, I am excited to see our knowledge about algal partnerships, interactions and interdependencies expand so that we can more fully resolve the rules which govern how individual species or groups of algae interact with each other, associated heterotrophs, and their chemical environment. Collectively, this knowledge will better resolve ecosystem resiliency on a changing planet.

Thomas Mock, University of East Anglia, t.mock@uea.ac.uk

FROM POLE TO POLE – DIVERSITY AND ADAPTIVE EVOLUTION OF EUKARYOTIC PHYTOPLANKTON TO CONDITIONS OF GLOBAL CHANGE

Eukaryotic phytoplankton are main primary producers in nutrient rich and low temperature oceans underpinning some of the most productive food webs on Earth. Yet, evolutionary mechanisms and their environmental drivers critical for shaping their diversity and adaptive evolution remain enigmatic. This presentation will provide insights into drivers of spatial scaling of changes in microalgal diversity and their gene activity. Hence, I will discuss which physico-chemical differences between polar and non-polar surface oceans have an influence not only on changes in microalgal diversity but also their gene-expression activity from pole to pole. Furthermore, my presentation will provide insights into the adaptive genome evolution of a model microalgal species as revealed by long-term evolution experiments under conditions of global change.

Andrew E. Allen, Scripps Institution of Oceanography, University of California, San Diego & J. Craig Venter Institute, aallen@ucsd.edu

EVOLUTION AND METABOLIC CONFIGURATION OF NITROGEN AND IRON METABOLISM IN MARINE DIATOMS

Diatoms dominate phytoplankton communities by outcompeting other groups for nitrate, yet little is known about the mechanisms underpinning this ability. We have recently arrived at a systems-level understanding of how nitrogen is assimilated and distributed within the model diatom *P. tricornutum*. We propose that the unique configuration and high degree of metabolic integration between the major energy organelles allows diatoms to efficiently respond to changing nitrogen status, conferring an ecological advantage over other phytoplankton taxa. We have also recently obtained significant insights into molecular mechanisms that control iron metabolism in diatoms. For example, we have shown that diatoms utilize phytoferritin to access inorganic iron with remarkable efficiency, but this process is contingent on carbonate ion concentration. As ocean acidification reduces carbonate concentration, inorganic iron uptake may be discouraged in favor of carbonate-independent uptake. We described components of a reduction-dependent siderophore acquisition pathway that is not sensitive to carbonate availability but relies on a bacterial derived receptor protein and provides a viable alternative to inorganic iron uptake under certain conditions. This form of iron uptake entails close association between diatoms and siderophore producing organisms during low iron conditions. While recent studies have confirmed endocytosis to be required for acquisition of both inorganic and organic iron, proteins downstream of these cell surface associated uptake systems have been unknown. We propose key elements of a new model connecting cell surface iron binding, internalization and intracellular trafficking, followed by offloading to the chloroplast in *Phaeodactylum tricornutum*.

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ARE RED ALGAL PARASITES ACTUALLY TRANSMISSIBLE CANCERS?

Transmissible cancers are rare evolutionary events, where cells from an individual escape normal cell division controls but can also be infective to conspecifics. Most famously known from Tasmanian Devils, transmissible cancers have also evolved in bivalves and canines. Red algal parasites share many of the same characteristics of transmissible cancers in animals, but unlike their analogs in animals, they have independently evolved from different species over 100 times. Red algal parasites are small, host-specific and non-photosynthetic, rendering them reliant upon their photosynthetic red algal hosts for carbon and other metabolites. Using both morphological and molecular analyses, we examined growth and gene expression of the red algal parasite *Choreocolax polysiphoniae* over its lifecycle infecting *Vertebrata lanosa*. Morphological analyses confirmed the simultaneous development of internal and external parasite

structures and the creation of a nutrient gradient from uninfected host to parasite that prevents localized cell death, allowing *C. polysiphoniae* to reach reproductive maturity. Single-cell transcriptomics demonstrate that photosynthetic and carbohydrate metabolism are downregulated in infected *V. lanosa*, a crucial step in the establishment of a nutrient gradient. Amino acid and nucleotide biosynthesis, fatty acid metabolism, and membrane transporters are significantly upregulated throughout *C. polysiphoniae* development. Similarities in growth and metabolic requirements between *C. polysiphoniae* and animal transmissible cancers will be discussed.

IDEA Symposium (in order of presentation)

Ligia Collado-Vides, Florida International University, Miami, Florida, colladol@fiu.edu

REFLECTIONS ON DIVERSITY AND INCLUSIVENESS: A PERSPECTIVE FROM A PHYCOLOGIST

This talk will address some personal, group, and institutional experiences and perspectives that have influenced my career as a phycologist, from a diversity and inclusiveness point of views. I will offer examples on how experiences forced me to overcome challenges that were limiting and eventually strengthen my career. Finally, I will address some of the individual, collective and institutional efforts that are increasing the diversity in my lab, how that diversity is helping to bring awareness of the importance to recognize the others as we, and not as them. Just like red, brown and green algae, are representatives of a collective of forms and different evolutionary process that enrich diversity and ecosystem functioning; we as phycologists can increase our social impact by allowing ourselves to recognize the value and empowerment of diversity in our Phycological Society of America.

Camille Gaynus, University of Pennsylvania, Philadelphia, Pennsylvania, cgaynus@gmail.com

SCIENCE WILL ONLY BENEFIT FROM DIVERSITY

Camille Gaynus has prepared a talk that will take a deep dive at the work needed to diversify marine science. She will discuss her unique path as a Black marine scientist; the triumphs and difficulties. As a member of the Black in Marine Science leadership team and a co-owner of A WOC Space, she will explain how these organizations are creating the space to nurture Black marine scientist and changing the narrative around who is a scientist.

Austin Shelton, University of Guam, USA, austin.j.shelton@gmail.com

ISLANDERS IN MARINE SCIENCE AND SUSTAINABILITY

Traditional navigators remind the world that islands are distant but not alone. Oceans connected them for millenia. Over many generations, islanders have interacted in the immense biodiversity of their waters, including coral reefs, seagrass beds, rich pelagic fisheries, and more. The diverse perspectives of islanders and their ways of knowing belong in marine sciences. This presentation will discuss how islanders are creating opportunities and pathways in marine science for their students to understand and care for their natural resources.

Lang Lecture

Stacy Krueger-Hadfeld, University of Alabama, Birmingham, sakh@uab.edu

WHAT'S PLOIDY GOT TO DO WITH IT?

Sex is a crucial process that has molecular, genetic, cellular, organismal, and population-level consequences for eukaryotic evolutionary ecology. It is inextricably linked to the cycling of haploid and diploid stages and is responsible for generating spectacular life cycle diversity. Recent evolutionary models have established conditions under which sex will evolve, but still ignore the problem of why haploid and diploid stages are so diverse in form, function, and duration. A critical missing piece is establishing how selection in general, and ecology in particular, influence the evolution of life cycle diversity. Likewise, few quantitative studies of reproductive system variation exist outside diploid taxa, yet, the reproductive system not only controls, but is in turn controlled by standing genetic variability, thereby shaping evolutionary trajectories. Two major challenges exist for understanding the diversity of sex: (i) ***reconciling genetic (evolutionary) and ecological predictions of ploidy alternation in natural populations*** and (ii) ***quantitatively assessing the consequences of a prolonged haploid stage on reproductive systems***. I will discuss the progress we have made at the convergence of life cycles and reproductive systems, including insights made possible by the Lang Fellowship.

Bold Award Session (in order of presentation)

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PROTIST COMMUNITY STRUCTURE ACROSS INDONESIA AND ITS FUTURE IMPLICATIONS FOR MARINE PROTECTED AREA DESIGN

The Coral Triangle encompasses some of the most biodiverse ecosystems in the world, which are vital economic and food resources for countries across this region. Small-scale fisheries that rely on these reefs are particularly important in Indonesia, which puts these ecosystems at risk for overexploitation. In order to minimize the effects of harmful fishing practices, marine protected areas (MPAs) and fisheries management strategies have been implemented across this region with the goals of biodiversity conservation and promotion of sustainable fisheries. While these strategies have clear benefits for metazoan groups, the effects of fishing pressure and management on microbial communities at the base of the food web is not well studied. Our data suggest that fishing pressure and management play a minimal role in shaping protist community structure across Indonesia, further supported by a significant shift in protist diversity between the two most remote regions in the east. These two factors suggest that protist community structure across Indonesia is instead primarily driven by abiotic forces such as surface current patterns throughout the region. The structuring of these communities by surface currents could make these data useful in filling gaps left by traditional larval ecology methods of connectivity assessment which play a major role in design of MPAs across this region. While not a substitute for current methods

of assessing connectivity, protist community data could provide an additional layer of information to help improve future MPA design.

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THE ROLE OF HOST-ASSOCIATED MICROBIOMES IN PHOTOSYNTHETIC FUNCTIONING WITHIN THE HABITAT FORMING MACROALGAE, *HORMOSIRA BANKSII*

Emerging evidence from various organisms shows that microbiomes are crucial in the functioning of their eukaryotic host, resulting in the novel “holobionts” concept. This concept argues that to understand the functioning of biological systems, the relationships between hosts and their microbes must be studied holistically. There is an expansive body of evidence that marine communities are under threat by a suite of stressors with coastal ecosystems bearing the brunt of these. Although there is a broad understanding of what drives community productivity in these systems, the role host-microbiome interactions have in mediating ecosystem productivity in coastal systems remains poorly understood. This work was aimed at understanding the role of microbial taxa in host photosynthetic functioning within the intertidal alga *Hormosira banksii*. Individual alga’s (N = 110) microbiomes were disrupted with either antibiotics, bacteria isolated from the surface microbiome of the alga or a combination of both. Individuals whose microbiomes were disrupted showed significant decreases in photosynthetic efficiency. This effect was strongest when the microbiome was disrupted and then followed by inoculation with conditionally rare microbial taxa. All treatments (N=7), except disruption followed by inoculation, recovered within the experimental time frame (14 days). Our work shows that microbial taxa are fundamentally important to the functioning of their host, with potential impacts on how they structure the wider intertidal community.

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PREDICTIVE MODELLING ASSESSMENT OF SUITABLE HABITATS FOR STARRY STONEWORT (*NITELLOPSIS OBTUSA*) IN THE UPPER MIDWEST AND NORTHEAST (USA)

Nitellopsis obtusa was first reported in the St. Lawrence River in 1974 and has since then spread through human-assisted activity to Michigan and five other U.S. states. This invasive macroalga is a nuisance for native plants, animals, and recreational activities. Because eradication of invasive species is more difficult after establishment, early detection plans are an important tool in preventing and slowing their spread. Macro-scale data analyses have improved our ability to predict changes in freshwater ecosystems and are important to assess and control invasive species. Random forest, boosted regression and maxent were used to analyze occurrence records of *N. obtusa* from the C. V. Starr Virtual Herbarium (NY) and the Global Biodiversity Information Facility (GBIF), coupled with landscape and water quality parameters from the lake multiscale geospatial and temporal database (LAGOS), and climate variables from Worldclim to determine lakes across 17 U.S. states that could be suitable for invasion. Our analyses found

several environmental parameters including urbanized areas, bicarbonate concentrations and road density around lakes were important for predicting *N. obtusa* occurrence and furthering its spread in Michigan, Minnesota, New York, Ohio, and Wisconsin.

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ON THE DIVERSITY OF *DICTYOTA* J.V. LAMOUREUX IN BRAZIL

Dictyota is a phaeophycean genus found along tropical and temperate coasts worldwide, of which 14 species have their occurrence recognized in Flora do Brasil 2020, the Brazilian catalogue of algae, plants and fungi. To confirm them, most of the Brazilian coastline and its oceanic archipelagos were sampled from 2010 to 2017. The genomic material of selected specimens was extracted and amplicons of *psbA* were obtained via PCR, and then, sequenced. From the species of *D. dichotoma* complex cited to Brazil, only one was confirmed and it is part of *D. ceylanica* complex. Three species from *D. ciliolata*-*D. crenulata* complex were confirmed to Brazil, of which one is new occurrence to South Atlantic. A new species, part of *D. rigida* complex, was found broadly distributed in the northeastern region of Brazil. *Dictyota guineensis*, *D. pinnatifida* and *D. friabilis* were considered rare species and they were not found during sampling expeditions, but their occurrences were confirmed based on herbaria material. The presence of *D. bartayresiana* in Brazil could not be confirmed. From the species which type-locality is in Brazil, samples of *D. mertensii* belong to two unrelated clades, *D. dolabellana* was considered a cryptogenic species with unresolved systematic status, while the taxonomical status *D. cuneata* has been solved. As expected, differences on the catalogue and species occurring in Brazil were noted, *i.e.*, *D. implexa*, *D. spiralis*, *D. caribaea* and *D. crenulata* were not found and herbaria specimens were re-determined. These names should be removed from Flora do Brasil 2020.

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MICROBIOTA-MACROALGAL RELATIONSHIPS IN THE HAWAIIAN ARCHIPELAGO ARE INFLUENCED BY PHYLA AND MORPHOLOGICAL COMPLEXITY

Advances in high-throughput sequencing have allowed for microbiome studies on natural and artificial microbial communities permitting a deeper understanding of how microbes might be influencing host and biome health. Our understanding of the diversity and function of microbiota and their interactions with marine macroalgae is in its infancy. This project aims to understand and provide baseline data on the microbial communities of macroalgal species at varying depths in the Hawaiian Archipelago. Representative species from three macroalgal phyla were collected in triplicate from 'Ewa Beach, O'ahu, Hawaii, at low tide in May 2019. A second collection of dominant macroalgal species from each phylum was completed in July/August 2019 at Manawai. In addition to depth and location of each alga collected, each species was classified for calcification levels, morphological complexity, and whether or not it was a native or invasive/cryptogenic species. The SSU rRNA gene was amplified using universal bacterial primers for high-throughput sequencing to elucidate the core and variable algal microbiome. Variation in microbial-macroalgal associations was influenced by host phylum and morphological complexity. This study represents a great advance in our understanding of algal associated microbiota and the influence of host on microbial community composition. In particular, it provides further insight on the overall

ecosystem function and health of the macroalgal microbiota across the photic zone, and predicts the overarching impact of invasive macroalgae invisible to the naked eye.

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LABORATORY INDUCED EVOLUTION OF THERMAL TOLERANCE DIFFERS IN GENOTYPES OF THE SYMBIOTIC DINOFLAGELLATE *BREVIOLUM MINUTUM*

Ocean warming is causing increased stress to corals and their symbiotic dinoflagellates, resulting in recurring mass coral bleaching events. It is unknown if different symbiont species may adapt to elevated temperature and hence provide an avenue for corals to adapt to climate change. Using an experimental ratchet design, we show that genotypes of the symbiotic dinoflagellate *Breviolum minutum* differed in upper thermal tolerance limits, with three genotypes able to grow at 31°C and one at 32°C. After two years of growth at elevated temperature, two thermally selected (TS) genotypes (G1 and G2) exhibited functional trait adaptation during a reciprocal thermal transplant, and individual populations within these genotypes displayed distinct physiological profiles compared to wild type (WT) populations. Specifically, TS symbionts had significantly higher growth, photochemical efficiency, and carbon fixation at elevated temperatures than WT symbionts. At 32°C, G1 TS symbionts had lower gross photoinhibition and lower photo-repair and maintained similar net photoinhibition compared to WT symbionts at 28°C. Conversely, G2 TS symbionts had higher rates of gross and net photoinhibition and photorepair. Contrary to previous studies, all thermally selected populations produced greater reactive oxygen species relative to WT symbionts at their native temperatures. These findings confirm that genotypes can adapt to high temperature through a range of physiological pathways and highlight the potential for functional trait adaptation in these ecologically important dinoflagellates.

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PHOTOPROTECTION AS A POSSIBLE TARGET OF THE EX1-DEPENDENT ¹O₂ STRESS SIGNALING IN *CHLAMYDOMONAS REINHARDTII*

Light energy is the motive force of photosynthesis in plants and algae. The amount of light received by these organisms is often higher than their photosynthetic capacity. However, they have evolved sensors and signaling pathways that trigger protective systems to manage the excess energy. When this fails, destructive reactive oxygen species (ROS), including singlet oxygen (¹O₂), are formed leading to photoinhibition and photo-oxidative damage. Light-harvesting complexes (LHC) fine tune the amount of absorbed light energy. They both transmit light energy for photosynthesis and dissipate excess light as heat. In the green alga, *Chlamydomonas reinhardtii* (*Cr*), LHC stress-related (LHCSR) genes are upregulated to assist in non-photochemical quenching. In plants, ¹O₂ signaling is controlled by two distinct pathways triggered from photosystem (PS) II cores or the grana margins. In the latter, the protein Executer 1 (EX1), plays the major signaling role. We identified an ortholog of EX1 in *Cr*. Our results show that in the *Cr ex1* mutant compared to the wild type (WT), and in response to increasing concentrations of ¹O₂, the LHCSR1 is not detectable. This contrasts with the expression of LHCSR1 in response to high light (HL) and in comparison to the increase in LHCSR3 accumulation. This suggests that ¹O₂ signaling could be transmitted via two separate pathways in *Cr*. We conclude that the LHCSR1 might be a target of EX1-dependent ¹O₂ signaling.

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MICROBIOME CHANGES IN A STRANDING SIMULATION OF THE HOLOPELAGIC MACROALGAE *SARGASSUM NATANS* AND *SARGASSUM FLUITANS*

Since 2011, massive amounts of holopelagic *Sargassum* have been stranding on the Caribbean, Brazilian, and African shorelines potentially introducing exogenous microorganisms, representing an unexplored threat to these coastal ecosystems. In this study we described the microbiome associated with *Sargassum* before stranding, and how the microbiome changes during a stranding simulation. We collected healthy specimens of *Sargassum fluitans* III and *S. natans* VIII in the North Equatorial Recirculation Region, and characterized their microbiomes at 0 hr (right after sampling *Sargassum* from the seawater), after 24, and 48 hours of a simulated stranding experiment under *in situ* environmental conditions (N=18). Amplicon sequencing of 16S rRNA gene V4 hypervariable regions resulted in a total of 2005 ASVs, of which more than 600 were shared between *Sargassum* species. Only 30 ASVs were consistently identified throughout the stranding simulation. The stranding simulation caused significant changes in the *Sargassum* microbiome: in the first 24 hrs Alteromonadales and Vibrionales drastically increased in abundance, outweighing the most abundant taxa present at time zero. Vibrionales reached up to 91% in relative abundance of the microbial community. These findings suggest that after stranding, the *Sargassum* microbiome undergoes dysbiosis and its biomass becomes a fertile ground for potentially pathogenic bacteria such as *Vibrio*, presenting a potential threat to coastal areas where *Sargassum* strands.

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HOW DOES YOUR COCCOLITHOPHORE GROW? EXCRETION AND UTILISATION OF DOM AND DON BY CULTURED *EMILIANA HUXLEYI*

The DOM from phytoplankton primary production is important in supporting bacterial growth and production. Diatoms and coccolithophores are capable of utilising DOM, DON and DOP as nutrient sources during periods of nutrient limitation. Dinoflagellates and coccolithophores utilise bacteria for growth under nutrient limitation (mixotrophy). As phytoplankton are leaky these dynamics will be reflected in the DOM pool and its composition. Traditional methods of DOM determination based on oxidation and combustion of preserved samples provides headline figures for the DOM pool but do not reveal the actual dynamics. In our research we applied Size Exclusion Chromatography (SEC)-Liquid Chromatography(LC)-Organic Carbon Detection (OCD)- Organic Nitrogen Detection(OND) (Huber, Balz et al. 2010) to look at evolution of the DOM and DON pool that develops in exponentially growing cultures of *E. huxleyi* under luxury uptake conditions. During exponential growth *E.huxleyi* excreted up to 70% of the fixed carbon as DOC and there was only a net production of DOM in 5 out of 9 days. Up to 45% of fixed inorganic nitrogen was released as DON while previous workers showed DOP release of ~29%. These results show that *E. huxleyi* utilises its own excreted DOM pool to enhance its growth during luxury uptake and discuss these results in terms of algal nutrition, global success and our understanding of nutrient (re)cycling in marine systems.

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GOING WITH THE FLOW: PHYTOPLANKTON MORTALITY AND COMMUNITY DYNAMICS

Phytoplankton communities consist of a dynamic assemblage of organisms, existing in an ever-changing environment. Both abiotic (light, temperature, nutrients) and biotic factors (grazing, species interactions) have been considered to regulate phytoplankton growth, but other factors may be at play that we know much less about – loss processes and cell mortality. Traditionally, losses are thought to be due to sedimentation or grazing, with little consideration of environmental factors and their influence on cell mortality. Knowing that phytoplankton communities undergo changes in composition throughout the seasons, we studied the phytoplankton community and cell death in a small urban pond in southeastern Wisconsin for three years. Using flow cytometry, phytoplankton groups were resolved using red and orange fluorescence, and cell mortality was determined using the mortal stain, Sytox Green®. Of eleven populations tracked, five were intermittent, ranging from undetectable to over 200 cells/L, while six populations were persistent and stable with populations in the range of 200-1,200 cells/L. The proportion of dead cells generally varied with abundance, from < 10% in dominant groups to almost all cells dead in rare species at their lowest populations. Abundance and cell death poorly correlated with most abiotic factors but some populations exhibited correlations with others, suggesting possible biotic interactions (e.g. allelopathy) may be driving community dynamics.

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AN ANALYTICAL APPROACH TO MONITORING SURFACE CHEMISTRY OF SMALL-SCALE *SKELETONEMA MARINOI* ALGAL BLOOMS

The changing biogeochemistry of algal systems throughout their bloom alters both the air-seawater interface, giving rise to dynamic changes in sea spray aerosol composition. To understand the temporal change at the sea surface and subsequent sea spray aerosol production, we investigate the marine-relevant diatom *Skeletonema marinoi*. We explore in situ the temporal surface properties of small-scale *S. marinoi* monocultures by utilizing the surface techniques of Brewster angle microscopy (BAM) imaging, vibrational sum frequency generation (SFG) spectroscopy, and infrared reflection absorption spectroscopy (IRRAS). BAM images show morphological structural changes and heterogeneity in the interfacial films, revealing an ~5 nm thick surface region in the late stages of the bloom. Our surface-specific SFG spectroscopy results show significant diminishing in surface water molecules, consistent with organic algal species partitioning to the surface. IRRAS confirms the presence of organic molecules at the surface as we observe increasing intensity of vibrational alkyl modes and the appearance of a proteinaceous amide band in the late stage of the bloom. By coupling surface imaging and vibrational spectroscopies to complex, time-evolving, marine systems, we begin to unravel the complex role of algae as the “ocean’s elevator” which acts to transfer biogenics between bulk seawater and the air-seawater interface.

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THE CLONING AND ENGINEERING OF DIATOM MITOCHONDRIAL GENOMES IN YEAST AND BACTERIA

Algae are attractive organisms for biotechnology applications, such as the production of biofuels and other high-value compounds due to their genetic diversity and metabolic processes. As new species are domesticated, rapid nuclear and organelle genome engineering methods need to be developed and optimized. To that end, the mitochondrial genomes of *Thalassiosira pseudonana* and *Phaeodactylum tricornutum* were cloned into yeast and transformed into bacteria for analysis. No significant host burden between mitochondrial harbouring yeast or bacteria and their respective empty vector controls was observed by growth rate analysis. However, plasmid stability assays found that over 60 generations, 17% of *T. pseudonana* mitochondrial genomes were mutated compared to 0% for *P. tricornutum*. Consequently, analyses of genome integrity will be required following propagation in bacteria prior to use in downstream applications.

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EVOLUTION OF SPAWNING CAULIFLOWER CORALS CORRESPOND TO THE SPECIATION OF MUTUALISTIC MICROALGAE

More than just discerning elementary taxonomic units in biology, the resolution of species provides insight into how each originated through ecological, biogeographic, and natural selection processes. Thus, species recognition is critical for deducing fundamental processes in ecology and evolution. The application of molecular genetics has reinvigorated and improved how species are defined and investigated scientifically, especially for morphologically cryptic micro-organisms such as mutualistic dinoflagellates (i.e. Symbiodiniaceae). Here we show how species recognition improves understanding of the ecology and evolution of mutualisms between reef-building corals and dinoflagellates. A combination of genetic, ecological, and morphological evidence defines two sibling species of *Cladocopium* (formerly *Symbiodinium* Clade C) each exhibiting genetic connectivity across the tropical and sub-tropical Pacific Ocean. They are specific only to corals in the genus *Pocillopora*. *Cladocopium latusorum* sp. nov. is common to *P. grandis* (= *P. eydouxi*) and *P. meandrina* while *C. pacificum* sp. nov. associates with *P. verrucosa*. Both symbiont species form mutualisms with the brooding species *P. acuta* and *P. damicornis*. Molecular clock estimates of their origination correspond to a time when their hosts were also diversifying and gives further evidence for adaptive radiation among *Cladocopium* during the late Pliocene and early Pleistocene epochs when the Earth underwent cycles of precipitous cooling and warming. The long temporal and spatial maintenance of high host fidelity, as well as genetic connectivity across thousands of kilometers, indicates that distinct ecological attributes and close evolutionary histories will restrain the adaptive responses of corals and their specialized symbionts to rapid climate warming.

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THREE SEX PHENOTYPES IN A HAPLOID ALGAL SPECIES GIVE INSIGHTS INTO THE EVOLUTIONARY TRANSITION TO A SELF-COMPATIBLE MATING SYSTEM

Mating systems of haploid species such as fungi, algae, and bryophytes are either heterothallic (self-incompatible and unisexual) with two sex phenotypes (male or female) of clones or homothallic (self-compatible and bisexual) with only a single sex phenotype producing zygotes within a clone. The anisogamous volvocine green alga *Pleodorina starrii* is a haploid species previously reported to have a heterothallic mating system. Here, we found that two additional culture strains originating from the same water system of *P. starrii* were taxonomically identified as *P. starrii* and produced male and female gametes and zygotes within a clone (bisexual). Sequences of rapidly evolving plastid genome regions were identical between the bisexual and unisexual (male or female) *P. starrii* strains. Intercrossings between the bisexual and unisexual strains demonstrated normal hypozygotes and high survivability of F1 strains. Thus, these strains belong to the same biological species. *P. starrii* has a new haploid mating system that is unique in having three sex phenotypes; namely, male, female, and bisexual. Genetic analyses suggested the existence of autosomal “bisexual factor” locus independent of volvocine male and female determining regions. The present findings increase our understanding of the initial evolutionary step of transition from heterothallism to homothallism in haploid species.

Algae In Education (in order of presentation)

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ALGAE FOUNDATION'S ALGAE TECHNOLOGY EDUCATIONAL CONSORTIUM (ATEC) AND ALGAE ACADEMY (AA) SERVING 100,000 STUDENTS AND BIOECONOMY TRAINEES

The Algae Foundation, dedicated to all forms of algal-based education and training, served over 100,000 students and trainees over the past four years. This is the sixth year of the ATEC initiative to develop algal-based bioeconomy education and training programs for: 1. Two college certificate degrees in Cultivation and Algal Biotechnology; 2. Algae Cultivation Extension Short-courses-ACES (microalgae and seaweeds); 3. Algae Academy (K-12 STEM education); 4. Massive Open Online Courses; 5. Micro Credentialing Digital Badging Program; and 6. Gamification of Algae training and education (recently initiated). The Algae Foundation's efforts has attracted individuals from the United States and 45 countries. The Algae Foundation's DOE award included the development of an algal-based retraining

program entitled, Algae Cultivation Extension Short-courses (ACES) supporting existing aquaculturists in expanding their skill sets and assisting with the development of multitrophic aquaculture enterprises. Lastly, the Algae Academy reached ~ 80,000 students in 49 states, 1 territory and 3 countries in 2020-2021 academic year. This year's current estimate includes the K-12 STEM education effort reaching 36,000 students from all 49 USA states. As a result of Covid-19 on the global educational systems; we have converted our in class curriculum to both blended and asynchronous online instruction. Accomplishments include: Graduation of first college class, May 2018; Formal adoption of ATEC curriculum by 20 colleges with nearly 1700 students involved with the algal-based curriculum; Alga MOOCs #1 and #2 have attracted ~ 20,000 students with a 98 % approval rating; ACES Part 1 – Seaweed and Part two – Microalgae have been taken by 1700 students in 45 countries and national endorsement of the ATEC micro-credentialing digital badging program by the Algae Biomass Organization was secured in July 2019.

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ALGAE ACADEMY: EDUCATING STUDENTS ON THE POWER OF ALGAE

The Algae Academy is a unique K-12 education module that teaches the fundamentals of algae and how they can be applied as a solution for today's global dilemmas. the K-12 educational initiative of the Algae Foundation is a 501C(3) nonprofit organization that sees a future that embraces algae as an essential solution for a sustainable and healthy planet. The Foundation's mission is to create that future through education, mentoring, and public outreach and engagement. The Algae Academy was created in response to the national need for new science curriculum to meet the Next Generation Science Standards (NGSS). Since its inception in 2015, the Algae Academy has reached over 75,000 students nationwide and continues to grow exponentially. The STEM kits are a "drop-in" ready 5-day curriculum that has students cultivate algae, monitor its growth, analyze and interpret data, and make connections as to how algae production has a positive impact on the global environment. The curriculum is tailored by age and has grade level specific NGSS-aligned objectives for elementary, middle, and high school classes. With the pandemic impacting in-person education, the Algae Academy converted all its curriculum to be accessible completely online. Through our work with the Algae Academy, we noticed a need for quality educator trainings and developed the Summer Algae Science Institute (SASI). The SASI offers an immersive algae-centered science workshop for educators to provide the time and resources necessary to fully understand a new science topic and collaborate with other educators to increase their teaching and leadership skills. Our session will present the advancements and accomplishments of both the Academy and SASI for the 2020-2021 academic year. Come and hear how you can help excite the next generation of algae farmers, scientists and business professionals!

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ATEC - ALGAE WORKFORCE TRAINING FOR THE 21ST CENTURY

The US DOE and the Algae Foundation are funding the creation of a two-year certificate in Algae Cultivation at Santa Fe Community College as part of the Algae Technology Educational Consortium (ATEC) project. The first cohort graduated in 2018 and all have either continued their education at university or found jobs with benefits. This hands-on STEM curriculum is teaching necessary skills for

educated technicians involved in sustainable algae production for algae-based products, fuel and foods. Through algal education students learn and develop the skills practical applications of farming and biotechnology. Due to Covid-19 the State of New Mexico closed all colleges and mandated that all classes move to online instruction. The algae program was rapidly moved online and changed so that the lectures are online and the hands-on labs are short 1-2 week classes small enough to minimize the risks associated with large groups. These labs include micro-credentials (digital badges) that are based on industry input on required skills. Digital badges are a fast-track skill-based credential that does not require academic enrollment. Eighteen Algae Cultivation digital badges are approved for delivery with the SFCC Lab courses. These algae farming skill-sets have been validated by the Algae Biomass Organization. SFCC has adopted the Acclaim platform for issuing micro-credentials. Digital badges will be used to provide credentialing for both credit and non-credit pathways. This 5-year project of the Algae Foundation is funded by the DOE's Bioenergy Technologies Office (BETO).

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ALGAE IN THE DARK – USING ALGAE GROWN HETEROTROPHICALLY AS A TEACHING TOOL

This presentation outlines efforts by ATEC, the Algae Technology Education Consortium, to encourage colleges to implement programs that give students experience with growing algae using heterotrophic methods. In this curriculum students use a variety of carbon sources to grow algae to produce food supplements, protein, or specialty chemicals. The effort included input by industry professionals, representatives of the national laboratories, and college faculty to develop lecture outlines and laboratory experiments appropriate for adoption by any college. Results from pilot projects give preliminary indication of the value of the new curriculum.

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REDESIGNING OF UPPER DIVISION UNDERGRADUATE BIOCHEMISTRY LABORATORY COURSE WITH FOCUS ON ALGAL BIOTECHNOLOGY

Algae-based products have gained significant importance for its potential as a next-generation resource to meet the demand of the growing population that possess a great challenge to the food, agricultural and biotech industries. The biological diversity of these photosynthetic organisms provides a wide scope of research that can be efficiently leveraged to generate essential bioproducts derived naturally or by genetic engineering. It is therefore critical to integrate and infuse the knowledge of algal chemistry with emphasis on biotechnology in STEM education and curriculum. This objective was achieved by incorporating and redesigning the upper-division biochemistry laboratory course offered to graduating seniors in the Spring of 2021 at Fresno State. The course was redesigned by adopting modules developed by the Algae Technology Educational Consortium (ATEC). The focus of the course involved the culturing of microalgae and monitoring their growth in photobioreactors followed by the extraction of the lipid, protein, starch, and DNA from the biomass of the harvested algae. This hands-on experiential lab played a critical role in providing knowledge to students about the importance and scope associated with algal chemistry. The use of algae as an alternate resource and its emerging importance to the food, biotech, and agricultural industries was well relayed to the students through these learning modules.

Contributed Sessions (alphabetized by surname)

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INORGANIC NUTRIENT METABOLISM OF DIATOM ENRICHMENTS FROM THE LAURENTIAN GREAT LAKE MICHIGAN: GROWTH THROUGH THE NIGHT PHASE WITH ADEQUATE DAYTIME LIGHT

Diatom enrichments from summer expeditions to offshore Lake Michigan (LM) were acclimated to a 14L:10D light:dark cycle in filtered LM water enriched with NO_3^- , HPO_4^- , and SiO_2 . Large cultures were divided into many vessels for incubation at 14L:10D 5000K LED illumination with frequent sampling, or for 20-1000 $\mu\text{Einst}/\text{m}^2/\text{s}$ light gradient 14L and 14L:10D endpoint sampling. Initial comparison of one day-night cycle in time series and L-L/D light gradient at $\text{CHLa} < 10 \mu\text{g}/\text{L}$ and daytime light $> 150 \mu\text{E}$ showed both dSIL and NO_3^- to be assimilated unbroken through the L-D transition and at night. Sub-saturated uptake was observed as low as $34 \mu\text{E}$ relative to dark. $25 \mu\text{M}$ NH_4^+ completely blocked nitrate uptake and was consumed completely within one day-night cycle. PvsI-based photosynthetic maximum was 13% higher with NH_4^+ but low light response was unaltered. DIC decreased by $> 100 \mu\text{M}$ in one day. In a second project, 4 L/D cycles were followed with $150 \mu\text{E}$ LED daylight in side- vs under-lit batch incubations. Consumption of dSIL across the day-night cycle mirrored an increase in particulate silicate. Total chlorophyll pigment and cellular P increased exponentially but chl slowed perceptibly at night, while cellular P accumulated for one whole L:D cycle after replication and chl synthesis had stopped from Si exhaustion. Over the 45-100h span, pigment, biogenic silica, and particulate P increased with doubling times of 22.9, 22.2, and 23.2 h respectively, while P accumulation was much faster after growth ceased. In shallow stratified waters, night growth can affect nutrient and biomass budgets.

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EXPANDING THE DISTRIBUTION OF *OCULATELLA* (OCULATELLACEAE, CYANOBACTERIA): NEW DISCOVERIES FROM NIGERIA, CHINA AND NEW MEXICO

Oculatella is unique among the cyanobacteria in that members of the genus all share a synapomorphy not present in any other genus, a reddish rhodopsin-containing organelle in the apical cell of the filament that is phototactic. First described in 2012 from Italian caves, the genus has been collected in numerous localities and now contains 13 described species, including species from Chile, California, Utah, Germany, Mexico, Hawaii, Arctic Spitzbergen, and Ukraine. We recently recovered more populations of this interesting genus, including four strains from Nigeria as well as new populations from New Mexico. An additional isolate was obtained from soils in China. These new strains were analyzed morphologically and molecularly (16S rRNA and 16S-123S ITS). The ITS regions were particularly informative, based on secondary structure, percent dissimilarity, and phylogenetic analysis. We determined that the Nigerian material represents three new species to science. The Chinese strain was very surprising, being a 100% match in sequence of both the 16s rRNA gene and the 16S-23S ITS region to *O. dilatavagina*, a species described from desert soils in Mexico. This is the only instance in which any molecularly defined species of Synechococcales has been definitively found on different continents.

Oculatella will likely continue to be discovered, and given its morphological synapomorphy and well studied ribosomal sequences, will be a model genus for uncovering the possible extent of molecular diversity in the simple filamentous forms of cyanobacteria.

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THE GENUS *ACHNANTHES* (BACILLARIOPHYCEAE) AS A MODEL TO INVESTIGATE THE NATURE OF PUTATIVELY OBLIGATE EPIZOIC DIATOMS

After years of increased focus on collecting and describing diatoms from epizoic surfaces, such as manatees and sea turtles, it is becoming evident that some diatom taxa are exclusive to or show a clear preference towards these habitats. As we move beyond the “novelty” of these putatively obligate epizoic (POE) diatoms, we can channel greater effort into understanding the nature of this specialization, which has now been documented in several genetically disparate diatom genera. In this presentation we will discuss the potential for the raphe-bearing pennate diatom genus *Achnanthes* Bory as a model system to investigate questions about diatom host specificity, dispersal, morphological and molecular adaptations, and their interactions with prokaryotic partners unique to the epizoic habitat. The genus *Achnanthes* can be found in a variety of marine benthic habitats and includes several POE taxa. These POE taxa have been found on both manatees and sea turtles from multiple oceans and so far, appear to represent a single radiation from non-POE *Achnanthes* species. The marine *Achnanthes*, including the POE taxa, also appear to grow robustly in laboratory culture, which raises more questions about the nature of their relationship to their animal hosts in the wild.

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PAST CLIMATE-DRIVEN RANGE SHIFTS STRUCTURING INTRASPECIFIC BIODIVERSITY LEVELS OF THE GIANT KELP (*MACROCYSTIS PYRIFERA*) AT GLOBAL SCALES

The paradigm of past climate-driven range shifts structuring intraspecific biodiversity is well established in the marine realm, but lacks replication at broad geographical scales. Studies addressing the potential effects of glacial-interglacial cycles of the Quaternary generally miss biological models exposed to comparable extreme environmental conditions in independent geographic regions. Our objective was to fill in this gap by estimating population genetic diversity and structure of the giant kelp (*Macrocystis pyrifera*) across its entire distributional range (from Alaska to the Southern Ocean) and comparing it with past range shifts and refugial regions of long-term persistence from the Last Glacial Maximum to the present. Using high polymorphic microsatellite markers to genotype 115 populations across the present range and species distribution models to hincast past ranges, we showed that the broad antitropical distribution of *Macrocystis pyrifera* is composed by 6 significantly differentiated genetic populations, for

which present genetic diversity matches expectations derived from predicting past ranges by modelling. Past range shifts structured low latitude refugial regions where genetic relics with higher and unique diversity were found, while post-glacial expansions following ~40% global range contraction explained extensive regions with homogenous reduced diversity. These traits were analogous between hemispheres, largely supporting the role of climate changes on structuring the intraspecific levels of marine biodiversity at global scales.

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HIGHLY TOXIC STRAIN OF *PRYMNESIUM PARVUM* IS AN ALLODIPLOID HYBRID

Prymnesium parvum is a globally distributed, toxic bloom forming Haptophyte alga. Initial genome surveys indicated a high degree of variation in both genome size and ploidy levels across the species. To investigate the drivers of this genome variation, we sequenced and assembled the genomes of 14 strains of *P. parvum* from around the world. Analysis of the highly contiguous long-read assembly (scaffolded with Hi-C sequencing data) of a highly toxic strain isolated from Texas revealed that the strain is an allodiploid hybrid. Evolutionary genomic analysis of the two subgenomes of this Texas strain revealed that the parental lineages are distantly related, with subgenome A clustering with other North American strains and subgenome B grouping closer to strains from Europe. Preliminary analysis of polyketide synthase (PKS) genes potentially involved in toxin production identified 80 PKS genes, the most of any published eukaryotic genome thus far. PKS genes are often arranged in physical clusters and we observed 12 clusters within both subgenomes, while 9 and 3 clusters were uniquely present in subgenome A and B, respectively. These results implicate hybridization as an underappreciated source of evolutionary innovation in toxic algae.

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PROTOPLAST ISOLATION AND REGENERATION FROM THE POTENTIAL ECONOMIC BROWN ALGA *PETALONIA FASCIA* (ECTOCARPALES, PHAEOPHYCEAE)

Petalonia fascia is a widespread brown alga with economic potential due to its use as raw or dried good, and in the biomedical field. Protoplasts are plant cells devoid of cell wall with a wide range of applications in basic and applied research, especially in crop improvement, and as a seedstock in seaweeds. Protoplasts have been previously isolated from *P. fascia*; however, their regeneration ability, an important prerequisite for protoplast applications, has not been explored. In this work, we report the protoplast isolation and successful regeneration from *Petalonia fascia* using the commercially available enzymes. Protoplast production was enhanced under increased osmolarity, with chelation pre-treatment, and short incubation time. Our protocol produced more than 14 times the number of protoplasts obtained using previously reported protocols. After 4 weeks in culture, protoplasts developed into prostrate, discoid, and mixed thallus, as well as cell clumps. Blades mostly emerged from prostrate thalli. Antibiotics were not crucial for improving protoplast regeneration, and temperature did not affect the development of the morphological forms and blades. Our results show that high yields of protoplasts (10^7 protoplasts g^{-1} FW) with good regeneration ability can be obtained from *P. fascia* using a simple mixture of commercial enzymes. This represents the first report of successful protoplast regeneration in *P. fascia*.

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KINETIC AND THERMODYNAMICS INVESTIGATION OF THE PYROLYSIS OF FRESHWATER MACROALGAE, *SPIROGYRA CRASA*

The demand for renewable energy resources has been increased in the last two decades. There are several reasons behind the production of clean energy, like greenhouse gases, cost of the fossil fuels and its diminishing nature. Algae biomass is one of the renewable bioenergy source with many advantages in terms of food and bioenergy. Here we analyzed the conversion of biomass of freshwater macroalgae *Spirogyra crasa* into biofuel products through pyrolysis. This biomass conversion into bioenergy and other useful contents through pyrolysis helps in determination of the kinetic triplet, master plot and thermodynamics parameters. The thermogravimetric data provided four unique stages of pyrolysis. The activation energy calculated through the four iso-conversional methods for these four stages are in the range of 120 - 217 kJ mol⁻¹. The fitting of the kinetic data into master plot showed the reaction of mechanism of each individual pyrolysis stage. The thermodynamic parameters showed the favorable nature of *Spirogyra* biomass as a biofuel source and a possible choice of renewable energy in the future.

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UNRAVELLING FUcoxANTHIN BIOSYNTHESIS IN DIATOMS

Fucoxanthin is the main light-harvesting carotenoid in diatoms. It also plays a role in photoprotection and contributes to the overall brownish appearance of diatoms and kelps. While several pathways for fucoxanthin biosynthesis have been proposed, the actual process has remained elusive. We used a reverse genetics approach in the diatom *Phaeodactylum tricoratum* to isolate *vd12*, *zep1* and *criso5* mutants. These mutants exhibit a green color in contrast to the brown wild type. High-performance liquid chromatography (HPLC) analysis confirmed the change is due to the absence of fucoxanthin and also revealed the appearance of novel intermediate carotenoids. Reduced growth rates under low light conditions, photosynthesis-irradiance curves, and functional absorption cross sections of PSII all suggested less effective light harvesting in these mutants compared to the wild type. These mutants also showed no capacity for non-photochemical quenching (NPQ). Overall, our results reveal the fucoxanthin biosynthesis pathway in *P. tricoratum* and show its required role for high photosynthetic efficiency.

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A COMPARISON OF PHYSIOLOGICAL RESPONSES BETWEEN ATTACHED AND FLOATING POPULATIONS OF BLOOM FORMING *SARGASSUM HORNERI* UNDER NUTRIENT AND LIGHT STRESSES

Sargassum horneri blooms (floating) have been observed in Jeju Island (Korea) and the southwest of the Korean Peninsula, causing serious problems for seaweed and abalone farms as well as for fisheries, tourism and recreational industries. The present study explored the physiological responses of two different *S. horneri* populations (an attached and floating), to environmental stressors of nutrients and light. *Sargassum horneri* populations (floating and attached) were cultivated at two different nutrient levels (HN: 50 μM of nitrogen and 5 μM of phosphorus and LN: 5 μM of nitrogen and 0.5 μM of phosphorus) and three photosynthetically active radiation (PAR) levels (H-PAR: 250 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$; M-PAR: 150 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$ and L-PAR: 50 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$) for 25 days. Relative growth rates (RGR) were significantly lower in the floating population than that in the attached population. All thalli from the floating population died within 20 days. Pigment contents (chlorophyll *a* and *c*, and carotenoids) were significantly higher at HN than at LN, and decreased as PAR increased for both populations. In the attached population, photosynthetic rate, tissue nitrogen, and carbon and nitrogen removal were also significantly higher at HN than at LN. These results suggest that the floating population grow slowly, or even stop growing after a long journey from their origin. Low nutrient and higher PAR may diminish the impacts of *Sargassum* blooms.

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PHOTOSYNTHETIC PROTISTAN DIVERSITY ALONG A SPATIAL GRADIENT IN THE NEW RIVER, BELIZE

Freshwater habitats provide extensive ecological and economic services. Total microbial biodiversity and species dynamics can aid in determining the availability of resources. Evaluating interactions and correlations between environmental data and metagenomic data (18S rRNA) can provide a more in depth look at species dynamics. We investigated the environmental drivers of protistan diversity in the largest river system in Belize. The New River varies from oligotrophic to hypereutrophic due to nutrient inputs from agricultural and urban (e.g., sewage) areas and the lower portions vary in salinity due to proximity and water exchange with the ocean. We observed differences in abundance of photosynthetic protists along the spatial gradient with chlamydomonads, cryptomonads, diatoms and chrysophytes abundant throughout the river, while prasinophytes, dictyochophytes, porphyridiales, and sphaeroplealeans were also present. Heterotrophic cryptomonads were especially dominant in sites with high conductivity, but also appeared in high abundances in the New River lagoon. Chlamydomonads were present in high abundances in the lagoon compared to areas around the mouth of the river and in Corozal Bay. The high abundance of photosynthetic protists suggests a highly productive system along the New River, Belize.

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CO-CULTURE REMODELS THE TRANSCRIPTOMES OF *PROCHLOROCOCCUS*, *SYNECHOCOCCUS* AND ‘HELPER’ BACTERIUM *ALTEROMONAS* DURING HIGH CO₂ GROWTH

Prochlorococcus and *Synechococcus* depend on heterotrophic bacteria for accomplishing essential functions. The effect of elevated CO₂, however, can break such interaction. We aimed to understand the effects of co-culture on cyanobacteria and the ‘helper’ bacterium *Alteromonas* during high CO₂ growth. We have co-cultured one strain of *Prochlorococcus* (*P. marinus* MIT9312) and two different strains of *Synechococcus* (sp. CC9311 and sp. WH8102) along with the heterotrophic bacterium *Alteromonas* sp. EZ55 at either current (400 ppm) or year 2100 CO₂ concentrations (800 ppm). We have extracted and sequenced RNA from each co-cultured cyanobacterium and EZ55, as well as EZ55 in axenic culture, and performed a differential gene expression RNA analysis using the *edgeR* pipeline. Our data showed that *Prochlorococcus* significantly decreased expression of carbon fixation and high-light inducible (HLI) genes. None of these responses were observed in *Synechococcus* WH8102. The response of *Synechococcus* CC9311 was unclear, but HLI genes were also differentially expressed. In response to high CO₂, EZ55 had 116 and 17 down- and up-regulated genes, respectively. Remarkably, the effect of co-culture resulted in a much higher number of down- and up-regulated genes (579 and 564, respectively). Pathway analysis revealed significantly different expression of ribosomes, bacterial chemotaxis, flagellar assembly, biosynthesis of amino acids, carbon metabolism and glyoxylate metabolism. These results showed that the response of co-culture increased the magnitude of change when compared strictly to high CO₂.

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TEMPERATE KELP FOREST COLLAPSE BY HERBIVORY: A DEMOGRAPHIC STUDY

Kelp forest dominate rocky shores of temperate latitudes, acting as foundation species. Beyond their importance to marine ecosystems, kelp forest also received considerable attention for their decline in many regions around the world. Climate change has been considered one of the main drivers of deforestation, both through abiotic stress and/or through distortion of biotic interactions (e.g., grazing pressure). In NW Spain, golden kelp (*Laminaria ochroleuca*) canopy forests have declined within the limits of Islas Atlánticas Marine National Park (MPA) in recent years. To investigate this decline, a wide-ranging seasonal demographic study was carried out over one year in eight *L. ochroleuca* reefs inside and outside the MPA. We measured 15 morphological traits to assess population structure, and developed an Herbivory Pressure Index (HPI) to assess grazing on kelp blades. Results showed contrasting demographic structures inside and outside the MPA. Outside reefs had kelps covering a wide range of size classes year round while inside reefs were exclusively composed of small, recently recruited kelps in spring-summer. Most kelps showed herbivory marks both outside and inside the MPA. However, the HPI showed that herbivory intensity was low outside the MPA (<25% of the blade edge grazed in most kelps) but very high inside, particularly in winter when all kelps had been degraded to meristemless seaweeds by grazers. As a result, inside populations could be considered as ecologically dead by winter, never reaching the canopy forest stage.

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A COMPARISON OF REPRODUCTIVE TIMING OF *MACROCYSTIS PYRIFERA* AND INVASIVE *SARGASSUM HORNERI* ON CATALINA ISLAND

Observations of terrestrial species shifting their reproductive windows in response to climate change beg the question: Could this occur in aquatic environments too? Giant kelp, *Macrocystis pyrifera*, is the foundational species along much of California's coastlines and islands, but in the aftermath of the 2015-16 El Nino on Catalina Island, it appeared to struggle to regain its dominance in the face of an invasive furoid *Sargassum horneri*. As a part of a master's studying the life history interactions between these two species, I performed monthly population and reproductive surveys, July 2018-August 2019, to address when each species was investing most in biomass, reproductive biomass, reproductive output, and if there was a correlation between biomass and output in these species. The annual *S. horneri* dedicated much of its reproductive effort to a few short months in the spring (Feb.- April) and had a strong relationship between individual size and reproductive output. The perennial *M. pyrifera* peaked in reproductive output in late summer (July-August) and had a weak relationship between an individual's size and reproduction. The observed timing was surprising as kelp is expected to peak in reproduction in the spring when upwelling is at its strongest. These observations on the kelp forests of Catalina could be an artifact of multiple stressful years of El Nino, heatwaves, and invasive species, but they also ask us to think about the assumptions we have about the classic timing & cycling of algal life histories.

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WHOLE GENOME SEQUENCING OF THE KELP GENUS *ALARIA* (PHAEOPHYCEAE) REVEALS FORGOTTEN LINEAGES AND HYBRIDIZATION AMONG SPECIES

Genomic datasets are increasingly applied to the field of phycology, yet emphasis remains on drafting genomes and phylogenetic analysis of organelles. We applied WGS datasets to survey diversity in the kelp genus *Alaria*, compare phylogenetic signal across organellar and nuclear genomes, and test for evolutionary scenarios, including relationships among species and hybridization events. Genomes were sequenced in *Alaria crassifolia*, *A. praelonga*, *A. crispa*, *A. marginata*, and *A. esculenta*, representing over 550 GB of data and over 2.2 billion paired reads. Organellar genomes were *de novo* assembled and aligned, while reads were mapped to reference nuclear scaffolds generated from a gametophyte culture of *A. esculenta*. Genomic datasets retrieved 3814, 4536, and 24,242 Single Nucleotide Polymorphisms (SNPs) for mitochondrial, chloroplast, and nuclear genomes, respectively. An Arctic lineage of *Alaria* was revealed, which we hypothesize represents defunct *A. grandifolia*. The SNP datasets also revealed incongruent topologies across genomic compartments and signals of hybridization among Pacific *A. praelonga*, *A. crispa*, and Arctic *Alaria*, and within lineages of the *A. marginata* complex. Our analysis demonstrates the potential of WGS data to advance our understanding of evolution and diversity beyond amplicon sequencing and the importance of integrating phylogenetic information across genomic compartments, particularly in algal lineages where cryptic diversity and hybridization dynamics are known or suspected.

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BRILLIANT AND BRIGHT: THERE'S MORE TO STRUCTURAL COLOUR IN THE SEAWEEDS THAN MEETS THE EYE

Structural colour is widespread in the marine environment and we perceive it as vivid, saturated colours. In the seaweeds, it is known in six orders of Rhodophyta (reds) two of the Phaeophyceae (browns) seaweeds, and although barely reported in the Chlorophyta (greens) our most recent work indicates that it is widespread in at least one order. Until our studies, the phenomenon of structural colour in seaweeds was largely unexplored. The functional purpose is also largely unknown, although we hypothesise that it is a photoprotective mechanism to mitigate the harmful effects of uv radiation. Production of colour in the seaweeds includes multi-layered structures (reds), iridescent bodies (reds and browns) and microfibril arrays (greens), structures which are also found in the charophytes (Charophyta) and land plants (Magnoliophyta). This raises evolutionary questions for these photosynthetic organisms across the tree of life. The origin of structural colour in the algae is unknown. However, there is a correlation over geological time of the date of the algal groups with structural colour and temperature peaks on Earth. Also, structural colour in the reds is only found in a subclass that split approximately 580-442 million years ago, coinciding with the Cambrian explosion (c. 530-520 million years ago) when a wide range of marine invertebrates were found. I will present an overview of our work, including anatomical and optical studies, reviewing phylogenetic signals, distribution and depth data, microbiomes, and the potential for new materials.

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MOLECULAR AND MORPHOLOGICAL ANALYSES REVEAL NEW TAXA ADDITIONS TO THE TRIBE STREBLOCLADIEAE (RHODOMELACEAE, RHODOPHYTA)

The recent segregation of 12 genera in the tribe Streblocladieae suggests that the taxonomy of some species belonging to *Polysiphonia* sensu lato is updated with the transfer and the proposal of new combinations. Accordingly, six new additions to the tribe Streblocladieae on the basis of morphological and molecular analyses are presented as a consequence of this new segregation. These additions include the description of the new species *Carradoriella platensis* sp. nov., the proposal of the following new combinations *Eutrichosiphonia paniculata* comb. nov., *E. tapinocarpa* comb. nov., and the reinstatement of *Vertebrata curta*, *V. decipiens*, and *V. patersonis*. Additionally, our morphological observations identified additional diagnostic features for two genera of the Streblocladieae. *Carradoriella* has branches with sexual reproductive structures arranged adaxially on branchlets, and the recently described *Eutrichosiphonia* has rhizoids with multicellular digitate haptera. Our study gives insights in regards to the distribution, the diagnostic features for delimiting genera morphologically, and the molecular evolutionary relationships in the Streblocladieae.

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CHARACTERIZING PSEUDOCRYPTIC DIVERSITY IN HAWAIIAN MESOPHOTIC RED BLADES OF THE GENUS *CROISSETTEA*

Recent investigations into the species diversity of expanded red blades in Hawai'i have revealed several pseudocryptic species, highlighting the need for a more thorough taxonomic assessment of these algae. Expanded to lobed red blades preliminarily identified as belonging to the genus *Croissetea* M.J.Wynne were studied morphologically using light microscopy and with molecular analyses using COI-5P (mitochondrial) and *rbcL* (plastidial) markers. *Croissetea* currently includes three species: *C. requienii* (J.Agardh) Kützing (the generitype), *C. australis* (Womersley & R.E.Norris) G.W.Saunders, and *C. tasmanica* (Harvey) G.W.Saunders. The genus has a wide and disjunct distribution in the North Atlantic, Pacific, and Indian Ocean. Four new deep water (mesophotic) Hawaiian *Croissetea* species are described based on our combined molecular and morphological analyses. Each taxon was resolved as a unique genetic lineage with varying distances between relatives. Gross morphology alone was an inadequate discriminator, but the incorporation of distribution patterns and depth ranges facilitated species identifications. The discovery of these four novel mesophotic species highlights pseudocryptic diversity among red blades, and indicates that Hawaiian mesophotic reefs still have a high level of undescribed algal biodiversity, particularly in expanded red blades. The significance of this discovery inspired cultural naming collaborations that referenced mauka (land) to makai (ocean) connections and kupuna (elders) who contributed to the discovery and conservation efforts of the Hawaiian biota.

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TYPE SPECIMEN SEQUENCING AND DNA-BASED SPECIES DELIMITATION RESOLVE THE COSMOPOLITAN *CORALLINA BERTEROI* AND OCCURRENCE OF *C. CHAMBERLAINE* IN CHILE

Molecular studies of *Corallina* systematics have focused primarily on resolving whether or not species belong in the genus and on correctly applying names by sequencing type material. Herein, we provide additional examples of the necessity to sequence type specimens to apply names and of the inadequacy of morpho-anatomical characters to distinguish *Corallina* species. A total of 108 specimens of coralline were collected in Australia, Chile, China, England, Japan, Korea, Mexico, Peru, and USA to perform a multilocus phylogeny and five DNA-based methods (ABGD, GMYC, SPN, bPTP, and BPP) for three molecular markers (COI, *psbA* and *rbcL*) to delimit species in *Corallina*. We show the non-congruence of different markers for resolving the phylogenetic relationships among *Corallina* species. We found that *C. berteroi* (type locality: Chile) is the oldest available name for the *Corallina* species currently known as *C. ferreyrae* (type locality: Peru) and that *C. pinnatifolia* (type locality: California, USA) is also a junior synonym, as is the morpho-anatomically divergent *C. melobesioides* with an extensive base and unigeniculate uprights (type locality: Japan). *C. berteroi* has been confirmed from temperate waters worldwide, including the western and eastern coasts of North America, southwestern Pacific Ocean, Pacific coast of South America, western and eastern Atlantic, East Asia, and the southern Indian Ocean.

In addition, we expand the distribution of *C. chamberlainiae* from the southern Atlantic (Falkland and Tristan da Cunha Islands) and New Zealand, to include central and southern Chile.

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MULTI-OMICS INVESTIGATION OF ABIOTIC STRESS RESPONSES IN ALGAL BIOFUEL STRAINS

Microalgae are of interest for applications in biofuel production due to their ability to convert carbon dioxide into lipids. During outdoor cultivation, algae are exposed to environmental changes, but the underlying mechanisms that control and regulate physiological responses and adaptation to environmental pressures are largely unknown. Systems-level characterization enabled by functional genomics can help identify biochemical pathways that promote stability and productivity of algae. Screening of candidate production strains has identified top performers in lab-based cultivation simulations and outdoor testbed facilities, including *Scenedesmus* sp. NREL 46B-D3 and *Monoraphidium minutum* 26B-AM, which showed robust growth in the summer and winter screens, respectively. We applied our multi-omics pipeline to profile these high potential strains under temperature and salt perturbations. Metabolomics and transcriptomics measurements were taken as a time course on samples grown under environmental perturbations. We observed that osmolytes, such as trehalose, proline and betaine, increase in abundance under salt stress, coinciding with upregulation of genes involved in proline biosynthesis and antioxidant processes. Through coexpression analysis, transcription factors with correlated expression to differentially expressed metabolism genes were identified as potential target genes for engineering. This multi-omics analysis provides a foundation for strain improvement in biofuel applications and expands our general understanding of metabolic and regulatory mechanisms in algae.

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METABARCODING REVEALS HIGH GENETIC DIVERSITY OF HARMFUL ALGAE ON THE COAST OF TEXAS (GULF OF MEXICO): A CASE STUDY

Environmental-DNA (eDNA) for metabarcoding is a rapid and effective means to investigate microplankton community composition and species diversity. The objective of this study was to examine the genetic diversity of the phytoplankton community in the Gulf of Mexico, with particular emphasis on harmful algal bloom species. Samples were collected on a cruise at stations along the coast of Texas in September 2017 in the aftermath of Hurricane Harvey. Metabarcodes were generated from the eDNA targeting both the V4 and V8-V9 regions of the 18S rDNA gene. Evaluation of the metabarcodes revealed an unexpectedly high number of harmful algal species not documented in this region previously. A total

of 29 and 31 harmful algal species could be differentiated based on V4 and V8-V9 metabarcoding phylogeny, respectively. Based on the taxonomic resolution of the V4 or V8-V9 marker region, not all species can be differentiated using solely one marker. For example, some genera can be resolved using the V4 region (e.g., *Heterocapsa*), while others are resolved using V8-V9 (e.g., *Prorocentrum*). In other cases, species must be differentiated using a combination of both (e.g., *Karenia*). In the Gulf of Mexico, 6 species of *Karenia* have been recognized, so it was of interest to find that *K. mikimotoi* and *K. brevis* cannot be differentiated using the V4 region but *K. selliformis* can be differentiated. Conversely, the V8-V9 region could distinguish *K. brevis* and *K. mikimotoi*. We conclude that no single marker can delineate all species, so it is recommended monitoring programs use more than one marker.

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IDENTIFICATION OF ENVIRONMENTAL DRIVERS OF MICROBIOME STRUCTURE FROM THE BROWN ALGA *FUCUS VESICULOSUS* (PHAEOPHYCEAE)

Latitudinal biodiversity gradients provide a robust framework to consider the distributions of intertidal algae because they reflect historical and contemporary environmental gradients in light availability and temperature. However, it is unknown if these environmental factors govern the composition and abundance of macroalgal microbiomes. We characterized bacterial communities of *Fucus vesiculosus* across its entire North Atlantic range (Greenland – North Carolina and Norway - Spain) using 16S rRNA gene amplicon sequencing across three tissues (holdfasts, receptacles, vegetative tips). Bacterial community structure was weakly correlated with environmental variables, but vegetative tips had the strongest correlation. Often the relative abundances of amplicon sequence variants (ASVs) across latitude were highly correlated with one or more of a small subset of environmental parameters (air temperature, humidity, SST, tidal height), and not with the one (photoperiod) caused directly by latitude. Overall, ASV relative abundance correlated with specific stresses such as desiccation, inferred by wind speed and tidal height (*Blastopirellula_t628*), or heat stress (*Sulfitobacter_7351*). Additionally, we report an apparent range retraction of *F. vesiculosus* in North Carolina. This correlates with warmer air temperatures and more tropical storms affecting the intertidal biota at *Fucus*' previous range limit at Beaufort, N.C. Our studies suggest that similar environmental conditions may shape the distribution of hosts and their microbiomes.

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EFFECTS OF A MACROALGAL FOUNDATION SPECIES ON ABIOTIC HETEROGENEITY AND THE BETA DIVERSITY OF INTERTIDAL COMMUNITIES

Changes in species composition across space (spatial beta diversity) influence the multifunctionality, productivity, and resilience of communities. Thus, understanding the drivers of beta diversity is relevant, but most such drivers investigated to date are abiotic. We experimentally studied a biotic factor, the presence of a canopy-forming seaweed, as a driver of beta diversity in intertidal communities. Through field research done on the Chilean Pacific coast, we found that the dominant canopy-forming seaweed *Mazzaella laminarioides* decreases spatial variation in temperature and desiccation near the substrate. Based on these findings, we tested the hypothesis that this macroalga would decrease spatial beta diversity in communities. We experimentally created two treatments of *M. laminarioides* (canopy presence vs. absence) at the intertidal zone using replicate quadrats and kept both treatments for 32 months. Every 3 months, we measured the abundance of species in the quadrats and, then, we determined beta diversity for random pairs of quadrats. During the entire study period, canopy absence increased spatial beta diversity for the sessile species but had no effect on the beta diversity of mobile species, possibly because mobile species are less responsive to quadrat-scale conditions due to their high mobility. Overall, this study contributes novel insights into the community assembly mechanisms driving beta diversity, demonstrating that the loss of a foundation species can increase spatial environmental variation and spatial heterogeneity of the biological seascape.

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USE OF ALGAE IN A NOVEL WASTEWATER TREATMENT SYSTEM

There is an imminent need for sewage treatment systems that provide clean and safe water to an ever-growing human population, particularly in urban environments. Algae are capable of removing excess nutrients from wastewater that would otherwise be discharged into the Chicago River, causing blooms of disease-causing microbes. In collaboration with the Metropolitan Water Reclamation District of Greater Chicago and Gross-Wen Technologies, we are characterizing the algal communities of a Revolving Algal Biofilm system, an experimental, tertiary wastewater treatment in which algae grow on a vertical substrate that revolves through a tank that contains wastewater that has already undergone primary and secondary treatment. Algal samples were collected biweekly from the O'Brien Water Reclamation Plant in Skokie, Illinois, from 01/13/2021-02/24/2021 and examined with light microscopy at 1000x magnification. The most common species and their average relative abundances were *Sellaphora saugerresii* (76%), *Navicula cryptocephala* (12%), and *Nitzschia palea* (12%). Chlorophyll-*a*, which is a measure of algal biomass, averaged 2.59 $\mu\text{g}/\text{cm}^2$. The algal biomass, which removed an average of 28% of total nitrogen and 75% of total phosphorus from the wastewater, can be harvested and repurposed for fertilizer and other valuable bioproducts. Ongoing research will also examine the impact of the algal treatment system on the microbial communities in the wastewater effluent.

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GRATELOUPIA LANCEOLA (HALYMENIACEAE, RHODOPHYTA) IS THE CORRECT NAME OF THE NON-NATIVE SPECIES IN ALGIERS COAST KNOWN AS *G. LANCEOLATA*?

Grateloupia species are the most reported introduced species of red algae in Mediterranean waters. Several specimens of the order of *Halymeniales* were collected along the Algiers coast, during the last three years. Because of their morphological similarity, many of these specimens were placed on comparative genes sequences analysis. A morphological and histological analysis on numerous individuals showed the identification of three species (*G.lanceola*- *G.turuturu*-*G.lanceolata*). The blade is purplish red with a characteristic emerald green coloration at the base. The blade has a short stipe and marginal proliferations. The thallus is multiaxial with a length arrives up to 80 cm long. Based on Identification using mitochondrial COI-5P and plastid rbcL sequences, *G. lanceola* resolved as a distinct monophyly (100% ML, 1.0 BPP), clearly separated from other *Grateloupia* species. In the rbcL (1249 bp) phylogeny, *Grateloupia lanceola* from Algeria formed a monophyletic clade (100% ML, 1.0 BPP) with those from Malaga and La Coruña, Spain. Phylogenetic relationships of *G. lanceola* with other species were not resolved.

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AN EFFECTIVE APPROACH TO THE STUDY OF EUGLENIDS

Taxonomic research on photosynthetic euglenids dates back to 1830, when Ehrenberg established the genus *Euglena*. For the next 190 years, euglenids have been studied based solely on morphological features. This resulted in many descriptions of new genera, hundreds of new species and artificial intra-generic classification systems. During this time, the understanding of morphological features continued to change, and more recently the use of molecular methods had a lasting impact on interpreting them in the context of evolution. Unfortunately, further studies are limited by material accessibility. Nearly all strains deposited in culture collections have already been studied thoroughly and the only possibility of subsequent research is to isolate strains from natural populations. However, this is time-consuming and laborious, with no guarantee of success, as many species do not survive in laboratory cultures. Therefore, isolation of cells of selected species with a micropipette directly from environment samples without establishing cultures is a much more effective method. Using this strategy we have increased the number of species in phylogenetic analyses, what enabled us (1) to indicate the diagnostic features of many common species, which have been difficult to distinguish so far, e.g. *Lepocinclis ovum* from *L. globulus* (the type species of the genus *Lepocinclis*) or species in the *L. acus*-like, *L. tripteris*-like, *Phacus longicauda*-like groups (among others), (2) describe the new genus *Flexiglana*.

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ADAPTATIONS OF *MICROCYSTIS FLOS-AQUAE* TO THE PRESENCE OF *PSEUDOKIRCHNERIELLA SUBCAPITATA* AND UV-B EXPOSURE CORRELATE WITH CHANGES IN THE METABOLITES PROFILE OF THE CYANOBACTERIUM

Among the conditions that drive the formation of blooms of harmful cyanobacteria is the increase in the intensity of ultraviolet (UV) radiation. The impact of UV-B on the metabolites profile of toxin-producing strains of *Microcystis* during allelopathic interactions has been poorly reported. This study aimed to investigate the influence of UV-B on the metabolites profile of *Microcystis flos-aquae* during allelopathic interactions with *Pseudokirchneriella subcapitata*. UVB stimulated the growth of *M. flos-aquae* at the expense of the green microalgae: no noticeable impact of the latter on the growth of the former. The profile of the cultures exposed to UV was distinct from those co-cultures without UV treatment and the monoculture controls. Aucubin, Myo-inositol, L-isoleucine, phenylalanine, serine, L-tyrosine, valine, octadecadienoic acid, and hexadecenoic acid were closely strongly positively associated with the monocultures and co-cultures exposed to UV. Metabolites such as D-galactopyranose, n-pentadecanoic, octadecanoic, D-glucopyranoside, indole-3-ethanamine, talopyranose, atenolol, and alanine had a negative relationship with treatments with UV. These findings show that metabolites involved in amino acid metabolism, glycolysis and gluconeogenesis, carbon fixation and metabolism, fatty acid metabolism, and the biosynthesis of secondary metabolites are significantly affected by UV exposure. Our study reveals that the metabolites profile of *M. flos-aquae* correlates with its adaptation to increasing UV levels, probably leading to superior growth rates.

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FUNCTIONAL STRUCTURE OF A HYPEREUTROPHIC TROPICAL BAY IN RIO DE JANEIRO, BRAZIL

Functional Diversity (FD) is an approach widely used for ecological analysis of ecosystems. Over a five-year period, the benthic communities of Guanabara Bay (GB), a heavily polluted bay, were studied at three zones: entrance (EN), channel (CH), and inner zone (IN). A transect was used in the meso-littoral region at each location to create seasonal photographic samples with five squares of 30x30cm randomly placed. The photos were analyzed to determine the FD using the Rao Index, in which algae and invertebrates were classified into functional groups (FGs). Additionally, niche overlapping between FGs was assessed through null models. In total, fourteen FGs were recorded, in which foliose and filamentous chlorophytes, corticated and crustose calcareous rhodophytes, filter feeders, and bacterial biofilm were characteristic of the benthic communities of GB. The EN zone had the highest functional richness and some exclusive FGs, while the IN zone had the lowest richness and the highest frequency of bacterial biofilm, forming an environmental gradient. Macroalgae with simple morphology and opportunistic life strategies were characteristic of the zone with the highest level of pollution (IN). The FGs at the EN zone overlapped their niches more than would be expected by chance, while there was a predominance of competitive exclusion among the FGs that occurred at IN zone. A competitive exclusion relationship was shown between two rhodophytes FGs. Thus, a functional gradient in space and changes in the functional structure was recorded in a hypereutrophic bay throughout five years.

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DEPENDENCE OF BIOCHEMICAL COMPOSITION AND BIOMASS PRODUCTION OF *CLADOPHORA SP* ON NUTRIENTS AND LIGHT INTENSITY IN PROLONGED LABORATORY ENRICHMENT

A vigorous green clump of Western Lake Michigan benthic *Cladophora* filaments was diver collected in late spring off Chicago at 15m depth. Filaments were repeatedly washed in 0.2 μ m filtered lake water (FLW) and gently disentangled. The microscopically "clean" mass was blotted semi-dry, divided into equal weighed portions, and resuspended in FLW in 250mL PC bottles. Replicates with No add (CON), +1000 μ M NO₃⁻ (+N), and +N +100 μ M HPO₄⁼ (+NP) were incubated for 3 weeks on a rotating wheel at 10C at 0, 30, 57, 135, 335, and 752 μ Einst/m²/s. Filtered aliquots were analyzed for nutrients at intervals to assess growth. End-point filaments were filtered and the pads dried in a vacuum desiccator. Weighed portions were ground with a glass pestle-grinder to powder and analyzed for biochemical constituents. Visually, 30-57 μ E produced little growth but had purple Cyanobacterial filaments and 752 μ E golden filaments were covered with epiphytic scale-like (not stalked) diatoms – midlevel light filaments were nearly naked. Dry weight doubled at 752 μ E and had small increases at low light in + or -P. CHL-a/mg DW decreased from 2-3 at lowest light to <1 at 752 μ E in either + or -P. TP/mg DW was inversely proportional to light (IP2L) from 40 to 16 in +P but P2L from 40 to 140 in -P. N:P (mol) in -P was 19-22 in moderate-high light but only 3-4 with P addition. Inorganic nutrient availability had little effect on *Cladophora* growth over one doubling of biomass but substantially altered the elemental composition of the total biomass produced. Epiphytes prospered at extreme light conditions.

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THE ANTARCTIC CHLAMYDOMONAS SP. UWO241 HAS A REDUCED REPERTOIRE OF PHOTORECEPTOR GENES AND AN ABERRANT PHOTOTACTIC RESPONSES

The Antarctic green alga *Chlamydomonas* sp. UWO241 is an obligate cold extremophile (psychrophile) and an emerging model for photosynthetic adaptation to extreme conditions. UWO241 originates from the ice-covered Lake Bonney, an extreme but highly stable environment. In addition to the permanent cold (~5°C), this alga thrives under highly unusual light conditions with very low light levels (~15 μ mol/m² s⁻¹), a narrow spectrum enriched in blue light, and an extreme photoperiod. Genomic sequencing of UWO241 exposed an unusually large genome, hundreds of gene duplicates and expanded gene families, some of which could be aiding its survival in extreme conditions. In this work, we demonstrate that the gene encoding the blue-light photoreceptor phototropin is duplicated in UWO241; however, the photoreceptor gene family is significantly reduced compared to the model mesophile *Chlamydomonas reinhardtii*. Mirroring this, the gene family encoding for light harvesting complex (LHC) proteins also contains gene duplicates, but UWO241 lacks certain LHC homologs when compared to *C. reinhardtii*. UWO241 also possesses a very small eyespot and exhibits an aberrant phototactic response. We saw similar trends the genomic repertoire for photoreceptor and LHC genes in another Antarctic alga, the closely related *Chlamydomonas* sp. ICE. This suggests significant differences in the ability of low-light adapted polar algae to perceive and respond to light when compared to their mesophilic relatives, with implications on their evolution and survival under extreme conditions.

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TEMPORAL DYNAMICS AND FUNCTIONAL REDUNDANCY IN THE MICROBIOME OF A MACROALGAL FOUNDATION SPECIES

The scales at which microbiomes of marine hosts vary in time and space, and the biotic and abiotic drivers of variation are poorly understood. Functional redundancy can maintain key microbe-mediated processes despite taxonomic variation, but it is unclear if these functions are stable following changes in the host or host environment. We repeatedly sampled the microbiome of the same *Fucus distichus* individuals through time and compared host-associated bacterial (16S rRNA gene), eukaryotic (18S rRNA gene), and functional (shotgun metagenomic) diversity to source pools of microbes in the surrounding environment. Temporal variation in biotic filters (the host) and the abiotic environment were partially decoupled by sampling co-occurring host individuals at different life stages over time. Synchronous temporal turnover in microbial taxa occurred at the host population-level but interindividual variation in specific ASVs was high and minimally explained by differences in host ontogeny or spatial distance within the host population. In contrast, interindividual variation in microbial functional repertoire was low, suggesting high functional redundancy. We also observed consistent and habitat-specific temporal turnover in microbial functions indicating functional change is driven by seasonal variation across host-associated and abiotic intertidal habitats. This research makes a novel contribution to understanding the selective filters determining microbiome compositional dynamics and functions in an ecologically important marine host.

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DIATOMS AND DINOFLAGELLATES DIVERSITY INHABITING A COASTAL UPWELLING SYSTEM: A METABARCODING APPROACH

Small eukaryotic plankton has been traditionally characterized using conventional microscopy techniques. Current advances in sequencing technologies allow the cost-effective study the diversity within microbial plankton based on DNA sequences. This technique has been implemented in the last 15 years for investigating prokaryotic diversity, but its application to unravel the diversity and ecology of eukaryotic organisms is still incipient. In this study we analyze the diversity of the diatoms and dinoflagellates in the marine communities using rDNA sequencing techniques, as well as the taxonomic resolution provided by the V4 region of the 18S rRNA gene. Twenty monthly 6L seawater samples for DNA metabarcoding were collected and filtered through 3 µm polycarbonate filter in a station off the Ría de A Coruña (NW Iberian Peninsula). DNA was extracted, the V4 region of the 18S rRNA was PCR amplified and subsequently sequenced using the High Throughput Sequencing (HTS) platform Illumina. Amplicon sequence variants (ASVs) were differentiated using DADA2 implemented in R. Sequences were aligned against PR2 v4.12.0 and SILVA 132 18S rRNA databases as references, as well as studied using BLAST and phylogenetic trees. *Sequence-based taxonomic* approach found 128 and 416 metabarcodes corresponding to diatoms and dinoflagellates, respectively. Sequences had limited resolution at species or even genus level, and overall the taxonomic resolution of diatoms was substantially higher than those of dinoflagellates.

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PAN-ARCTICA : HORIZONTAL GENE TRANSFERS DEFINE THE CONVERGENT EVOLUTION OF DISTANTLY RELATED ALGAE FROM THE SAME OCEAN

Anthropogenic climate change is rendering the Arctic Ocean a warmer, fresher, and more oligotrophic environment. This is impacting the composition of the phytoplankton communities supporting the entire Arctic food chain, with an initial spring pulse of diatoms being increasingly replaced by a phylogenetically diverse range of small algal species (e.g. cryptomonads, haptophytes, pelagophytes and chrysophytes), whose biology remains poorly understood. Here, we present genomes of four new small Arctic algal species isolated from the Pikialasorsuaq/ Northwater Polynya, alongside comparative analyses of a densely sampled algal sequence dataset, to unveil adaptive features underpinning the Arctic algal pan-genome. We note striking convergences in the biology of small Arctic algae, compared to non-Arctic relatives; although this is largely exclusive of Arctic diatoms. Using high-throughput phylogenetic approaches, incorporating environmental sequence data from *Tara* Oceans, we demonstrate that this convergence is not only driven by gene family expansions and contractions, but also by horizontal gene transfers (HGTs) of over 30 discrete gene families between Arctic species, exemplified by genes encoding ice-binding domains. These Arctic-specific genes have been repeatedly transferred between Arctic algae, and are independent of equivalent HGTs in the Antarctic Southern Ocean. Our data provide insights into the specialized Arctic marine microbiome, and underlines the role of geographically-limited HGT as a driver of environmental adaptation in eukaryotic algae.

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DECIPHERING CORAL REEF ECOLOGICAL PUZZLE USING PROPER ALGAL TAXONOMIC RESOLUTION

The Florida Keys Reefs have experienced severe (>75%) coral loss in the last 50 years where, despite effective long-term protection, corals have failed to recover. Several studies have described failure in coral recruitment and survival likely related to unsuitable habitats but no detailed (high taxonomic resolution) benthic surveys have been conducted in order to evaluate this hypothesis. We conducted surveys in 2016 to study the benthic composition of three low-relief and three high-relief coral reefs in the Upper Florida Keys and their relationship with coral recruitment. We further analyzed macroalgal community composition and its association with sediment. We found low-relief reefs dominated (>40%) by a stable matrix of turf-forming algae (18 taxa dominated by *Digenea simplex*) associated with sediment (> 0.5 cm thick). As expected, coral recruitment was negatively correlated with sediment depth and abundance of this matrix. In high relief reefs, *Dictyota* spp. turf-forming algae, and crustose coralline algae (CCA) such as *Mesophyllum* spp. covered over 70% of the benthos. It was surprising that even in areas dominated by CCA (some species can facilitate coral recruitment) density of coral recruits was very low. Neither of these two reef types was seemingly suitable for coral recruits (average density 10 ind m⁻²) however, higher taxonomic resolution studies are needed to explain this ecological puzzle.

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TISSUE SPECIFICITY AND CROSS-ATLANTIC, NORTH TO SOUTH LATITUDINAL DIFFERENTIATION OF HOST MICROBIOMES OF THE BROWN ALGA *FUCUS VESICULOSUS* (PHAEOPHYCEAE)

Latitudinal diversity gradients provide insights into species differentiation and community processes. The intertidal-zone is well-studied, yet little is known about latitudinal diversity in microbiomes associated with habitat-forming hosts. We investigated microbiomes of *Fucus vesiculosus* because of deep understanding of this model system and its latitudinally large, cross-Atlantic range. Given multiple environmental effects, we predicted that cross-Atlantic microbiomes of the *Fucus* microbiome would be similar at similar latitudes. We compared host bacterial communities along the entire Atlantic range from Greenland to North Carolina (USA) in the western Atlantic and from Norway to Spain in the eastern Atlantic with 16S rRNA gene amplicon sequencing of holdfasts, vegetative tips, and receptacles of *F. vesiculosus* from 16 sites in 2 summers (2015, 2016). *F. vesiculosus* microbiomes were strikingly different from environmental microbiomes collected from adjacent seawater or substrata. Community structure and individual amplicon sequencing variants (ASVs) showed distinctive latitudinal distributions, but alpha diversity did not. Latitudinal differentiation was consistent among the three sampled tissues, but with strong tissue specificity between holdfasts and vegetative tips/receptacles. Latitudinal differentiation was mostly driven by ASVs that were more abundant in cold temperate to subarctic or warm temperate latitudes. We suggest cross-Atlantic microbial structure of *F. vesiculosus* is related to a combination of past (glacial-cycle) and contemporary environmental drivers.

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IN A NUTSHELL – A LOOK AT THE PHYLOGENETICS OF GENUS *STROMBOMONAS* (EUGLENOPHYTA)

Many Protists are known to create outer envelopes around their cells. Such is the case of *Strombomonas*, one of the two loricate genera among autotrophic euglenids – cosmopolitan, freshwater-dwelling Eukaryotes. The cells are surrounded by a metal incrustated shell, termed the lorica, which acts as the key diagnostic trait for the loricate taxa. Genus *Strombomonas*, though separated in 1930 by Deflandre based on envelope shape, is still poorly represented on current phylogenetic trees, despite having over 80 taxonomically accepted species. Moreover, the existing sequences are either identified only on the genus level, or most likely misidentified, as species of different names locate together in common clades. This is quite probably the result of the following issues: a) lack of specific morphological diagnostic traits, b) difficulties with DNA isolation due to the presence of lorica, c) lack of representatives in algae culture collections. As such, a taxonomic verification focusing on both morphological and molecular data was conducted, yielding a phylogenetic tree of the genus *Strombomonas* (based on 18S rDNA) with 12 new sequences representing 5 different species. The descriptions of the species were emended and their clades designated, including that of *S. verrucosa* – the type species, for which an epitype is suggested. As a result, the tree currently consists of 30 sequences, representing 8 species and 2 unidentified specimens.

The sequences were obtained from environmental samples collected across Poland, as the lorica is sensitive to ontogenetic and environmental changes.

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RESISTANCE AND EARLY RECOVERY OF *DURVILLAEA INCURVATA* DOMINATED - COMMUNITIES TO A PULSE DISTURBANCE IN A CHILEAN SOUTHERN ROCKY SHORE

Large canopy-forming seaweeds are essential to support biodiversity through habitat provision and amelioration in coastal ecosystems worldwide. However, environmental, and anthropogenic disturbances may induce changes in community functioning and the benefits provided by coastal ecosystems to mankind. Thus, understanding the ability of coastal communities to resist and recover from severe disturbances, such as the local extinction of canopies, is of widespread relevance for fundamental and applied ecology. We manipulated the presence of *Durvillaea incurvata* in field experimental plots (n=20), to assess canopy loss effects on community composition and function. We focused on their ability to remain unchanged under external stress (resistance) as well on their ability to return to its former reference state (recovery). Canopies were completely removed once in half of the plots and then we monitored species cover and density in all plots each three months, to indirectly estimate community biomass. After the pulse disturbance, a notable increase (relative to controls) in barnacles, red calcified seaweeds *Lithothamnion* sp. and *Corallina officinallis* was observed. A high recruitment of *D. incurvata* enhanced the compositional resistance of the disturbed communities, while community biomass was almost fully recovered a year after the disturbance. Hence, we conclude that functional and compositional resistance were low, however a high compositional and functional recovery within a relatively short time (i.e. a year), highly the ability of this community to cope with disturbances.

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GLOBAL SPECIES RICHNESS PATTERNS OF MARINE FORESTS OF LARGE BROWN MACROALGAE

Large brown macroalgae create essential coastal habitats, supporting invaluable ecological services. While marine forests are globally declining due to human-dominated disturbances, their global distribution and species richness patterns are still poorly studied, precluding a global perspective on conservation and management priorities. To address this gap, we used a global dataset of brown macroalgae (orders: Laminariales, Tilopteridales, Desmarestiales and Fucales) together with biologically meaningful environmental predictors, to develop species distribution models and stacked them across species to infer species richness estimates. We found that temperature and light availability at the seafloor are the main predictors shaping the distribution of subtidal species, while wave energy, temperature and salinity drive the distribution of intertidal species. Richness hotspots were located in the Northeast Pacific

and North Atlantic for kelp (max regional richness: 32 species in California-Alaska) and in Australasia and central Indo-Pacific (max regional richness: 53 species in southern Australia) for fucoids. Despite regional differences, coldspots of richness coincided and were mainly found at higher latitudes and the Baltic Sea, where extreme conditions prevail. Our findings reveal the major environmental drivers shaping the distribution of marine forests and identify regions of high and low species richness, providing baseline estimates at global scales. We discuss the findings in light of current environmental conditions and long-term evolutionary processes.

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NEW DEEPWATER SPECIES OF RED ALGAE GROWING IN RHODOLITH BEDS IN THE NW GULF OF MEXICO

This talk will focus on recently collected new species of marine red algae growing on the surface of rhodoliths at 56-85m depth in the northwestern Gulf of Mexico. On the basis of comparative *rbcl* sequence analysis and developmental morphology, the new taxa being discussed belong in the genus *Waldoia* W.R.Taylor (Rhodomelaceae, Ceramiales), *Chondrymenia* Zanardini (Chondrymeniaceae, Gigartinales), *Anatheca* F.Schmitz (Solieriaceae, Gigartinales), and *Chrysymenia* J.Agardh (Rhodymeniaceae, Rhodymeniales). The phylogenetic position of each of the new species will be discussed. *Waldoia* sp. nov. is nested along with the generitype *W. antillana* W.R.Taylor 1962 from Tobago (B.W.I.) within a clade of species previously considered to belong in *Chondria*. *Waldoia* is here redefined to include a dozen *Chondria* species characterized by thalli that are either terete throughout, or at least partly terete and secondarily compressed to flattened, with acute or blunt branch apices, deciduous trichoblasts that originate from the central cells, and lack of cell wall thickenings. Two new species of *Chondrymenia* Zanardini, a former monospecific genus hitherto only reported from the Mediterranean Sea (*Chondrymenia lobata* (Menegheni) Zanardini 1860), are recognized from offshore Louisiana and Texas. The distribution of *Flahaultia tegetiformans* W.R.Taylor 1942, a former monospecific genus described from Tobago (B.W.I.), is here expanded to the Campeche Banks (SW Gulf of Mexico), Caribbean Panama, and Martinique (F.W.I.). *Flahaultia* is newly placed in the Chondrymeniaceae, and its relationship to *Chondrymenia* will be discussed.

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COMPARATIVE GENOMICS OF SYMBIODINIACEAE AND SYMBIOSIS AS A DRIVER OF DIVERSIFICATION

Dinoflagellates in the family Symbiodiniaceae are important photosynthetic symbionts associated with cnidarians (such as corals) and other reef organisms. Breakdown of the coral-dinoflagellate symbiosis due to environmental stress (*i.e.* coral bleaching) can lead to coral death and the potential collapse of reef

ecosystems. However, evolution of Symbiodiniaceae genomes, and its implications for the hosts, is little understood. Genome sequences of Symbiodiniaceae remain scarce due in part to their large genome sizes (1–5 Gbp) and idiosyncratic genome features. Here, we present *de novo* genome assemblies of seven members of the genus *Symbiodinium*, of which two are free-living, one is an opportunistic symbiont, and the remainder are mutualistic symbionts. Integrating other available data, we compare 15 dinoflagellate genomes revealing high sequence and structural divergence. Divergence among some *Symbiodinium* isolates is comparable to that among distinct genera of Symbiodiniaceae. An in-depth comparison between the genomes of the symbiotic *Symbiodinium tridacnidorum* (isolated from a coral) and the free-living *Symbiodinium natans* reveals a greater prevalence of transposable elements, genetic duplication, structural rearrangements, and pseudogenization in the symbiotic species. Our results support the hypothesis impact of symbiosis as a driver of genome divergence and diversification of *Symbiodinium*, and more broadly of Symbiodiniaceae.

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NEW PARTS FROM OLD: EVOLUTION OF THE CRYPTOPHYTE PHYCOBILIPROTEIN ANTENNA

Cryptophyte algae acquired their plastids from a red alga by secondary endosymbiosis, along with many nuclear-encoded genes for plastid proteins. Unlike other algal groups with secondary plastids which completely lost all trace of the primary red algal antenna, the phycobilisome (PBS), the cryptophytes retained one of its proteins, the plastid-encoded β subunit of phycoerythrin. It became paired with a small nuclear-encoded protein (8–10 kDa) to evolve a completely novel light-harvesting antenna system. This “new α ” subunit is a natively disordered protein that can only fold into its final shape by binding onto the hydrophobic surface of a β subunit to form the $\alpha\beta$ protomer, which then dimerizes to form the $(\alpha\beta)_2$ light-harvesting antenna. So where did this new protein come from? Searching databases for amino acid sequence similarity gave no clue. Approaching it from a different direction, searching the recently published cryo-EM structures of two red algal PBS on the basis of protein fold rather than protein sequence, revealed a minor family of PBS linker proteins that possess one or more copies of a cryptophyte- α -like domain. They serve to bind unpaired β subunits to conserved positions on the surface of the PBS. We propose that after endosymbiosis one of these proteins could have provided a stable binding partner for the β subunit, rescuing it from oblivion and in the process giving rise to a novel antenna. In fact, it might have outcompeted the original binding partner of the β subunit, thus contributing to the demise of the PBS.

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ASSESSING CHANGES IN COASTAL ECOSYSTEM ENGINEERS AND ASSOCIATED COMMUNITIES IN NARRAGANSETT BAY

Habitat-forming seaweeds are ecosystem engineers that form dynamic habitats in cool-water regions and support complex food webs. Rockweeds are dominant temperate seaweeds in the intertidal and shallow

subtidal of rocky shorelines, while kelps form complex habitats in the subtidal. Changes in the distribution or abundance of habitat-forming seaweeds can have consequences for the associated food webs and ecosystem health. We hypothesized that the abundance of rockweed and kelp and their associated invertebrate and fish have shifted over time in Narragansett Bay. Our research project assessed the current health of economically and ecologically important habitats by revisiting 24 sites that were historically surveyed (1970s and 1980s) and determining how these communities have changed. Video surveys were conducted via SCUBA diving in both the fall and summer using a diver-operated metal ski mounted with GoPro cameras, underwater lasers, and lights along a 30m transect in order to document seaweeds, invertebrates, and fishes at all sites. Current percent cover of rockweed and kelp at all 24 sites was determined by analysis of the seaweed videos. Our initial results indicate that there has been a significant decline in the percent cover of kelp in Narragansett Bay. Rockweed percent cover has also changed significantly over the past 4 decades and we documented a decline in rockweed in the northern part of the bay, but an increase in percent cover at southern sites. Future research and analyses will determine the consequences of these changes for the wider ecosystem.

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MOLECULAR SYSTEMATICS OF HAWAIIAN GRACILARIALES (RHODOPHYTA) BASED ON RBCL DNA SEQUENCE ANALYSES

To date, 10 Gracilariales species have been reported in the main Hawaiian Islands: *Gracilaria abbotiana*, *G. coronopifolia*, *G. dawsonii*, *G. parvispora*, *G. epihippisor*, *G. dotyi*, *Gracilariopsis lemaneiformis*, and the introduced species *G. salicornia*, *G. tikvahiae*, and *Hydropuntia perplexa*. *Gracilaria abbotiana*, *G. dawsonii*, *G. epihippisor*, and *G. dotyi* are considered Hawaiian endemics. In the literature, *G. coronopifolia* has been cited for the Western Pacific Ocean, but current knowledge also recognizes *G. coronopifolia* as a Hawaiian endemic. We use *rbcL* DNA sequences to test species boundaries and phylogenetic relationships among all Hawaiian Gracilariales. Maximum likelihood and Bayesian phylogenies show that (1) *G. dotyi* is conspecific with *G. coronopifolia*, (2) *G. epihippisor* is conspecific with *G. salicornia*, (3) *G. dawsonii* and *G. abbotiana* are sister species who share a recent common ancestor with *G. coronopifolia*, (4) *Gracilariopsis lemaneiformis* from Hawaii is a new species, and (5) a flat deep-water *Gracilaria* species from Molokai is a new species. The clade *G. coronopifolia*-*G. dawsonii*-*G. abbotiana* suggests a case of in-island species radiation. Our results reset the Gracilariales flora from the Hawaiian Islands to nine species: *G. abbotiana*, *G. coronopifolia*, *G. dawsonii*, *G. parvispora*, *G. salicornia*, *G. tikvahiae*, *G. sp. nov.*, *H. perplexa*, and *Gracilariopsis sp. nov.* Descriptions for the new species will be reported elsewhere.

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REAL-TIME MONITORING TO ADDRESS HARMFUL ALGAL BLOOMS IN THE INDIAN RIVER LAGOON, FLORIDA

The Indian River Lagoon Observatory Network of Environmental Sensors (IRLON) is comprised of 13 stations at ecologically important sites in the Indian River Lagoon (IRL) and St. Lucie Estuary (SLE) related to the dynamic interface between oceanic water from inlets and freshwater inputs from rivers, canals, and Lake Okeechobee. Each station consists of a custom suite of biogeochemical instrumentation coupled with meteorological sensors to provide real-time, high-accuracy and high-resolution water

quality/weather data via a dedicated interactive website (www.irlon.org). In 2020-2021, new capabilities are enhancing IRLON to address harmful algal blooms (HABs). In the northern IRL, HABs have been a significant threat for a decade, beginning in 2011 with the “Super Bloom” comprised of an unidentified pedinophyte, followed in 2012 by brown tide (*Aureoumbra lagunensis*) which has continued to 2021, along with significant amounts of picocyanobacteria. These blooms have led to catastrophic seagrass loss, unprecedented fish kills, and high mortality of the endangered Florida manatee. To the south, toxic cyanobacteria blooms (*Microcystis aeruginosa*) originating in Lake Okeechobee are routinely occurring in the SLE causing impacts to marine resources and humans. For improved HAB monitoring, we have added Turner Designs C3 Submersible Fluorometers to monitor phycocyanin, phycoerythrin, and chlorophyll fluorescence at all IRLON stations, an unprecedented capability to monitor the spatial and temporal distribution of HABs in this system. These data will also be incorporated with data relevant to the growing HAB problem, i.e., cell counts, toxin levels, satellite imagery, acoustics, and novel advance technology (e.g., cybotbots) by other colleagues to enhance visualization capabilities and to facilitate modeling efforts of HABs in the IRL system.

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WHO CARES MORE ABOUT CHEMICAL DEFENCES IN THE RED SEAWEED *PLOCAMIUM* SP. – THE SEAWEED OR ITS ONLY GRAZER?

Chemically-based inter- and intraspecific interactions between organisms can involve communication, environmental sensing, or defense and are often mediated by secondary metabolites. Sessile marine organisms such as macroalgae commonly produce chemical defenses against grazers, pathogens, and biofoulers. *Plocamium* sp. is a finely branched red understory alga common in Antarctic macroalgal forests. It supports a very high abundance of amphipods of which most are not able to feed on this heavily chemically defended host with the exception of *Paradexamine fissicauda*. Different *Plocamium* sp. individuals produce differing mixtures of halogenated secondary metabolites (= chemogroups). Near Palmer Station (Anvers Is.) 15 different chemogroups were identified. A subset was used to identify whether the feeding rate of *P. fissicauda* differed between individuals that vary in chemogroup production and to assess differences in growth rate and reproductive output of *P. fissicauda* when held on a chemogroup-specific diet. Some chemogroups were consumed at a significantly slower rate than others whereas amphipod growth rate did not differ significantly between most of the treatments. Between two chemogroups examined for effects on amphipod reproduction, the one consumed at a significantly slower rate also led to the amphipod having a diminished growth rate in terms of weight (but not length) and producing fewer embryos. Overall, there seems to be a fitness cost associated with the consumption of some chemogroups, and a benefit to *Plocamium* sp. in producing certain chemogroups over others.

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TERRESTRIALIZATION OF ZYGNEMATOPHYCEAE: HOW ADAPTATION TO STRESSFUL ENVIRONMENTS SHAPED THEIR TRANSITION TO LAND

Over the past decade, a large dataset was gathered on abiotic stress tolerance in Zygnematophyceae which helped to understand their prerequisites for terrestrialization. Among the most challenging abiotic stresses are limited water availability and light stress. Upon experimental desiccation, particularly young cultures of *Zygnema* sp. reacted with severe transcriptomic changes, whereas older cultures that had formed pre-akinetes showed less regulation at the transcript level. These data were compared with field studies of *Zygnema* from the Arctic, showing the highest transcript regulation in the upper layer of a mat when compared to the lower layer. The upper layer is more likely exposed to desiccating conditions as well as strong irradiation. A correlative metabolite profiling showed in the upper layer a readily production of metabolites that prevent damage from the expected stresses e.g. osmotically active compounds. In an experimental approach, metabolite profiling of young versus nitrogen-starved cultures showed similar metabolic signatures. Thus, we can conclude, that pre-akinetete formation involves a re-allocation of photosynthetically fixed energy into storage instead of growth, supporting survival of extreme environmental conditions. Studies with experimental UV-irradiation moreover demonstrated that pre-akinetes tolerate this stress, but young cells are more dynamic in their physiological responses. Transition to pre-akinetes is a strictly vegetative process and asexual reproduction is usually favored in open, extreme or transient, unpredictable environments, where colonizing ability and rapid population growth are important. However, sexual reproduction commonly found in alpine regions results in the formation of resistant zygospores, likely crucial for long-term survival.

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THE *TETRADESMUS (SCENEDESMUS) OBLIQUUS* PAN-GENOME

As part of our commitment to research in bioenergy and the environment, the DOE Joint Genome Institute has initiated several projects to produce high quality whole genome scale data and analysis, increasing both the taxonomic depth and species strain breadth available to the broader eukaryotic algal research community (<https://phycocosm.jgi.doe.gov/>). Recently, we have sequenced and annotated the genomes for several strains of *Tetrademus (Scenedesmus) obliquus*, a Chlorophyte microalga, and other members of the Scenedesmaceae family. *T. obliquus* is ubiquitous in freshwater environments. This species is known to be oleaginous, accumulating oil bodies under environmental stresses, and is a recent model organism in the context of biofuel feedstock development. Investigations of patterns of shared protein families between closely related strains, known as the species pan-genome, is a powerful tool for uncovering genes related to strain-specific phenotypes. We have successfully applied a pan-genome software workflow, originally developed for fungi, to a set of six haploid *T. obliquus* genomes. In contrast to more traditional gene family homolog clustering, this method uses sequence similarity paired with available synteny information to resolve paralogy, producing single-ortholog clusters (SOCs). Closer examination of these SOC demonstrates gene set enrichment for strain specificity due to factors such as copy number expansion in pairs of unique SOC or patterns of enzyme class presence/absence. Additional

development efforts have extended this methodology to routine pan-genome analysis as additional *T. obliquus* genomes are sequenced and released.

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MECHANICS AND EVOLUTION OF CELL SHEET FOLDING – EMBRYONIC INVERSION IN *VOLVOX*

Cell sheet folding is an essential process during multi-cellular development, examples including gastrulation, neurulation and organogenesis. It is poorly understood how mechanisms at the molecular and cellular level give rise to deformations at the tissue level. The inversion process in the multicellular green microalga *Volvox* is a powerful model to illuminate these relations. During inversion the spherical *Volvox* embryos undergo invagination and eventually turn themselves inside-out, in order to expose their flagella. As in animals, cell sheet folding in *Volvox* is driven by cell shape changes. These are possible as embryonic cells of *Volvox* do not possess a cell wall. Different types of cell sheet deformations have evolved in different *Volvox* species and are associated with different environmental conditions as well as physical constraints. A combination of light sheet fluorescence microscopy and mathematical modelling revealed that equatorial invagination during type B inversion has to be complemented by active contraction and expansion in the posterior and anterior hemisphere, respectively. While inversion is achieved by a single wave of cell-wedging in type A inversion (*V. carteri*), different areas exhibit different cell shapes in type B inversion (*V. globator*). As a result, the anterior hemisphere is pulled over an inflection point by contraction rather than bending of the cell sheet. This differential cell behaviour suggests a transition towards a higher complexity of embryonic development within the family Volvocaceae.

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EXTRATERRESTRIAL AND INTRATERRESTRIAL CYANOBACTERIA, DIATOMS AND OTHER MICROALGAE: TOWARD A NEW PARADIGM CONCERNING THE ORIGIN AND DISTRIBUTION OF BIOSPHERES

The origin and distribution of biospheres is one of the great unanswered questions of Science. The accepted paradigm is the biosphere arose after long, slow abiotic synthesis of organic carbon compounds and biomolecules led to self-replicating cells in Earth's primordial oceans. The panspermia hypothesis (life originated elsewhere in the Cosmos and was delivered to Hadean Earth by comets and asteroids) is strengthened by IR data on interstellar dust and Scanning Electron Microscopy (SEM) discoveries of fossil microalgae in carbonaceous meteorites. Small pennate diatoms and cyanobacteria found are similar to those of deep biospheres of Earth. SEM studies at NASA/MSFC imaged intraterrestrial microorganisms from deep hot rocks of the Rainbow hydrothermal vent; South Africa's Driefontein gold mine and cold Biospheres-Polar ice caves and deep Vostok ice cores. SEM studies at MSFC, PIN, Cardiff Univ. and Joint Institute of Nuclear Research showed the low-density stones that fell in Polonnaruwa, Sri Lanka on Dec. 29, 2012 contain astonishingly well-preserved extinct hystrichospheres, cyanobacteria and diatoms. These stones are unlike all known meteorites but have properties similar to the Apollo 14 VHK

lunar KREEP basalts and low-density dark boulders of asteroid Ryugu. Epithermal Neutron Activation Analysis studies at JINR found that these meteorites contain very high level of incompatible radiogenic Heat Producing Elements (^{40}K , ^{235}U , ^{238}U , ^{232}Th) and provides insights for a possible mechanism for the interstellar transfer of viable biospheres between planetary systems.

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EFFECT OF ELEVATED CO₂ AND TEMPERATURE ON THE GROWTH, PHOTOSYNTHETIC PIGMENTS AND NUTRIENT UPTAKE OF *GRATELOUPIA FILICINA*

Ocean acidification and global warming have been environment concerns worldwide. A red alga, *Grateloupia filicina*, is known as a cosmopolitan species, inhabiting in all continents except for Antarctica. This study was to determine the effect of elevated CO₂ and temperature on *G. filicina*. *Grateloupia filicina* blades were exposed to 500 (control), 900 and 1800 ppm of CO₂ at 18 and 25°C for 20 days. In addition, to determine the effect of aeration, a blank control without seaweed was placed at the same conditions. Specific growth rate (SGR), photosynthetic pigments (PE: Phycoerythrin; PC: Phycocyanin; Chlorophyll *a*; and Carotenoids) and nutrients (phosphorus and nitrate) uptake rates were measured every 5 days. No significant differences of photosynthetic pigments were observed at all conditions. CO₂ did not affect SGR, but the high temperature (25°C) significantly reduced the growth of *G. filicina* when cultivated at 1800 ppm. Phosphorus and nitrate uptake rates were decreased as temperature and CO₂ concentration increased. These results suggest that the combined effects of ocean acidification and warming may negatively affect the growth and nutrient uptake of *G. filicina*.

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PRELIMINARY ASSESSMENT OF MICROBIAL COMMUNITY STRUCTURE OF WIND-TIDAL FLATS IN THE LAGUNA MADRE, TEXAS, USA

Aside from two samples collected nearly 50 years ago, little is known about the microbial composition of wind tidal flats in the hypersaline Laguna Madre, Texas. These mats account for ~42% of the lagoon's area. These microbial communities were sampled in the Laguna Madre, including Laguna Madre Field Station (LMFS), Nighthawk Bay (NH), and two locations in Kenedy Ranch (KRN and KRS). Amplicon sequencing of 16S genes determined the presence of 51 prokaryotic phyla dominated by Bacteroidota, Chloroflexi, Cyanobacteria, Desulfobacteria, Firmicutes, Halobacteria, and Proteobacteria. The microbial community structure of NH and KR is significantly different from LMFS, in which Bacteroidota and Proteobacteria were most abundant. Twenty-three cyanobacterial taxa were identified via genomic analysis, whereas 45 cyanobacterial taxa were identified using morphological analysis, containing large filamentous forms on the surface, and smaller, motile filamentous and coccoid forms in subsurface mat layers. Sample sites were dominated by species in Oscillatoriaceae (i.e., Lyngbya) and Coleofasciculaceae (i.e., Coleofasciculus). A total of 73 cyanobacterial bioactive metabolites were identified using ultra-performance liquid chromatography-Orbitrap MS analysis from these communities. Laguna Madre seems unique compared to other sabkhas in terms of its microbiology.

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DECIPHERING PHOTOSYNTHETIC CARBON PARTITIONING AND ITS REGULATION IN RESPONSE TO VERY-LOW AND HIGH CO₂ IN *MICROCHLOROPSIS GADITANA* NIES 2587 BY QUALITATIVE PROTEOMICS

Photosynthetic organisms fix inorganic carbon through carbon capture machinery (CCM) that regulates the assimilation and accumulation of carbon around ribulose-1,5-bisphosphate carboxylase / oxygenase (Rubisco). However, few constraints that govern the central carbon metabolism are regulated by the carbon capture and partitioning machinery. In order to divert the cellular metabolism toward lipids and/or biorenewables it is important to investigate and understand the molecular mechanisms of the CO₂-driven carbon partitioning. In this context, strategies for enhancement of CO₂ fixation which will increase the overall biomass and lipid yields, can provide clues on understanding the carbon assimilation pathway, and may lead to new targets for genetic engineering in microalgae. In the present study, we have focused on the deciphering the response occurring within marine oleaginous microalgae *Microchloropsis gaditana* NIES 2587, under the influence of very-low CO₂ (VLC; 300 ppm, or 0.03%) and high CO₂ (HC; 30,000 ppm, or 3% v/v). Our results demonstrate that HC supplementation in *M. gaditana* channelizes the carbon flux toward the production of long chain polyunsaturated fatty acids (LC-PUFAs) and also increases the overall biomass productivities (up to 2.0 fold). Further, the qualitative proteomics has identified nearly 900 proteins, among which significantly upregulated are acetyl coA carboxylase, citrate synthase, succinate dehydrogenase in HC while phosphoglycolate phosphatase, malate dehydrogenase, NADH ubiquinone oxidoreductase in VLC. In conclusion, our focus is to understand the entire carbon partitioning and its regulation within these photosynthetic cell factories, which will be further evaluated through multiomics approach for enhanced productivities of biomass, biofuels, and bioproducts (B³).

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SYNTHETIC PROMOTERS FOR CONTROL OF GENE EXPRESSION IN THE MODEL DIATOM *PHAEODACTYLUM TRICORNUTUM*

Developing genetic approaches for efficient and scalable disruption or activation of gene expression has multifaceted advantages. It can aid in dissecting mechanisms governing cellular processes, studying gene function, enable high throughput genome-scale screens and assist in redirecting metabolic flux towards high-value metabolites. Chemical-inducible expression systems have been employed for precise dynamic control over genetically engineered traits. However, the current systems for controlled transgene expression in diatoms are limited to endogenous promoters that respond to different environmental factors. We developed a highly efficient, tunable, and reversible episome-based transcriptional control system in the model diatom *Phaeodactylum tricorutum*. We assessed the time- and dose-response dynamics of each expression system using a reporter protein (eYFP) as a readout. Using our circuit configuration, we found two inducible expression systems with high dynamic range and confirmed the suitability of episome expression platform for synthetic biology applications in diatoms. Addition of a chemical inducer (β -estradiol) to transgenic strains activates transcription with a dynamic range of up to ~180-fold. We demonstrated that our episome-based transcriptional control systems are tunable and

reversible in a dose- and time-dependent manner. Using droplet digital PCR, we also confirmed inducer dependent transcriptional activation starts within minutes of inducer application without any detectable expression in the uninduced controls. The system described here expands the molecular and synthetic biology toolkits in algae and will facilitate future gene discovery and metabolic engineering efforts. This research is supported by the Office of Biological and Environmental Research in the DOE Office of Science – grant # DE-SC0008595

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A NEW CRUSTOSE SPECIES OF *PHYMATOLITHON* (HAPALIDIALES, CORALLINOPHYCIDAE) FROM THE MEDITERRANEAN SEA (ABU QIR, EGYPT)?

Phymatolithon is one of the most studied and ecologically important crustose coralline algae (CCA) because of their dominance in various marine ecosystems worldwide. The taxonomic history of the genus has been complex, and the genus has been revised multiple times on the basis of morphological and molecular analyses. As part of recent macroalgal diversity survey in the Mediterranean and Red Sea, we report on CCA specimens collected in June 2011 via snorkeling along rocky reef habitats of Abu Qir on the Mediterranean coast of Egypt. Comparative DNA sequence analysis of the plastid genes *rbcL* and *psbA* suggests a potentially new species of *Phymatolithon*. SEM revealed coaxial thallus construction, the presence of cell fusions and absence of secondary pit connections in the perithallium, and an epithallium with 1-2 cell layers. Sequencing of additional genes and morphological analyses are ongoing to confirm unambiguous species identity.

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PHOTOSYNTHETIC RESPONSE TO A WINTER HEATWAVE IN LEADING AND TRAILING EDGE POPULATIONS OF AN INTERTIDAL RED ALGAE

Global and local instabilities related to anthropogenic actions are affecting terrestrial and marine ecosystems. Especially habitat-forming macroalgae species like coralline algae, play vital roles in temperate intertidal and coastal ecosystems, however, warming in countless regions around the world negatively affected abundance as well as distribution patterns. Marine heatwaves (MHWs) caused by anthropogenic climate change are developing to become forceful key factors of change on an ecosystem level and are increasing in intensity, duration and frequency. Despite recent research efforts, knowledge about variability in fitness-related physiological traits in trailing (i.e., warmer, low latitude) versus leading (i.e., colder, high latitude) edge populations is limited. We tested if leading (Iceland) and trailing (Spain) marginal populations of the fundamentally important intertidal macroalgae *Corallina officinalis* show photophysiological resilience and recovery capability when exposed to an ambient and future winter MHW scenario. Our study reveals that ambient and future winter sea surface temperature conditions in

the intertidal environment including local MHWs do not negatively impact northern margin populations of *C. officinalis* which present a relatively constant photosynthetic. Against expectations, southern populations showed an increase in photosynthetic. Our findings indicate MHWs have no significant negative impact on the. We also show a strong regional but not population-level effect on these marginal populations. We confirm differentiation of thermal strain responses between leading and trailing margins, but responses rest on local population traits and are consequently not foreseeable only based on thermal pressures.

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ON DETECTION, IDENTIFICATION, AND DELIMITATION OF PLANKTONIC DIATOM SPECIES IN METABARCODE DATA, EXAMPLES FROM *CHAETOCEROS* AND *BACTERIASTRUM*

We used a haplotype network algorithm to detect, identify and delimit biologically meaningful species among metabarcode haplotypes in the diatom genera *Chaetoceros* and *Bacteriastrium*. Haplotypes were obtained from 48 plankton samples collected at our Neapolitan LTER Station (18S rRNA gene V4 region), and from geographic samples of Ocean Sampling Day (OSD; V4-region) and Tara Oceans (V9-region). Network analysis of haplotypes in, for instance, the *C. curvisetus* complex uncovered major (read-rich) haplotypes, each surrounded by networks of minor ones in OSD and Tara Oceans datasets. Major haplotypes were identified using reference sequences, which also enabled linking V4-haplotypes in the OSD network with V9-haplotypes in that of Tara Oceans. Both networks included major haplotypes without reference (unknown species). The species-complex as a whole was ubiquitous, but the individual species therein showed geographic patterning. To assess if close haplotypes represent biologically distinct species, we inferred haplotype networks from the LTER time-series data and mapped timing of the reads onto the haplotypes. Closely related haplotypes with an offset or distinct distribution belong to different species. In several cases, we had reference sequences for both. Thus, network analysis and info on seasonality help sorting metabarcode haplotypes into biologically meaningful species and can be deployed to validate results of ASV- or MOTU-algorithms in taxonomic groups of interest.

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PHYCOCOSM: SEQUENCING THE ALGAL TREE OF LIFE

Algae, defined as photosynthetic eukaryotes other than plants, are responsible for 50% of global primary production as phytoplankton, seaweeds, and coral and lichen photobionts. Algae cycle carbon, anchor food webs, form toxic blooms, and source a growing suite of bioproducts. However, “Algae” is a polyphyletic and paraphyletic term, since multiple distinct eukaryotic lineages acquired photosynthesis through endosymbiosis. Algae are today found in at least 9 deeply diverging clades of the eukaryotic tree of life, of which one encompasses all land plants and their sibling green algae. To fully exploit the vast fundamental diversity of algae, the US Department of Energy Joint Genome Institute (JGI) has, in collaboration with researchers from around the world, sequenced, assembled, annotated, and released to the public genomes representative of most of the major clades, often including the 1st or only genome of that clade to be sequenced. Over 100 algal genomes are available from JGI’s algal genomics resource PhycoCosm (<https://PhycoCosm.jgi.doe.gov/>) equipped with web-based genome analysis tools. With the

addition of genomes of non-photosynthetic relatives, plus an increasing variety of -omics data that complement genomics, PhycoCosm facilitates comprehensive and sophisticated comparative genomics and multiomics analyses of algae. The JGI Community Science Program (<https://jgi.doe.gov/user-programs/program-info/how-to-propose-a-csp-project/>) provides a way to collaborate with JGI to add yet more genomes and -omic datasets, and to join the PhycoCosm community.

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TROPICAL CYANOBACTERIAL DIVERSITY ALONG A TROPHIC GRADIENT IN THE NEW RIVER, BELIZE

The New River is situated in northern Belize and has a trophic gradient due to several points of anthropogenic influence including agricultural, urban, and industrial run-off. In the fall of 2019 this system experienced a severe drought, leading to fish kills and reports of harmful algal blooms (HABs) along much of the river. A study was conducted to determine the trophic state, cyanobacterial community structure, and cyanotoxin concentrations along the river from the non-impacted lagoon downstream through impacted areas and into Corozal Bay. The trophic state varied spatially along the river, starting from oligotrophic in the lagoon and increasing in trophic state near impacted areas, with *in situ* chlorophyll *a* concentrations typically exceeding 20 µg/L in these areas. Cyanobacterial community structure, and cyanotoxin concentrations varied spatially along the river and cyanobacterial HABs were seen in various locations along the river as both planktonic blooms and dislodged benthic mats. 16S metagenomic analysis detected that community structure varied along the trophic gradient. *Synechococcus* dominated throughout much of the river, though toxigenic species, such as *Microcystis aeruginosa* were also found along much of the river along with microcystins in several locations.

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PHYLOTRANSCRIPTOMICS INDICATES MULTIPLE INDEPENDENT ORIGINS OF MULTICELLULARITY AND CELLULAR DIFFERENTIATION IN THE VOLVOCINE ALGAE

The volvocine algae, which include the single-celled species *Chlamydomonas reinhardtii* and the colonial species *Volvox carteri*, serve as a model for studying the evolution of multicellularity and cellular differentiation. Many phylogenetic studies tracing the evolutionary history of this group have relied on datasets of one to a few genes for phylogenetic inference and ancestral character state reconstruction. These studies suggest that multicellularity evolved only once in the volvocine algae, that each of the three colonial families is monophyletic, and that there have been at least three independent origins of cellular differentiation in this group. We performed RNA-Seq on 55 strains representing 46 volvocine algal species, then generated a dataset consisting of transcripts from 40 single-copy, protein-coding nuclear genes. The predicted amino acid sequences of these genes were subjected to maximum likelihood, Bayesian inference, and coalescent-based analyses. These phylogenetic inferences suggest that multicellularity has evolved independently at least twice among the volvocine algae, and that the multicellular species do not form a clade, as previously thought. We also find that the colonial family Goniaceae is not monophyletic. Our analyses further suggest that cellular differentiation independently

evolved at least four and possibly as many as six times within this group. These results represent the most taxonomically comprehensive phylogeny yet produced using a nuclear dataset for the volvocine algae.

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METABARCODING OF AUTOTROPHIC EUGLENIDS BASED ON V2 18S rDNA MARKER, CURATED REFERENCE DATABASE AND OPTIMIZED PROTOCOL OF DNA ISOLATION

Although autotrophic euglenids are widespread and common in freshwater environments, their ecology is still rather poorly understood. The DNA metabarcoding, that has become a powerful molecular tool frequently used for biodiversity assessment for various groups of algae, gives very little new data concerning euglenids, because they are underrepresented in most HTS-based environmental surveys. It is mostly due to the long and highly variable nSSU rDNA sequences that are difficult to amplify with universal eukaryotic primers and the lack of curated reference database that can hamper correct euglenid species identification. Herein we designed and tested euglenid targeted metabarcoding approach based on V2 18S rDNA marker, newly designed euglenid specific primers and curated database of reference sequences. We also investigated the performance of DNA capture and extraction methods for environmental samples. The GeneMATRIX Soil DNA Purification Kit (Eurx) was chosen as the most suitable method of DNA isolation due to the best quality and quantity of obtained DNA as well as the relatively low costs and workload. From the studied biomass harvesting methods, centrifugation gave similar results to filtering and the choice between them is not crucial for the reliability of the analysis. Using proposed metabarcoding approach resulted in obtaining a high fraction (85%) of euglenid reads and species-level identification of almost 90% of them. Fifty species were detected by metabarcoding method, including almost all species observed using a light microscope.

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CAN THE GREEN MICROALGAE HELP IN REDUCING WATER SCARCITY IN JORDAN?

Jordan is one of the most water-scarce countries in the world, water scarcity affects the economic development and the stability of the country. Safe reusing of the treated wastewater in the agriculture sector that consumes around 60% of the freshwater resources will reduce the pressure on freshwater resources. Green microalgae can be applied in large-scale High Rate Algal Pond (HRAP) for wastewater treatment as an environmentally friendly process, but this application has many challenges. To achieve the sustainability in HARP system, it has to remove excess nutrients in wastewater efficiently at relatively low capital and operational costs. Thus, this work aims to isolate, identify, and evaluate locally adapted green microalgae isolates that grow rapidly, removes nutrients efficiently and be harvested easily by gravity to be applied to HRAP systems in Jordan. Water samples were collected from WWTPs and freshwater resources, eight different green microalgae isolates were obtained and characterized using the *18SrRNA* gene and ITS1-5.8S-ITS2 sequences. The isolates belong to *Desmodesmus*, *Chlorella*, *Acutodesmus*, and *Coelastrrella* genera. The isolates were assessed based on their growth rate in wastewater, efficiency in removing nutrients (e.g. phosphorus and nitrogen), and their settleability by gravity. After ranking the isolates two promising candidates on small scale were obtained, Jordan_18 and Jordan_29 to be applied on large-scale evaluation in the future

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MOLECULAR ANALYSES FOR THE SNOW-INHABITING MICROORGANISM, *CHIONASTER NIVALIS*

In thawing snow and glaciers, food webs are composed of cold-adapted microorganisms such as algae, heterotrophic protists, rotifers, fungi, and bacteria. To reveal the biodiversity of those ecosystems, we have conducted taxonomic studies for snow-inhabiting algae at species level, based on cultured materials as well as field-collected cysts (e.g., Matsuzaki et al. 2019, *PLoS One*). *Chionaster nivalis* is one of the typical unicellular microorganisms found in the ecosystems in Northern Hemisphere, especially in blooms of snow-inhabiting algae (i.e., colored snow). Despite the many previous reports, the taxonomic position of *C. nivalis* above genus level has long been unclear, possibly due to the reason that the species has been uncultured. To unveil the taxonomic position of *C. nivalis*, we obtained the ribosomal RNA operon sequences of the species, using the DNA extracted from more than 200 cells of *C. nivalis* isolated from a Japanese colored snow material. Our molecular phylogeny using the concatenated 18S and 28S ribosomal DNA sequences of the Japanese specimens strongly indicated that the species is sister to *Bartheletia paradoxa* (Bartheletiomycetes), which is a filamentous fungus associated with fallen *Ginkgo biloba* leaves and is known as an orphan basal lineage of the subphylum, Agaricomycotina. We also detected the sequences assignable to *C. nivalis* in the previously examined meta-amplicon sequencing datasets from snowpacks and glaciers in Northern Hemisphere as well as Antarctica.

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HARMFUL ALGAL BLOOM DYNAMICS IN THE LAKE OKEECHOBEE SYSTEM: PRELIMINARY FINDINGS FROM MONTHLY FIELD MONITORING AND EXPERIMENTAL MESOCOSMS

A collaborative project is underway to better understand harmful algal bloom (HAB) ecology in the Lake Okeechobee system and provide information to management agencies that will help guide mitigation and control of HABs. Monthly field surveys are being conducted to understand patterns and drivers of phytoplankton assemblage structure, cyanotoxin and cyanotoxin-gene concentrations in Lake Okeechobee and the connected Caloosahatchee and St. Lucie Rivers. In-situ mesocosm experiments are conducted three times a year on the Caloosahatchee River to test the effects of nitrate (NO₃), ammonium (NH₄), and phosphate (PO₄) enrichment on phytoplankton assemblages and toxin production. In 2019, algal cell densities were highest in the northwestern region of the lake where the influence of freshwater inflows from the Kissimmee River and several canals is greatest. The phytoplankton assemblage was dominated

by cyanobacteria. The most abundant toxin-producing genera were *Microcystis*, *Dolichospermum*, and *Raphidiopsis*. Microcystin and cylindrospermopsin were the most frequently detected toxins. Saxitoxin and anatoxin were also detected at much lower concentrations. The cyanotoxin-genes *mcyE*, *cyrA*, *anaC*, and *sxtA* were all detected. The NO_3 , NH_4 , and PO_4 treatments in the first mesocosm (September 2019) did not have significant effects on phytoplankton assemblage (PERMANOVA $P > 0.05$) or cyanotoxins (MANOVA $P > 0.05$). However, total algal cell density, chlorophyll-a and phycocyanin concentrations increased significantly ($P < 0.05$) over the 72-hour study regardless of treatment suggesting that nutrients were not limiting to algal growth in September mesocosms but that some other limiting factor, potentially light, became more available.

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HELLO DARKNESS: RED ALGAL PATCH DYNAMICS ON TEMPERATE ROCKY REEFS

This study simulated storm disturbances of varying frequency and magnitude in two geographically distinct regions in California (Monterey, San Diego) and assessed the subtidal community's response via benthic presence and photosynthetic capabilities. We sought to understand how a kelp forest may respond to the physical removal of brown algae canopy and sub-canopy layers, and what patterns of succession may take place. From pre and post-manipulation surveys, we saw a significant increase in red algal biomass within removal plots (i.e. simulated canopy removal), but did not see differences in red algal biomass or community assemblages across treatments. Rather, simple patchiness in red algae communities accounted for most of the variation observed in both locations, suggesting that community organization likely results from individual species' life history characteristics, their ecologies, and stochastic processes. We then sought to understand the responses of red algae to these disturbances, and to subtly understand their photosynthetic-capabilities, which can be thought of as a proxy for ecological success, to better understand if their responses were due to light adaptations from competitive release. In comparing photosynthetic properties (α and p_{max}), we found that sites, seasons, and the interaction between treatment and season were major drivers of red algal photosynthetic capability. Our results suggest that light adaptations in red algae reinforce patch dynamics in temperate reef communities.

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CHLOROPLAST mRNAs ARE 3' POLYURIDYLYLATED IN THE GREEN ALGA *PITHOPHORA ROETTLERI* (CLADOPHORALES)

Species within the green algal order, Cladophorales, have an unconventional plastome structure where individual coding regions or small numbers of genes occur as linear single-stranded DNAs folded into hairpin structures. Another group of photosynthetic organisms with an equivalently reduced chloroplast genome are the peridinin dinoflagellates of the Alveolata eukaryotic lineage whose plastomes are mini-circles carrying one or a few genes required for photosynthesis. One unusual aspect of the Alveolata is the polyuridylylation of mRNA 3' ends among dinoflagellates, and the chromerid algae. This study was

conducted to understand if an unconventional highly-reduced plastome structure co-occurs with unconventional RNA processing. Evidence of several processing events were collected, most notably the 3' termini of six of the eight genes were polyuridylylated, which has not been reported for any lineage outside of the Alveolata. Other processing events include poly(A) and heteropolymeric 3' additions, 5' primary transcript start sites, as well as the presence of circularized RNAs. Five other species representing other green algal lineages were also tested and poly(U) additions appear to be limited to the order Cladophorales. These results demonstrate that chloroplast mRNA polyuridylylation is not the sole provenance of photosynthetic alveolates and may have convergently evolved in two distinct photosynthetic lineages.

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ALL MIXED UP: RECONCILING DIVERGENT EVOLUTIONARY RESPONSES OF MIXOTROPHS TO CLIMATE CHANGE

Plastidic protozoa, or phytoplankton that eat, combine photosynthesis and heterotrophy to meet their energetic and material needs. These mixotrophs vary in the extent to which they rely on these two forms of metabolism, and their relative investment in each may evolve as the ocean warms. We combined mathematical models and evolution experiments to test the prediction that mixotrophs should become more heterotrophic at warmer temperatures because aerobic respiration increases more rapidly with temperature than photosynthesis. Our numerical simulations supported this prediction, showing that mixotrophs should increase their investment in heterotrophy (and reduce their investment in photosynthesis) as part of an evolutionarily stable strategy at warmer temperatures. However, our evolution experiments using the genus *Ochromonas* show that these mixotrophs evolve to maintain, and even increase, their investment in photosynthesis at warmer temperatures. This evolved strategy appears to be adaptive, as evolved lineages have higher growth rates than lineages evolved at ancestral temperatures. We argue that an understanding of physiological and ecological tradeoffs may explain these contradictory predictions: First, if mixotrophs feed to obtain nutrients as well as prey carbon, heterotrophy and phototrophy can be synergistic. Second, increased heterotrophy by mixotrophs suppresses prey populations, creating an ecological feedback that can alter the direction of selection to favor photosynthesis at hot temperatures.

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IDENTIFICATION OF LATITUDINAL AND TISSUE-SPECIFIC AMPLICON SEQUENCE VARIANTS OF BACTERIA IN HOST MICROBIOMES OF THE BROWN ALGA *FUCUS VESICULOSUS* (PHAEOPHYCEAE)

We investigated microbiomes of *Fucus vesiculosus* because of its large, cross-Atlantic range and ecological importance. We compared host bacterial communities along the entire eastern and western Atlantic range with 16S rRNA gene amplicon sequencing of holdfasts, vegetative tips, and receptacle samples of *F. vesiculosus* from 16 sites in 2 summers (2015, 2016). Rather than using taxonomic identification or 97% overall sequence identity to define operational taxonomic units, we looked for

biologically significant sequence variation using Minimum Entropy Decomposition, which defined amplicon sequence variants (ASVs). We discovered a wealth of diversity within specific genera, most notably, 86 distinct *Granulosicoccus* ASVs. We aligned our ASVs with reference *Granulosicoccus* 16S sequences and ASVs from the Pacific brown algae *Nereocystis* and *Macrocystis* (Weigel and Pfister 2019). The highly abundant *Granulosicoccus*_t3260 is identical to the V4 region of a bacterial sequence cloned from the surface of *F. vesiculosus* (Lachnit et al., 2011), and many North-Central ASVs were similar/identical to reported sequences from other brown algae. Most *Granulosicoccus* ASVs were holdfast or vegetative specialists. Forty-two ASVs were distributed predominantly in the host's North (22), Central (7), or South (13) latitudinal range. Some closely related ASVs in *Blastopirellula*, *Octadecabacter*, and *Roseobacter* had contrasting tissue and/or biogeographic distributions, showing that minor differences in the 16S gene can suggest phylogeographic or functional distinctions worthy of further study.

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THE PATCHWORK PLASTID PROTEOMES OF FUCOXANTHIN DINOFLAGELLATES

Kareniaaceae is a group of mixotrophic marine dinoflagellates known for producing toxins and causing harmful algal blooms. These algae harbor fucoxanthin-containing complex plastids derived from haptophytes that replaced the evolutionarily ancestral peridinin plastids in a serial endosymbiotic event, possibly after a period of secondary heterotrophy. As a result, these plastids function on a mix of proteins originated from both the early plastid and the extant plastid, as well as host-derived proteins and proteins gained laterally from other algal sources, congruent with the “shopping bag” model. In order to be able to observe the larger picture of this evolutionary patchwork and use its compositions and patterns of occurrence in different metabolic pathways to draw conclusions about the history of plastid loss and regain in this lineage, we sequenced five new transcriptomes, obtained *in silico* proteome datasets using a kareniaaceae-specific targeting prediction, and performed a large-scale analysis of their evolutionary origin employing automatic generation and sorting of single-gene trees for all the putative plastid protein sequences. Our results based on more than 20,000 trees from seven transcriptomes show that the abundance of haptophyte (plastid-late) proteins differs notably between the studied genera and that the evolutionary pattern in plastid metabolic pathways is not as consistent as we expected, especially in the case of *Takayama helix*, suggesting that the evolutionary history of its plastid might have taken a different path.

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RE-DISCOVERY OF THE THIRD MATING SYSTEM OF “VOLVOX AFRICANUS“ FROM CULTURES ORIGINATING FROM THE HOMETOWN OF DINOSAURS IN THAILAND*

Diversity and evolution of mating systems attract biologists in a broad range of eukaryotic taxa. Freshwater green algae are convenient research materials of sexuality because their sexual reproduction can be easily induced in culture. Until 2006, molecular genetic studies of sexuality mainly used unicellular *Chlamydomonas* by Drs P. J. Ferris and U. W. Goodenough and their group. *Chlamydomonas*

is isogamous, but its related multicellular volvocine algae represent male and female differentiation and various mating systems. Thus, our 2006 discovery of the male-specific gene *PlestMID* (“*OTOKOGP*”) in anisogamous *Pleodorina* became the breakthrough for subsequent molecular genetic studies of evolution of male and female using volvocine algae. On the other hand, Dr. R. C. Starr in 1971 reported four mating systems in world-wide strains identified as “*Volvox africanus*” (VxAf). Although Dr. A. W. Coleman in 1999 determined ITS-2 sequences of these strains, most of them were extinct. In 2015, we rediscovered VxAf strains with two mating systems (heterothallic, homothallic with male and bisexual spheroids) from the Japanese ancient lake “Lake Biwa”, and we are revealing the molecular genetic bases of VxAf mating system diversity. In the present study, we obtained VxAf strains with the third mating system (homothallic with male and female sexual spheroids) from Kalasin Province, the hometown of dinosaurs in Thailand. We will report on its morphology and classification. [*Dedicated to the memory of Dr. Patrick J. Ferris]

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SUNGMINIACEAE FAM. NOV. (RALFSIALES, PHAEOPHYCEAE), *SUNGMINIA* GEN. NOV. AND THREE NEW *SUNGMINIA* SPECIES FROM KOREA BASED ON MOLECULAR AND MORPHOLOGICAL ANALYSES

The crustose brown algal order Ralfsiales Nakamura ex P.-E. Lim and H. Kawai is composed of five families: Hapalospongiaceae, Mesosporaceae, Neoralfsiaceae, Pseudoralfsiaceae and Ralfsiaceae. The Ralfsiales is identified by discoid development during initial stage; one to several chloroplasts without pyrenoids; plurilocular zoidangia with sterile terminal cell(s) and terminal unilocular zoidangia; presence of crustose gametophytic or sporophytic stage(s) in the life history. In this study, we describe a new family within the Ralfsiales, Sungminiaceae fam. nov. from Korea based on molecular and morphological analyses. Sungminiaceae fam. nov. is characterized by small crusts, erect filaments laterally adjoined but partially separate with pressure and not tapered, with apical vegetative cells larger than other cells, intercalary plurangia capped with a sterile cell, unilocular sporangia on the terminal part of erect filaments with associated paraphyses. Our phylogenetic analyses of *rbcL* and COI-5P genes reveals that Sungminiaceae is sister to Mesosporaceae, with a strong bootstrap supporting value.

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ALGAE-BASED DAIRY MANURE WASTEWATER TREATMENT INTEGRATED WITH ANIMAL FEED PRODUCTION

In this study, six different strains of microalgae from *Chlorella* and *Scenedesmus* genera were screened to test their capabilities to remove nutrients present in wastewater collected from a dairy farm. Based on the best removal capacity, *Chlorella sorokiniana* UTEX1230 was cultivated in a custom designed floating plastic photobioreactors (FP-PBR) operated in batch mode and fed with coagulated, filtered and 1/4 diluted farm wastewater. Removal rates of 59.4%, 64.2% and 95.7% were obtained for total phosphorus, total nitrogen, and chemical oxygen demand, while biomass concentration of 1.8 g/L was achieved. To demonstrate a circular bioeconomy case by upcycling agricultural wastewater nutrients, microalgal biomass was further explored as potential feed formulations for livestock and aquaculturing operations. For this purpose, biochemical characterization including protein, carbohydrate, lipid content, vitamin,

amino acid, and FAME profiles were determined. Total lipid content of 22.6%, monomeric sugar content of 47.3%, and total hydro-soluble protein content of 28.7% were measured in harvested microalgal biomass. All essential amino acids, B3, B9, B12, C, and E vitamins and beta carotene were detected and quantified in the biomass. Palmitate, stearate, linolenate and linoleate fatty acids were also quantified. Overall, the study was aiming to optimize general and specific parameters of a low-cost microalgae-based agricultural wastewater treatment applications and generate value added bio-feed products for sustainable livestock production and aquaculturing facilities.

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MITIGATING HARMFUL CYANOBACTERIAL BLOOMS IN A HOTTER, HYDROLOGICALLY MORE EXTREME WORLD

Managing and mitigating the global expansion of toxic cyanobacterial harmful blooms (CyanoHABs) is a major challenge facing researchers and water resource managers. A variety of approaches including nutrient load reduction, artificial mixing and flushing, omnivorous fish removal, algacide applications and sediment dredging have been used to reduce bloom occurrences. However, managers now face the additional challenge of having to address the effects of climate change on watershed hydrologic and nutrient load dynamics, water temperature, mixing regime and internal nutrient cycling. Rising temperatures, increasing frequencies and magnitudes of extreme weather events, including tropical cyclones, extra-tropical storms, floods and droughts all promote CyanoHABs and influence the efficacy of ecosystem remediation measures. These climatic changes will likely require setting stricter nutrient (including both nitrogen and phosphorus) reduction targets for bloom control in impacted waters. In addition, the efficacy of currently used methods to reduce CyanoHABs will need to be re-evaluated in light of the synergistic effects of climate change with nutrient enrichment.

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YOU ARE THE PLASTID YOU STEAL: PREY SPECIES INGESTED IMPACTS PHYSIOLOGICAL AND TRANSCRIPTIONAL RESPONSE IN THE CILIATE *MESODINIUM CHAMAELEON*

A number of eukaryotic protists obtain their ability to photosynthesize through kleptoplasty, the retention of photosynthetically active chloroplasts from their prey. Organisms capable of kleptoplasty use the photosystems of ingested prey to produce sugars that make up a significant amount of the carbon captured and energy demands of the host. Kleptoplasty has independently evolved multiple times in diverse lineages, but the mechanisms involved in kleptoplasty evolution, acquired plastid maintenance, and regulation are not well understood. Here, we focused on the mechanisms that enable plasticity--especially the use of plastids from multiple prey types--in kleptoplastidic organisms. We fed the kleptoplastidic ciliate *Mesodinium chamaeleon* four different species of cryptophyte prey and used transcriptomics to get

insights into the metabolism in both well-fed and starved states. Prey species identity had the largest impact on ciliate regulation and expression patterns. Interestingly prey identity had a larger impact on ciliate expression than whether the ciliate was well fed or starved, and the greater the phylogenetic distance between prey types the greater the difference in ciliate expression. In part, these differences may have been driven by physiological performance of the stolen chloroplasts, as plastid origin affected maximum photosynthetic capacity, ciliate growth rates, and tolerance of starvation.

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A NEW SPECIES OF *TIMAVIELLA* (OCULATELLACEAE, CYANOBACTERIA) FROM CANYONLANDS NATIONAL PARK

Timaviella was described four years ago with two species from Giant Cave in Trieste, Italy. Since that time two new species were described from subaerial habitats in Utah, USA, and a species formerly in *Plectonema* was transferred to the genus. We recently sequenced a strain isolated from soil crusts in Canyonlands National Park, Utah that had putatively been placed in *Leptolyngbya*. We found that this strain actually belonged to *Timaviella*. Upon analysis of the 16S-23S ITS region in species of this genus, we found that it is a species separate from the five named species in the genus. However, it was close to two unnamed strains in the genus, one from the epilithon of a lake, and the other from soil crust in the White Mountains Wilderness Area in California. Secondary structures of the conserved domains of the ITS region supported placement of the three strains in a new species. Percent dissimilarity among ITS sequences in the different species of *Timaviella* were all >13% dissimilar, strong evidence that they are distinct species. The three strains in our new species have ITS dissimilarity ranging from 2-4%, and given the discontinuity between dissimilarity values, we conclude that they should be placed within the same new species. We propose to name this species after Jayne Belnap, who has long conducted studies of biological soil crusts, especially in Canyonlands National Park.

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RESISTANCE THROUGH SEX: INSIGHTS INTO THE CONJUGATION PROCESS AND ZYGOSPORE STRUCTURE IN FIELD SAMPLED *MOUGEOTIA* SP. (ZYGNEMATOPHYCEAE)

Zygnematophyceae are the ancestors of all land plants, and a variety of adaptation strategies to terrestrial habitats are known. To better understand their evolutionary success, we studied their sexual reproduction process by conjugation and the resulting features of the zygospores. Field samples of *Mougeotia* were collected in the Austrian Alps and assigned to the two species *M. parvula* and *M. disjuncta*. The main difference was found in the surface structure of the zygospores. During the conjugation process pectins, xyloglucans, xylans, arabinogalactan proteins and extensins, were detected by glycan microarray analysis and *in situ* staining. Upon maturation, the zygospores darkened, accumulated storage compounds and got

surrounded by a thick multi-layered cell wall. Transmission electron micrographs showed a three-layered architecture of the zygospore wall, consisting of a polysaccharide rich endo- and exospore, interrupted by a massive electron dense mesospore. An additional layer with a lipid-like appearance was observed between the two inner layers, possibly resembling a precursor of the mesospore. Raman imaging detected carbohydrates in the endo- and exospore, while an enrichment of lipids and an aromatic-rich layer were found in the mesospore, likely containing sporopollenin-like components. Overall, a major reorganization of the zygospore wall during maturation, leading to a resistant and protective structure, was shown. It is likely that *Mougeotia* is able to survive unfavourable conditions by the formation of a water-proof layer in the zygospore wall.

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UNDERSTOREY CHANGES COMPOSITION AFTER TEMPERATE KELP FOREST COLLAPSE BUT KEEPS RICHNESS AND DIVERSITY

Kelps are foundation species that provide important ecosystem services in temperate rocky shores worldwide. Similarly to terrestrial forests, healthy kelp forests are structurally complex as they are often arranged as patches composed by a multi-layered understory of algae aggregations with different canopy adaptations. Over the last decades, several studies have reported a global kelp forest degradation, turning seascapes dominated by complex forest into structurally simpler mats of low-laying seaweeds. In NW Spain, golden kelp (*Laminaria ochroleuca*) canopy forests have recently receded within the limits of a MPA. This paradoxical loss inside a MPA allowed us to investigate the consequences of kelp forest collapse for other members of the biotic community, using nearby healthy kelp forest outside the MPA as a control. To assess these changes, four degraded sites within the MPA and four healthy kelp forest in nearby areas were sampled year round to assess the seasonal dynamics of understory algae. Healthy and degraded kelp reefs had significantly different understory assemblage compositions. However, unlike our expectations, these differences had little to none impact on the richness and diversity of the understory assemblage. Moreover, understory differences were only perceptible when the assemblages were compared at the lowest taxonomic resolution (species). Unlike other studies, comparisons based on functional groups (canopy, sub-canopy, turf and crust) failed to detect any significant difference between healthy and degraded kelp forest.

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RELYING ON LIGHT IN A LIGHT-LIMITED ENVIRONMENT: CHLOROPHYLL BIOSYNTHESIS IN THE ANTARCTIC PSYCHROPHILE *CHLAMYDOMONAS* SP. UWO241

You would not expect to find photosynthetic life 17 meters below the surface of a permanently ice-covered Antarctic lake, where there is only low blue light half the year and darkness the other half. Yet this is exactly where the green alga *Clamydomonas* sp. UWO241 thrives. Algae and plants produce chlorophyll (Chl) through a complex and well-regulated pathway, allowing them to absorb light from the sun to power photosynthetic reactions and carbon fixation. Despite its low light environment, UWO241 has lost the genes required for light independent Chl biosynthesis and instead relies on a light dependent enzyme. Curiously, a related green alga isolated from the same lake, *Chlamydomonas* sp. ICE-MDV, has retained the genes for Chl biosynthesis in the dark. Growth of both species under varied light quantities and qualities highlighted the effects of this loss on Chl biosynthesis. Under varied light conditions UWO241 has a reduced ability to alter Chl levels compared to ICE-MDV, and instead relies on alteration of Chl *a:b* ratios to acclimate to the different light conditions. Despite the ability of ICE-MDV to alter Chl levels to a greater degree than UWO241, its growth rates were significantly decreased in some light conditions. This suggests that the ability to synthesize Chl is not the single limiting factor in survival under varied light conditions. Future work aims to untangle the survival strategies used by these unique low-light thriving psychrophiles, providing insight into photosynthetic adaption under extreme shading.

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DIVERSITY OF EUCEUMATOID-ASSOCIATED EPIPHYTIC FILAMENTOUS RED ALGAE (EFA) IN MALAYSIA

Malaysia is one of the key players in the cultivation of the tropical red algal carrageenophytes *Kappaphycus* and *Euचेuma*, collectively termed the eucheumatoids. Infestation of the eucheumatoids by epiphytic filamentous red algae (EFAs) presents a persistent challenge in the cultivation of these crops globally. The infected eucheumatoids produced lower carrageenan yield and quality, resulting in reduced selling price. Hitherto, identification of these epiphytes is generally based on microscopic observations and until now they have been referred to members of the genera *Polysiphonia* or *Neosiphonia* (Rhodomelaceae, Ceramiales). The objective of this study is to assess the diversity and distribution of the epiphytic filamentous red algae (EFAs) associated with eucheumatoids in Sabah, Malaysia, via barcoding with *rbcL* and *cox1* genetic markers. The most prevalent EFA, identified as *Melanothamnus thailandicus* (formerly *Neosiphonia thailandica*), was present in all three species of *Kappaphycus* cultivated. Members of the Ceramiaceae, including *Gayliella* sp. and *Ceramium* sp., in addition to *Tolypocladia glomerulata* and *Chondria* sp. were also found to be epiphytic on the eucheumatoids, albeit with a weaker degree of attachment to the hosts. The results raise questions about the nature of the relationship of these epiphytes and whether they are host-specific or host generalists, but also the importance of taxonomy at the species and strain levels in being able to determine those conclusions.

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MITOCHONDRIAL MRNA PROCESSING IN THE CHLOROPHYTE ALGA *PEDIASTRUM DUPLEX* AND THE STREPTOPHYTE ALGA *CHARA VULGARIS* REVEALS AN EVOLUTIONARY BRANCH

Mitochondria carry the remnant of an ancestral bacterial chromosome and express those genes with a system separate and distinct from the nucleus. Mitochondrial genes are transcribed as poly-cistronic primary transcripts which are post-transcriptionally processed to create individual translationally competent mRNAs. In algae post-transcriptional processing has only been explored in *Chlamydomonas reinhardtii* (Class: Chlorophyceae) and the mature mRNAs are different than higher plants, having no 5' UTRs, much shorter and more variable 3' UTRs and polycytidylated mature mRNAs. In this study we analyzed transcript termini using circular RT-PCR and PacBio Iso-Seq to survey the 3' and 5' UTRs and termini for two green algae, *Pediastrum duplex* (Class: Chlorophyceae) and *Chara vulgaris* (Class: Charophyceae). This enabled the comparison of processing in the chlorophyte and charophyte clades of green algae to determine if the differences in mitochondrial mRNA processing pre-dates the invasion of land by embryophytes. We report that the 5' mRNA termini and non-template 3' termini additions in *P. duplex* resembles those of *C. reinhardtii* suggesting a conservation of mRNA processing among the chlorophyceae. We also report that *C. vulgaris* mRNA UTRs are much longer than chlorophytic examples, lack polycytidylation, and are polyadenylated similar to embryophytes. This demonstrates that some mitochondrial mRNA processing events diverged with the split between chlorophytic and streptophytic algae.

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EFFECTS OF LIGHT INTENSITY, PHOTOPERIOD AND NITRATE LEVELS ON FATTY ACIDS BIOMASS OF GREEN ALGAE *SCENEDESMUS DIMORPHUS*

The potential effects of various photoperiod, light intensity and of nitrate levels were examined on fatty acids biomass of *Scenedesmus dimorphus*. Three levels of photoperiod 12:12, 8:16 and 16:8 hours dark: light, light intensity of 3000, 5000 and 7000 lux and nitrate levels of 1.47, 2.94 and 4.41 mmol/l were set up. Pure culture of *Scenedesmus dimorphus* was carried out at 28±2 °C in BBM culture medium. Analyses of fatty acids revealed 3 fatty acid types. Saturated fatty acids varied between 0.83% up to 20.61% in different treatments. The highest concentration of fatty acids was observed at 5000 lux light intensity, 8:16 Photoperiod and 1.47 mmol/l nitrate levels and the lowest at 5000 lux light intensity, 16:8 Photoperiod and 4.41 mmol/l nitrate levels. The highest levels of monounsaturated fatty acid were detected at 5000 lux light intensity, 8:16 Photoperiod and 1.47 mmol/l nitrate levels. No monounsaturated fatty acid was observed in some treatments. The highest concentration of polyunsaturated fatty acids (46.45%) was recorded at 5000 lux light intensity, 16:8 photoperiod and 1.47 mmol/l nitrate. No polyunsaturated fatty acid was observed at 7000 lux light intensity, 12:12 photoperiod and 1.47 mmol/l nitrate levels.

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***CRUSTAPHYTUM?* SP. NOV., A NEW MAGNIFICENT AND EXPANSIVE SPECIES OF CRUSTOSE CORALLINE ALGAE FROM THE FLOWER GARDEN BANKS NATIONAL MARINE SANCTUARY**

Specimen collections and video observations performed with a remotely operated vehicle (ROV) in the Flower Garden Banks National Marine Sanctuary offshore Texas revealed the presence of a new and very interesting species of crustose coralline algae. Underwater video footage showed that this species forms expansive sheets that encrust upon rubble, sediment, and other material, and that it plays a significant role in consolidating the substratum and in primary production. Preliminary DNA sequence analyses of *rbcL* and *psbA* sequences showed that this species is closely related to both *Crustaphytum* and *Tectolithon* species. SEM observations revealed vegetative anatomy with coaxial construction, rhizoids on the ventral surface, perithallium with cell fusions present and secondary pit connections absent, tear-drop shaped intercalary meristematic cells, and an epithallium comprised of 1-2 cell layers. Rhizoids are hypothesized to play a role in anchoring this species to the substratum and assisting in consolidating the sediment and rubble. Specimens with multiporate conceptacles were observed, confirming the placement of this species in the Hapalidiales. Specimens with uniporate gametangial conceptacles were also observed.

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TROPHIC REGULATION OF ALGAL SIZE STRUCTURE

The presence of edible and inedible prey species in a food web can influence the strength that nutrients (bottom-up) or herbivores (top-down) have on primary production. In boreal peatlands, wetter more nutrient-rich conditions associated with ongoing climate change are expanding consumer access to aquatic habitat and promoting sources of primary production (i.e., algae) that are susceptible to trophic regulation. Here, we used an in-situ mesocosm experiment to evaluate the consequences of enhanced nutrient availability and food-web manipulation (herbivore and predator exclusion) on algal assemblage structure in an Alaskan fen. Owing to the potential for herbivores to selectively consume edible algae (small cells) in favor of more resistant forms, we predicted that the proportion of less-edible algae (large cells) would determine the strength of top-down or bottom-up effects. Consistent with these expectations, we observed an increase in algal-cell size in the presence of herbivores (2-tiered food web) that was absent in the presence of a trophic cascade (3-tiered food web), suggesting that predators indirectly prevented morphological changes in the algal assemblage by limiting herbivory. Increases in algal-cell size with herbivory were driven by a greater proportion of filamentous green algae and nitrogen-fixing cyanobacteria, whose size and morphological characteristics mechanically minimize consumption. While consumer-driven shifts in algal assemblage structure were significant, they did not prevent top-down regulation of biofilm development by herbivores. Our findings show that increasing wet periods in northern peatlands will provide new avenues for trophic regulation of algal production, including directly through consumption and indirectly via a trophic cascade.

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HEAVY METAL REMOVAL FROM INDUSTRIAL WASTEWATER BY MICROALGAE

Industrial wastewater contains various heavy metals which pose a risk to receiving water bodies and human health. Treatment of heavy metals using microalgae is a cheaper and sustainable alternative as microalgae are fastidious, photoautotrophic organisms and consumes high amounts of CO₂. In this study, we examined the removal efficiency of five heavy metals, namely, As, Cd, Cu, Pb, and Zn by microalgae treatment system. In Phase I, species with the highest tolerance among *Anabaena flos-aquae*, *Chlorella vulgaris*, *Coccomyxa subellipsoidea*, *Ettlia oleoabundans*, and *Tetraselmis suecica* was determined by challenging the growth metrics by exposure to individual heavy metals. The most effective metals limiting microalgae growth were Cu and Cd. *T. suecica* performed best survival against Cu and Cd, having IC₅₀ values 4.2±2.6 mg/L and 8.4±2.5 mg/L, respectively, whereas IC₅₀ values of other microalgae were around or below 1 mg/L for Cu and <4 mg/L for Cd. *T. suecica* also showed high tolerance against As, Pb, and Zn, with IC₅₀ values 105±50, 27±1, and 22±4 mg/L, respectively. In Phase II, a synthetic wastewater containing all five metals will be treated in an up-flow packed bed reactor filled with *T. suecica* cells immobilized into Ca-alginate capsules. Removal efficiency of the metals and treatment lifetime of the reactor will be determined.

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MOLECULAR STRATEGIES FOR ENHANCING PHOTOSYNTHETIC EFFICIENCY IN GREEN ALGAE

One of the major constraints limiting algae biofuel production is low biomass yield. LCA and TEA analyses indicate that 2- to 3-fold increases in algal biomass yields could help algal biofuels approach parity with petroleum-based fuels. One way to increase algal biomass yields is to increase photosynthetic efficiency. All plants and algae have inherent inefficiencies in photosynthesis achieving no more than 4% energy conversion efficiency. Theoretically, however, it is possible to achieve 11% photosynthetic efficiency. Furthermore, all algae light saturate photosynthesis at ¼ full sunlight intensity. Recently, we developed a strategy to better utilize photons at high light intensities by modulating the optical cross section of the photosynthetic light harvesting antenna. We modulate the optical cross section of the light harvesting antenna as a function of light intensity. This is achieved by regulating chlorophyll b (Chl b) synthesis using a light regulated translational repressor that regulates the translation of a hybrid chlorophyllide a oxygenase gene. Since Chl b is present only in the peripheral light harvesting antenna of green algae reductions in its accumulation result in a diminution of the antenna size. We determined that algae lacking one LHClI trimer, equivalent to a 30% reduction in Chl b content, had substantially higher rates of photosynthesis than wild-type algae while maintaining normal levels of non-photochemical quenching to mediate light stress. Light-dependent control of light harvesting antenna size results in a doubling of biomass yield.

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NEW PEYSSONNELIOID ALGAE SPECIES FROM HAWAI'I'S MESOPHOTIC CORAL ECOSYSTEMS

Collections made by submersibles and technical diving have yielded thousands of new algae specimens that we are analyzing in the context of what we know about the shallow water algae of Hawai'i, as well as the deep water (mesophotic) flora of other regions of the Pacific. Data highlighting some recent discoveries of algal diversity from the red algal Order Peyssonneliales from the mesophotic coral ecosystems of the Hawaiian Islands will be presented. These algae play a critical role as dominant assemblages in the Mediterranean and tropical Atlantic islands, and also in some parts of the Hawaiian archipelago. Moreover, some members of the Peyssonneliales exhibit invasive characteristics in the Caribbean and tropical western Pacific, overgrowing and smothering coral. The general morphology of these algae is typically crustose and less charismatic than many of the showier deep-water algae, but extensive cryptic or pseudocryptic diversity has been revealed through detailed microscopic observations paired with molecular phylogenetic reconstruction. These collections include undescribed species from the genera *Incendia*, *Peyssonnelia*, *Ramicrusta*, *Seiria*, and *Sonderophycus*. In the near future we will be characterizing many more collections from this order as well as from other groups of algae with the overall goals of: 1) describing new biodiversity, 2) learning more about how unique these mesophotic algae are relative to related shallow water species, and 3) enabling investigation into the ecological role of mesophotic algal communities in the Hawaiian archipelago.

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POLYPHASIC INVESTIGATIONS OF THE RARE HETEROCYTOUS CYANOBACTERIAL GENUS *CAMPTYLONEMOPSIS* FROM HAWAII AND INDIA

The rarely occurring heterocytous cyanobacterial genus *Camptylonemopsis* was sampled from parts of the Hawaii islands and central India with initial observations showing routine tapering filaments. A detailed polyphasic investigation using morphological, molecular, phylogenetic tools and folded structures of the 16S-23S ITS region indicated towards the presence of multiple putative new species of the genus *Camptylonemopsis*. Morphological features showed different levels of variability in all the isolates with the isolates differing in the presence/absence of necridia, amount of tapering and the sheath surrounding the trichomes. The 16S rRNA gene phylogeny indicated the Indian isolate LS3A-PS and the isolate from Hawaii, *Camptylonemopsis* sp. HA4241-MVI to be in the same cluster while the other two isolates from Hawaii, *Camptylonemopsis* sp. HA4241-MV5 and *Camptylonemopsis* sp. HA4241-MV6 occupied two distinct positions in the *Camptylonemopsis* cluster. Folding of the D1-D1', boxB, V2 and V3 regions of the 16S-23S ITS operons having both tRNAs and no tRNAs revealed interesting patterns that will enrich the diversity and taxonomy of this rarely described genus having very few previously reported species.

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THE POTENTIAL IMPACT OF CLIMATE WARMING ON THE FRESHWATER ALGAL FLORA OF ARCTIC LAKES: EVIDENCE FROM THE EOCENE

Craters formed during emplacement of kimberlites 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 when polar ice was lacking. The sediment records archived in some of the crater lakes span thousands of years, and often contain abundant concentrations of well preserved microfossils indicating thriving aquatic ecosystems. The Giraffe Pipe locality contains one such archive consisting of

65 meters of lake mudstones spanning thousands of years of geologic history. Climate reconstructions based on plant macrofossils yield wet and warm conditions, with 4x more precipitation, a mean annual temperature close to 20 °C warmer than today, and a lack of freezing winter conditions. Remains of more than 250 taxa have been uncovered and used to inform not only evolutionary history of the organisms, but ontogeny of the lake. Extensive numbers of synurophytes, chrysophytes, diatoms, and the green alga *Botryococcus* are found throughout the waterbody, with individual species often constrained to specific strata. Algal lineages found today in warm tropical and subtropical environments were common at Giraffe, supporting the elevated temperature reconstructions. Shifts in algal composition, coupled with remains of other organisms, identify periods of stable conditions separated by sharp shifts in pH, water depth and nutrient levels.

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EFFECT OF KELPAK® ON THE GROWTH AND THERMAL TOLERANCE OF *NEOPYROPIA YEZOENSIS*

Seaweed extracts have been widely used as plant biostimulants in agriculture. Kelpak® is a liquid extract derived from a brown alga, *Ecklonia maxima*. This study was to determine if the biostimulant, Kelpak® can enhance the growth and thermal tolerance of *Neopyropia yezoensis*. *Neopyropia yezoensis* blades (A1) were exposed to 0 ppm (control) and 5 ppm of Kelpak® solution (A1 treated) at 10 °C for 10 days and induced producing archeospores in 20 °C. Some of the young blades (A2) from these archeospores induced from control and A1 treated samples were cultivated in control medium at 10 and 20 °C for 20 days. Some A2 young blades induced from the control samples were exposed to 0 ppm and 5 ppm of Kelpak® solution (A2 treated) at 10 °C for 10 days. After exposure, the samples were cultivated at 10 and 20 °C for 20 days. All samples were cultured in von Stosch enriched (VSE, control) medium. The medium was replaced every 5 days. Specific growth rate (SGR), protein contents and reactive oxygen species (ROS) were measured. The A1 and A2 treated samples at 20 °C had significantly higher SGR than control samples at 20 °C. The A2 treated samples at 20 °C had significantly lower ROS contents than control at 10 °C. When *N. yezoensis* were treated with Kelpak®, an enhancement of growth was observed at high temperature, suggesting Kelpak® may increase the thermal tolerance of *N. yezoensis*. This result will provide critical information for potentiality of Kelpak® to be used in *Neopyropia* aquaculture considering climate change.

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INSIGHTS INTO THE EVOLUTION OF A PRIMARY ENDOSYMBIOSIS THROUGH ANALYSIS OF THE PAULINELLA GENOME

The photosynthetic plastid in eukaryotes putatively arose ca. 1.5 Ga from a single cyanobacterial primary endosymbiosis in the Archaeplastida ancestor. The only other known case of primary plastid origin occurred more recently (ca. 120 Ma) in the rhizarian amoeba *Paulinella*. *Paulinella*'s transition from a

heterotrophic to a photoautotroph lifestyle has resulted in significant remodeling of both the host and endosymbiont genomes. The host genome shows significant levels of genome instability, with a plethora of unannotatable “dark” genes, many of which are differentially expressed over the light-dark cycle, and novel regulatory mechanisms that have evolved to accommodate the endosymbiont, potentially as a response to damaging reactive oxygen species produced by photosynthesis. In contrast, the endosymbiont genome has undergone significant reduction when compared to the free-living ancestor lineage. The high light inducible (*hli*) genes which were transferred to the host genome from the endosymbiont comprise a large multigene family, many members of which are encoded in conserved outward facing pairs flanked by conserved repeat motifs. The two genes in these pairs, that may have arisen from different ancestral sequences, appear to have undergone gene duplication independently in different lineages, and may play different roles in the high light stress response of the host. The dynamic evolution of *hli* genes in *Paulinella* demonstrates how important these loci are to the host, that is still under strong selection to manage the novel organelle and its photosynthetic functions.

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MOLECULAR ANALYSIS OF DESERT STRAINS IN THE GENUS TRICHOCOLEUS (SYNECHOCOCCALES, CYANOBACTERIA)

Trichocoleus desertorum is a desert species that has been collected and sequenced from the Atacama Desert, Mojave Desert, and Colorado Plateau. Currently, *T. desertorum* is thought to be the only species of *Trichocoleus* sequenced due to the previous lack of support for new species recognition. Four strains of *Trichocoleus* collected from White Sands National Park were sequenced for the 16S and 16S-23S ITS regions and compared to previously published sequences in the genus. ITS analysis shows that the White Sands strains all have greater than 7% dissimilarity from each other as well as all other available sequences, indicating that each strain represents a different species. Multiple operons of the two tRNA allele found in one strain suggest that further cloning and sequencing of strains need to be performed to capture all operons and understand the true diversity of the genus.

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CONTRASTING RESULTS OF NATURAL AND FARMED POPULATIONS OF THE RED ALGA *AGAROPHYTON CHILENSE* AGAINST TEMPERATURE VARIATION

In Chile, as a result of unconscious selection and domestication process, farmed populations of the red alga *Agarophyton chilense* have most likely undergone a reduction in genetic diversity and a modification in life-history traits compared to wild populations. In order to evaluate how environmental factors may affect the productivity and photosynthetic responses of this Rhodophyta, a lab experiment was carried out in several populations and localities along the Chilean coast. Our experiment demonstrated that temperature variation affects different populations of this alga, being that wild population's growth decreased at extreme environmental conditions, while all the farmed populations respond in a very similar way. Furthermore, our results showed that photosynthetic activity was also affected by temperature treatments (e.g., different maximum maximal electron transport rate and quantum yield values depending on the population type and temperature). We propose that a possible outcome of farmers activity, in the

vegetatively propagated crops of *A. chilense*, could have been the selection of general-purpose-genotypes able to perform adequately across the range of temperature tested in our experiment. In a context of climate change, this red alga farmed populations may be better able to cope with impacts of anthropogenic activities than natural populations due to the buffer effect of their general-purpose-genotypes, tolerant to a wide range of conditions.

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EVALUATION OF THE CHLOROPLAST 16S GENE AS A DNA BARCODE MARKER ACROSS MAJOR ALGAL GROUPS

Delimiting and identifying species based on molecular data has become a standard procedure in phycology, but different marker genes (DNA barcodes) are being used in the different major algal groups, making comparisons among groups difficult. The 16S ribosomal RNA gene is commonly used as a standard taxonomic marker gene in bacteria and as metabarcode to characterise entire bacterial communities taxonomically. This gene is also present in the chloroplast genome of algae and could, at least in theory, help unify our knowledge of molecular species limits and biodiversity across algal groups, but the variability and taxonomic resolution of the 16S rRNA gene has not been studied in much detail. Based on analyses of 16S rRNA sequences obtained from 150 complete chloroplast genomes and 3.350 entries from the PR2 (PhytoRef) dataset, I aimed to characterise the variability and taxonomic resolution of the chloroplast 16S gene across the major groups of algae. Entropy plots of the variability in 16S alignments clearly distinguish the more conserved and variable regions of the gene, and the differences in variability patterns between major groups of algae. Compared to common DNA barcode markers, the 16S gene has a lower evolutionary rate (e.g. 36% of the rate of *tufA* in green algae). Evolutionary simulations based on the observed differences in evolutionary rates between classical DNA barcode markers and 16S suggest that when smaller regions of the gene are considered, as would typically be the case in a metabarcoding setting, 16S sequences that were clustered into OTUs (operational taxonomic units) at a 99% similarity threshold result in lower biodiversity estimates than classical DNA barcodes. In these circumstances, species-level resolution cannot be achieved with this marker, but full 16S sequences allow much better distinction between species in most groups of algae.

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DIFFERENTIAL PHYSIOLOGICAL RESPONSES OF *ULVA RIGIDA* TO WASTEWATER RELATED TOXIC COMPOUNDS

Sewage outfalls are one of the main anthropogenic impacts to coastal systems. Despite great progress, wastewater treatment plants (WWTP) effluents entering surface waters still present a major source of toxic pollutants. The presence and risk of many compounds, the so-called emergent pollutants, is sometimes unknown until they cause alterations in coastal communities. In this way, ecotoxicological bioassays have helped to identify the potential toxicity risks of anthropogenic derived effluents and related compounds. In this study we evaluated the toxicity of WWTP effluents, and two compounds frequently present in those inputs, such as zinc (Zn), a metal, and Benzophenone-3 (BP-3), a UV filter included in cosmetic formulas. The physiological responses of the macroalga *Ulva rigida*, such as growth, percentage of reproductive disks or maximum relative electron transport rate (rETR_{max}), and maximum quantum yield (F_v/F_m), was evaluated under different concentrations of these compounds. The results show that this macroalgal species shows a good and comparable sensitivity to other model organisms used in

ecotoxicological bioassays. However, there is no global indicator of the toxicity of these compounds, probably due to their differential effects on the macroalgal physiology. Therefore, more studies aiming to find a good indicator of the toxicity of different compounds to macroalgae are needed.

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EELGRASS-ASSOCIATED MESOGRAZERS LIMIT THE DISTRIBUTION OF *ULVA* SPP. VIA TOP-DOWN CONTROL OF ITS EARLY LIFE STAGES

Macroalgal blooms pose a threat to coastal ecosystems worldwide, especially in highly eutrophic environments. Excess nutrients often facilitate the proliferation of opportunistic algae, but in some systems grazing activity counterbalances its effects. The regulating role of mesograzers associated with eelgrass (*Zostera marina*) was evaluated in Elkhorn Slough, a eutrophic estuary where *Ulva* spp. blooms are frequent during the upwelling season. Recruitment and transplant success of *Ulva* spp. were monitored along transects placed across the edge of the largest *Z. marina* bed. Changes in abundance of *Ulva* spp. on transplants differed spatially and seasonally, and were significantly correlated with density of both small and large invertebrate groups. Of the large mesoinvertebrate groups, sea slugs had the strongest regulating effect on *Ulva* spp. Taylor's sea hare (*P. taylorii*), found almost exclusively on eelgrass, accounted for the majority (>90%) of individuals within this taxonomic group at the study site. Grazing affected not only adult *Ulva* spp. but also its early developmental stages, leading to decreased *Ulva* spp. abundance on transplants and minimal recruitment inside the *Z. marina* bed.

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ANALYZING THE FULL GENOMIC COMPLIMENT OF RIBOSOMAL RNA OPERONS, FOR TAXONOMIC DISAMBIGUATION OF THE CYANOBACTERIAL GENUS, *BRASILONEMA*

There is evidence that 16S rRNA sequences, used to designate novel prokaryotic species, lack resolution at the species level. Various cyanobacterial taxonomies remain paraphyletic or polyphyletic. Establishing innovative methods to identify cyanobacterial species, with strong statistical support, is vital to establishing monophyly. Analysis of the noncoding, intergenic, and potentially regulatory 16S-23S ITS region, could provide well supported species-level phylogenetic resolution. *Brasilonema*, a tropical, heterocytous genus in the Scytonemataceae (Nostocales), has global distribution but varies, on average, less than 2% in 16S rRNA coding sequences. The ITS regions in forty putative species within the genus *Brasilonema*, were analyzed. Through intensive cloning and sequencing, the number and nature of rRNA operons present in the genus was established. The 16S-23S ITS regions were cloned, and 12 clonal replicates were sequenced, for each strain. Consensus sequences, from multiple clonal replicates, were determined for each operon copy, via sequence alignments. Operon types were first designated as having either 2 tRNAs present or none, then sequence alignments and helical secondary structures were analyzed to further classify dissimilar operons. Three distinct operons were found to be inherent to *Brasilonema*, one copy containing no tRNAs and two operon copies containing two tRNA genes. All three operons were used in phylogenetic analysis and while agreeing with 16S rRNA phylogenies, they provided greater statistical support for species groups.

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BEYOND *E. HUXLEYI*: CELL SIZE, ELEMENTAL CONTENT AND ALLOMETRY OF A DIVERSE RANGE OF COCCOLITHOPHORE SPECIES

Coccolithophores are both photoautotrophs and calcifiers that play important roles in ecosystems and biogeochemical cycles. Some species form blooms in high-latitude waters, and low-latitude communities exhibit high diversity. Despite such diversity, our understanding of the clade relies on knowledge of *Emiliana huxleyi*. Our objective was to explore whether cellular carbon (C) and nitrogen (N) content is conserved within the coccolithophores, examine the clade's cell size spectrum, size-scaling relationships of growth, and elemental content compared with other phytoplankton. We examined the cell biochemistry of 9 strains from the main families of the calcifying Haptophyceae, as well as cell size frequency across extant species. Coccolithophore cell sizes are constrained, with ~71% of 159 species smaller than 10 μm in diameter. Growth rates scale with cell biovolume with an exponent close to metabolic theory. The coccolithophore-specific relationship between cell organic C content and biovolume indicates that coccolithophore cells are less organic C dense than other phytoplankton. Organic C to N ratios (~8.3 mol:mol) are similar to other phytoplankton, despite significant cellular investment in inorganic C. This implies little additional N cost for calcification and efficient retention and recycling of cell N. Our results support observations that coccolithophores are efficient competitors in low-nutrient conditions, able to photosynthesise, calcify and run the routine metabolic machinery necessary without any additional need for N relative to non-calcifying algae.

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HERITABILITY OF INCREASED BIOMASS IN THE GIANT KELP *MACROCYSTIS PYRIFERA* SUPPORTS THE DEVELOPMENT OF ITS GENOMIC BREEDING PROGRAM

Seaweed farms have existed globally for centuries but have only begun to emerge in the last few decades in the United States. As an industry in its infancy in the American economy, the need for rapid and efficient development is pinnacle to its success. The integration of a genomic breeding program to accelerate the optimization of traits of interest is a common technique for crop strains but has yet to be developed for targeted algal species in the United States. Of particular interest for aquaculture development is the giant kelp *Macrocystis pyrifera* due to its use for biofuel, its biostimulant properties, and its potential for nutrition supplementation. A first step to the development of a genomic breeding program is to measure the heritability of desirable traits. To this end, we used a common reference breeding design in which 500 females from four populations were crossed with a single male with five replicates per cross and outplanted in a pilot farm near Santa Barbara, California. Analysis of variance with genotype as a nested, random factor within population revealed significant genetic variation

($p < 0.001$) and broad-sense heritability for biomass yield of 0.22. These results suggest that future selection of the female genotype can be used for trait optimization. Surprisingly, source population did not have a significant effect on total biomass ($p = 0.0865$). Additional work is needed to correlate desirable phenotypic traits with specific genetic characteristics (i.e. GWAS) to further develop a giant kelp breeding program and inform the aquaculture of this alga.

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TOWARDS A SYNTHETIC ALGAL CHLOROPLAST: A STREAMLINED PLATFORM FOR CREATING DESIGNER CHLOROPLAST GENOMES IN *PHAEODACTYLUM TRICORNUTUM*

Chloroplasts represent a unique opportunity for the metabolic engineering of microalgae as characteristics of their prokaryotic-derived genomes and compartmentalized micro-environments render the organelle amenable to high levels of transgene expression and foreign protein accumulation. However, the development of the chloroplast as a synthetic biology tool has been limited by a lack of robust multigenic engineering techniques and methods for targeted delivery of large DNA inserts (>20 kb). The objective of this project is to first explore two cloning approaches for creating synthetic chloroplast genomes in the diatom *Phaeodactylum tricornutum*: (i) *in vivo* homologous recombination in yeast and (ii) *in vitro* golden gate assembly. The most efficient approach will then be used to genetically modify multiple loci throughout the exogenous chloroplast genome. Following this, we will explore different methods for the targeted delivery of whole synthetic genomes to the *P. tricornutum* chloroplast.

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EFFECTS OF IRRADIANCE, NUTRIENT ENRICHMENT, AND CO₂ ON PHOTOSYNTHETIC EFFICIENCY OF HAWAIIAN *CHONDRUS* SP. NOV. AND *HALYMENIA HAWAIIANA* (RHODOPHYTA)

Climate change is affecting our oceans and will direct our conservation efforts. How species will respond to future stressors can be used to predict the effects on ecosystems. Two red algal species commonly found on Hawaii Island, *Chondrus* sp. nov. and *Halymenia hawaiiiana*, were tested for their responses to increased irradiance, nutrient enrichment, and CO₂ enrichment. Photosystem II (PSII) efficiency was measured twice a week during the two-week-long experiments. *Halymenia hawaiiiana* did not show a significant difference between normal conditions and increased irradiance nor nutrient enrichment conditions. *Chondrus* sp. nov. performed best with lower nutrient enrichment and under lower irradiance. Both species displayed higher PSII efficiency when exposed to elevated CO₂ concentrations. Based on the results of this study, *H. hawaiiiana* may have the ability to withstand some altered environmental conditions caused by climate change, and may be a viable candidate for island aquaculture.

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A WINDOW TO THE PAST: CYANOBACTERIAL DIVERSITY AND BIOGEOGRAPHY IN HERBARIA SPECIMENS

During the HERBA project, a pilot study of the past diversity and biogeography of cyanobacteria in polar and alpine regions (till ca. 100 years BP) was performed on cyanobacterial samples preserved in the Drouet herbarium, Smithsonian Institution, USA. Amplicons based on the 16S rRNA gene V3-V4 segment were used for High-throughput sequencing (HTS). In total, the diversity of 12 samples was obtained, of which 2 samples were sequenced both by the 454 pyrosequencing and Illumina (MiSeq, 2x300 bp) technologies. The 12 samples were collected from 1897 to 1964 in Antarctica, Alaska, Yellowstone Park, and Austrian, Swiss and American glaciers. Both HTS technologies results were consistent and gave an identical dominant OTU. For the 10 samples analysed by 454 pyrosequencing, we obtained 46,889 good quality cyanobacterial reads. They ranged from 67 reads to 16,434 reads per sample and 86 OTUs (threshold 99% 16S rRNA similarity) were obtained. All four samples analysed by Illumina sequencing gave at least about 20,000 reads after quality check. Five of the 12 samples showed a complete identity between the morphological identification indicated on the label of the specimen and the dominant OTUs observed in the HTS sequencing data. Three other samples could be considered as showing a congruence between the two types of identifications if the taxonomic label based on morphology could be adapted to modern classification, like the assumption that the morphotype of *P. laminosum* could correspond in fact to the sequence of *Leptolyngbya*, as found in the older specimen of 1898. Four other specimens do not show an agreement between the molecular diversity and the label.

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ANTIOXIDANT PROPERTIES AND MINERAL COMPOSITION OF RED SEAWEED GRACILARIA VERRUCOSA

Seaweeds especially red ones are important polysaccharide and mineral sources and they also have antioxidant abilities. This study aimed to determine antioxidant capacity and essential mineral contents (Na, K, Mg, Fe, Cu, Zn, Mn, P, and Ni) in edible red seaweed *Gracilaria verrucosa*. The IC₅₀ values of the ethanolic extract of *G. verrucosa* were measured as 37.72± 0.20 mg/g ext. The inhibition rate was also found at 15.23±0.85 % and this red seaweed showed a medium free radical scavenging capacity in comparison with commercial antioxidant BHT (butylated hydroxytoluene). The seaweed sample was analyzed for mineral composition (K, Na, P, Ca, Mg, Fe, Mn, Zn, Cd, Cu, and Cr) by inductively coupled plasma optical emission spectroscopy (ICP-OES). The order of elemental concentrations in *G. verrucosa* was determined as Cr < Cd < Cu < Zn < Mn < Fe < P < Mg < Ca < Na < K. We found that Potassium (K) is the major element in *G. verrucosa*. The mineral composition of this red algae was found relatively higher as compared to the land vegetables. Our results show that *G. verrucosa* distributed in Çanakkale, Turkey can be used as a potential source of dietary supplements and functional foods.

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SEEKING SEAWEED SILICON: LOCALIZING SI IN DIVERSE ALGAE

Dissolved Si concentrations have been rising in Lake Michigan, from 10 μM in the 1980s to $>40 \mu\text{M}$ recently, but the reasons for this are unclear. To develop better Si budgets, we have been defining Si use by freshwater phytoplankton groups, as well as Si demand by dense coastal benthic algal communities of *Cladophora* plus epiphytes and freshwater macrophytes. An antipodean sabbatical provided opportunities to also make comparisons with marine *Cladophora* and other diverse seaweed taxa, collected from coastal sites in Tasmania. Biogenic Si (bSi) was analyzed following carbonate digestion. Si was localized within dense freshwater epiphytic communities on *Cladophora* and macrophytes by labeling with the Si incorporation dye 2-(4-pyridyl)-5-((4-(2-dimethylaminoethylaminocarbonyl)methoxy)phenyl)oxazole (PDMPO), viewed with epifluorescence microscopy. High bSi content of *Cladophora*-epiphyte assemblages correlated with diatom abundance, and marine samples showed lower epiphyte loads and bSi content than Lake Michigan samples. Across 72 seaweed taxa, there was no clear taxonomic or morphological correlation with bSi content, which ranged from <0.2 to $>4 \mu\text{g Si/mg dry mass}$. PDMPO effectively labelled bSi in diatoms but not in other taxa, despite extractable bSi. Si localization in selected seaweeds was examined using Rhodamine-123 with some evidence of Si localization in *Codium fragile* utricles and *Cladophora* cell walls. Understanding impacts of non-diatom taxa on marine and freshwater Si cycling, and the roles of Si in algal cells needs more detailed analysis of Si localization.

Poster Abstracts (alphabetized by surname)

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MACROALGAL COVER CORRELATED WITH ANNUAL SEA ICE COVER ALONG A LATITUDINAL GRADIENT ON THE CENTRAL WESTERN ANTARCTIC PENINSULA

Macroalgal forests dominate hard benthos in shallow waters along the northern portion of the western Antarctic Peninsula (WAP). Macroalgal biomass and species richness decline dramatically between southern Anvers Island and northern Marguerite Bay but observations in this gap have been limited to a few qualitative reports from the 1970s. We hypothesized that this pattern can be correlated with annual sea ice coverage patterns that govern light availability. We used satellite imagery of annual sea ice duration and extent as well as water turbidity during ice-free periods to identify 14 study sites that differed in ice coverage but were similar in terms of turbidity along the central WAP between the Terra Firma Islands in Marguerite Bay ($S 68^{\circ} 41.5'$) and the Joubin Islands west of southern Anvers Island ($S 64^{\circ} 46.4'$). Divers video recorded benthic organisms continuously on replicate vertical transects between 40 and 5 m depths with horizontal transects at every 5 m depth interval along each vertical transect. Macroalgae and invertebrates were collected by hand and airlift for species determinations and food web analyses. Fleishy macroalgal cover varied markedly with annual sea ice coverage, ranging from lush macroalgal forests with approximately 80% cover beneath the lowest annual ice cover to communities with no fleshy macroalgae where annual sea ice coverage was maximal. Brown macroalgae dominated at

most lower ice cover sites but red macroalgae increased in their contribution to overall macroalgal percent cover as annual ice cover increased.

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BCCM/ULC: A PUBLIC CULTURE COLLECTION AS RESERVOIR OF CYANOBACTERIAL DIVERSITY AND TAXONOMIC REFERENCE STRAINS

The BCCM/ULC public collection (<https://bccm.belspo.be/about-us/bccm-ulc>) aims to gather a representative portion of cyanobacterial strains from different ecosystems with a focus on the polar diversity. Amongst the 243 strains, for which the 16S rRNA gene sequence was determined, 93 OTU's (99% 16S rRNA similarity) could be detected. The collection includes several reference (or 'type') strains for newly described taxa. They include *Plectolyngbya hodgsonii* (ULC009), *Shackletoniella antarctica* (ULC037), *Timaviella circinata* (ULC401) and *T. karstica* (ULC402), *Cephalothrix komarekiana* (ULC718) and *Parakomarekiella sesnandensis* (ULC591). Recently, the BLCC (Berthold-Laughinghouse Culture Collection) deposited 196 strains with several new taxa from different ecosystems in Florida. These deposits include *Johannesbaptistia floridana* (ULC590) isolated from benthic coastal substrata, *Iningainema tapete* (ULC575), which is able to produce nodularin, from a greenhouse, *Brasilonema fioreae* (ULC548), *B. santannae* (ULC544) and *B. wernerae* (ULC573) from terrestrial environments, *Leptochromothrix* (ULC597), *Ophiophycus* (ULC599) and *Vermifilum* (ULC454) from benthic mats in mangrove forests and *Neolyngbya biscaynensis* (ULC530) and *Affixifilum floridanum* (ULC525) from marine benthic cyanobacterial mats. These ecosystems offer a huge and still largely unexplored diversity of cyanobacteria. Moreover, they are a potential source of novel secondary compounds. For example, species of *Neolyngbya* and *Brasilonema* have been shown to produce compounds with antibiotic and antifungal properties.

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CULTURE OF RED ALGAE *CHONDRACANTHUS CHAMISSOI* IN PERU

In Peru, macroalgae productions come mainly from extraction and correspond to the species *Macrocystis* spp., *Lessonia* spp., *Chondracanthus chamissoi*, *Gracilariopsis lemaneiformis* and *Pyropia* spp., which are mostly destined for the external market as raw material; only a part of the production of *C. chamissoi* and *Pyropia* spp. are destined for the national market for direct human consumption. Dried seaweed exports have tripled in the last 11 years (2009: 11,970 T and 2019: 35,000 T). The cultivation of red macroalgae in Peru has been studied since the 90s, but it is since 2010 that this activity has gained greater momentum due to the synergy between academia, private companies and artisanal fishermen. The main species that has been cultivated is *C. chamissoi* and it develops in the central and southern coast of Peru. The cultivation of *C. chamissoi* is carried out through vegetative propagation and sporoculture using artificial substrates for fixation and the generation of growing discs, a stage that takes place in a hatchery.

The seedlings produced are planted in marine concessions, where growth is monitored and the harvest is carried out, obtaining 2.5 to 4.5 MT of fresh product per hectare that is finally processed by various private companies for human consumption and as an input for industrial use. The cultivation of this species has been generating important jobs in Pisco, Ilo, San Juan de Marcona and Casma. It is expected that this activity will become massive and the extraction pressure will decrease.

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EXAMINING THE IMPACT OF ALGAE ON MICROBIAL COMMUNITIES IN WASTEWATER

In a partnership with the Metropolitan Water Reclamation District of Greater Chicago, we are examining an experimental tertiary treatment that would use algae to further clean wastewater. Because microbes work symbiotically with algae to remove excess nutrients and other pollutants from wastewater, our objective was to determine the impact of the tertiary algal treatment on the functional diversity of microbes. As a final step to further clean wastewater that has already undergone primary and secondary treatment, the tertiary algal treatment uses a 10-ft vertical belt that provides a substrate for algal biomass growth as it revolves in and out of a wastewater tank. We characterized the microbial communities in wastewater tanks with Biolog Ecoplates, which have thirty-one carbon substrates that microbes may consume. Principal Component Analysis (PCA) revealed that the microbial community in the tertiary algal treatment system was distinct from microbial communities in a control tank that lacked the vertical belt substrate, and from microbial communities in secondarily-treated wastewater. The microbial communities have importance because the treated wastewater will be discharged into the Chicago River, where microbes conduct ecosystem services such as degradation of organic matter and nutrient cycling.

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HOW UTILIZING AN IMLS GRANT FOR DIGITIZATION OF THE UCSB HERBARIUM'S SEAWEED COLLECTION PROVIDES VITAL DATA TO BETTER UNDERSTAND THE CHANGING MARINE ENVIRONMENT

The macroalgae collection of the UC Santa Barbara (UCSB) Herbarium has been utilized as a resource by students and researchers at UCSB. In order to increase the scientific value of the collection, we have initiated a digitization project to add to a growing data set being assembled by a consortium of seaweed herbaria. Collectively, these data can be used to address questions of changing climate, ocean currents, invasive species, and biodiversity along the Pacific Coast of North America. Our IMLS-funded digitization project is focused on digitizing ca. 10,000 specimens in our Pacific Coast of North America collection. Our digital data are currently available on two Symbiota-based web portals: The Consortium of California Herbaria 2 and the Macroalgal Herbarium Portal. Our data are also aggregated and shared worldwide through the Global Biodiversity Information Facility (GBIF). Our digitization project is not only creating high-quality public data, but also is providing ample opportunities for learning about algae

and the activities associated with curation in a natural history museum. USCB students, interns, and volunteers gain hands-on experience with our collections, seaweed identification, and phycological special events. The history and scientific insight that herbaria can tell argue for the importance of their preservation and for the continued need for new field collections. Reimagining these collections to present them to a wider audience increases the kinds of voices in science and the types of questions that can be asked about our changing world.

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THE INTRIGANT OCCURRENCE OF MANY GAS VESICLES IN BENTHIC MARINE CYANOBACTERIA

The occurrence of aerotopes in cyanobacteria is common in planktic species, in which these gas vesicles play an important role in buoyancy regulation in the water column. In some of these species, the aerotopes are easily visualized under optic microscopy. Recently, a great number of aerotopes were identified in two new benthic marine genera described from the Brazilian coastline, *Neolyngbya* and *Capilliphycus*. These two genera were collected in tidal pools or in the protected reef region on several substrate types, like rocks and sand. In *Neolyngbya* and *Capilliphycus* species, the gas vesicles occupy large areas in the interthylakoidal space. *Neolyngbya tenuis*, *C. salinus*, and *C. tropicalis* presented great densities of aerotopes, which occupy up to 50% of the total cellular area. Unlike planktonic species, in the aforementioned benthic ones, the aerotopes are not visible through optic microscopy. These structures were identified only under transmission electron microscopy in different phases of their life cycle. How the principal function of aerotopes in cyanobacteria is buoyancy control, what would be the role of these structures in benthic marine cyanobacteria? The presence of aerotopes in hormogonia can assist in the species dispersion because can keep the set of cells floating for a longer period. Additionally, gas vesicles also can help to keep the filaments upright in the water column to optimize photosynthesis. Thus, physiologic studies can help to better understand the functionality that the aerotopes play in these benthic organisms in the marine environments.

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MORPHOLOGICAL AND ECOLOGICAL CHARACTERIZATION OF THREE NEW SYMMETRIC BIRAPHID (NAVICULOID) DIATOM SPECIES FROM STREAMS OF THE ISLAND OF CYPRUS

Environmental parameters and diatom assemblages were studied in ca. 65 stations in a Cypriot stream network covering an area of about 5550 km² over the years 2011, 2018, 2019, 2020. The detailed taxonomic analysis using the latest taxonomic concepts allowed to uncover patterns and features of typical Mediterranean diatom communities. Many interesting taxa were found, and several species new to science were discovered and characterized from both taxonomic and ecological standpoints. In this contribution, three new symmetric biraphid species are proposed as new to science on the basis of LM and SEM studies, of careful comparison with the literature and with similar existing taxa, and of the analysis of our diatom-assemblage and environmental-factor multi-annual databases. *Craticula mediterranea* Lange-Bertalot et Cantonati sp. nov. is best distinguished by outline and striation density. *Mastogloia cyprica* Lange-Bertalot et Cantonati sp. nov. differs from similar species by outline, raphe

course (undulation), and stria density. *Navicula loumatensis* Lange-Bertalot et Cantonati sp. nov. is characterized by the combination of valve outline, shape and size of the central area, stria density, and by a high areola density. Mediterranean streams are affected by multiple stressors, and, in an increased manner, by their naturally fluctuating hydrology being increasingly influenced by climate changes. In-depth knowledge of diatom communities is of pivotal importance for robust assessment and monitoring, in particular in these critical decades.

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PREDATION AND MICROBIAL LANDSCAPE DYNAMICS IN CYANOBACTERIAL MAT METACOMMUNITIES

The mechanisms driving cyanobacterial mat dynamics on coral reefs remain largely unresolved despite their relevance to reef conservation priorities. Here, we applied a metacommunity framework to longitudinally document spatial dynamics of coral reef benthic cyanobacterial mats across multiple levels of ecological organization. Over a 49 day period from May – July 2019, we tracked individual mat communities (N=53) using repeat photographs, alongside metacommunity photoquadrat surveys (N=204) on a stretch of reef in Bonaire, Caribbean Netherlands. We developed a novel patch-matrix approach to quantify mat landscape statistics. Additionally, we documented predation from bacteriophages using paired shotgun metaomics (DNA/RNA), and predation from reef fishes using fixed-position video surveys. Finally, we conducted an experimental assessment of the influence of fish predation on spatial dynamics using a field-based enhanced predation experiment (N=27). Over the 7 weeks, we documented metacommunity stability despite substantial localized community extinction. Community extinctions were temporally asynchronous, occurring across 14 unique dates. Our results suggest that intermediate levels of predation pressure may promote community persistence, while heterogenous intra-site predation pressure may promote metacommunity persistence. Overall, our results suggest the mechanisms controlling coral reef benthic cyanobacterial mat spatial dynamics differ across spatial scales and levels of ecological organization, contributing to community ephemerality and metacommunity stability.

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SEASONAL SPECIES DIVERSITY OF SEA WEEDS IN THE INTERTIDAL ZONE OF WANDO-GUN, KOREA

This study investigated the diversity of seaweeds and their changes in the coastal rocky area of Jeongdo-ri, Wando-Gun, Korea from 2019 to 2020. 132 species were identified based on morphological and molecular approaches. Sheet form, filamentous form and coarsely branched form, which are ESG (ecological state group) II, were more than 60% in all season using Litter and Litter (1984) and Orfanidis *et al.* (2001). Using a 50x50 cm quadrat method, seasonal dominant species (highest value of IV) in upper, middle and lower areas of intertidal zone are *Gloiopeltis furcata*, *Monostroma nitidum* and *Chondracanthus tenellus* in winter; *Ulva australis*, *Corallina pilulifera* and *Corallina pilulifera* in spring; *Ulva australis*, *Sargassum fusiforme* and *Chondracanthus tenellus* in summer; *Chondracanthus intermedius*, *Chondria crassicaulis*, *Chondracanthus tenellus* in fall.

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THE CLONING AND ENGINEERING OF DIATOM MITOCHONDRIAL GENOMES IN YEAST AND BACTERIA

Algae are attractive organisms for biotechnology applications, such as the production of biofuels and other high-value compounds due to their genetic diversity and metabolic processes. As new species are domesticated, rapid nuclear and organelle genome engineering methods need to be developed and optimized. To that end, the mitochondrial genomes of *Thalassiosira pseudonana* and *Phaeodactylum tricorutum* were cloned into yeast and transformed into bacteria for analysis. No significant difference between mitochondrial harbouring yeast or bacteria and their respective empty vector controls was observed by growth rate analysis. However, plasmid stability assays found that over 60 generations, 17% of *T. pseudonana* mitochondrial genomes were mutated compared to 0% for *P. tricorutum*. Consequently, analyses of genome integrity will be required following propagation in bacteria.

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POTENTIALLY HARMFUL ALGAL BLOOMS IN A TROPICAL ESTUARINE GRADIENT—(BAHIA- BRAZIL)

The purpose of this study was to analyze the occurrence of potentially harmful algal blooms in the Paraguaçu River estuary. Sampling was carried along the estuarine for phytoplankton identification and counting and determining the concentration of nutrients (i.e. nitrite, nitrate and phosphate), in addition to obtaining rainfall and flow data. Four species blooms were recorded: *Skeletonema costatum* (1.16×10^7 cell L⁻¹) *Akashiwo sanguinea* (1.03×10^6 cell L⁻¹), *Scrippsiella acuminata* ($4.56 \times 10^6 \pm 2.16 \times 10^6$ cell L⁻¹) and *Planktothrix isoethrix* ($1.18 \times 10^6 \pm 1.05 \times 10^5$ cell L⁻¹). The blooms of *S. costatum*, *A. sanguinea* and *S. acuminata* were associated with variations in the concentration of nutrients, whereas the blooms of *P. isoethrix*, specie typical of reservoirs, in addition to the concentration of nutrients, was explained by the increased flow in the rainy season. None of the blooms registered had harmful effects observed on the system, and despite harmful species that can cause a huge negative impact in the trophic network when form a bloom, generally blooms can represents increases in system productivity in response to the increase of dissolved inorganic nutrients availability after rainfall, in this case. But it is important to continuously monitoring the area due to the occurrence of these potentially harmful species, as mariculture is an important economic activity for the surrounding community.

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DISTRIBUTION AND DIVERSITY OF ABUNDANT MACROALGAL ASSEMBLAGES IN COASTAL SOUTH CAROLINA: LOOKING IN ALL THE RIGHT PLACES

The Southeastern coastline of the United States is typified by sandy shorelines and estuaries, which are considered to host depauperate macroalgal communities. In particular, the macroalgal flora of South Carolina contains few records as compared to nearby North Carolina and Georgia. This study provides the first survey of marine macroalgae in South Carolina in over 30 years. Ten intertidal or shallow-water (<1 m) sites were sampled from Charleston to Murrell's Inlet, with habitats including floating docks, beaches, estuaries, and jetties. Sites were selected based on accessibility and abundance of macroalgae (>25% cover) based on visual estimates. The species composition of macroalgae on boat docks was spatially heterogeneous, ranging from 4 - 16 species per site, but had a higher diversity than estuarine habitats. The invasive alga *Agarophyton vermiculophyllum* was only found attached in mud flats and oyster reef environments. The jetty at Murrell's Inlet had the highest abundance and diversity (21 species), including the discovery of a new species of *Cryptonemia*. Several sites contained unique records, such as the occurrence of *Grateloupia gibesii* on a single boat dock. Our study suggests that the creation of artificial substrates, introduction of invasive species, and increase in hard substrata with oyster reef restoration enhance algal diversity and abundance in South Carolina. This study provides a baseline for future studies focusing on invasive species, climate change impacts, and changes in biodiversity in South Carolina's coastal environment.

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A SURVEY OF SILICATE UTILIZATION BY DIVERSE FRESHWATER ALGAL TAXA

Silicate availability in freshwater can influence algal community composition, but we still know relatively little about the processes driving freshwater silicate biogeochemical cycling. Though diatoms and chrysophytes are the prominent groups of algae which use silicate, some Si accumulation has been demonstrated in marine cyanobacteria. With this new finding, we sought to determine if non-silicifying freshwater phytoplankton could influence freshwater silicate cycles. We tested a range of freshwater taxa for silicate utilization. Algal cultures were grown in DYV medium with three Si treatments: Si-free DYV (<1 μM Si), DYV (~ 57-60 μM Si), and DYV with 30 μM GeO_2 added, a known inhibitor of diatom silicification expected to affect the growth of other silicifying organisms. Growth and dissolved Si in the medium was measured daily. Near the end of exponential phase of growth, cultures were filtered and tested for biogenic silicate (bSi) cellular content. Diatoms, *Cyclotella meneghiniana* and *Synedra sp* and the chrysophyte *Synura petersenii* showed significant growth inhibition with GeO_2 addition or Si omission ($p < 0.05$) and significant bSi accumulation. Freshwater cyanobacteria, green algae and another chrysophyte *Chrysocapsa* did not show growth differences or bSi accumulation. Si localization using SEM with energy dispersive x-ray spectroscopy to resolve elemental silica associated with cells is planned.

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EFFECT OF HERBIVORY AND NUTRIENTS ON INTERACTIONS AMONG COMMON CORAL REEF ALGAE OF FLORIDA KEYS

Defense mechanisms of algae include production of secondary metabolites in some species (e.g. *Dictyota* spp.), generation of calcium carbonate (e.g., *Amphiroa* spp) or quick replacement of tissue removed by herbivores (turf-algal species). Each strategy entails a response to herbivores as well as distinct allocation of resources that could determine the outcome of species-species interactions. We investigated the distribution and abundance of palatable algae as either single species-clusters or as mixes with unpalatable species in relation with levels of herbivory pressure. We quantified the frequency of mixes and single-species clusters of algae from surveys (n=90) carried out during summer 2015 in six reefs in the Florida Keys. A field experiment was conducted where species associations were manipulated under different levels of nutrient and herbivory. We found that sites with higher herbivore abundance had greater frequency of *Dictyota*-palatable spp. mixes while no single species-clusters of palatable species were observed. The experimental manipulation showed that when herbivores were excluded, the unpalatable species (*Dictyota* spp.) decreased and palatable species (*Jania* spp. and *Amphiroa* spp) increased over time. Thus, in coral reefs with high herbivore pressure, the unpalatable species (*Dictyota* spp.) functions as refuge for palatable species. These results show evidence of the importance herbivory pressure has in determining algal abundance, species interactions, and ultimately, community composition of reef benthic communities.

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MOLECULAR CHARACTERIZATION OF ALGAL LIPIDS FOR BIO-JET FUEL PRODUCTION

Civil aviation sector has been investigating bio-jet fuels which their biomass feedstocks (raw materials) are sustainable candidates to replace fossil resources. Microalgae, as a third-generation biomass feedstock, presents significant opportunities than other alternative sources; like low requirement to grow, rapid growth and abundant amount of lipid content. In this study, optimal growth conditions and lipid extraction pathways of several oleaginous microalgae species were investigated to achieve economically feasible, sustainable bio-jet fuel production. Different nutrient composition and concentrations were applied to observe the change in biomass productivity and lipid availability of the microalgae in both indoor and outdoor cultivation. Promising results shows that *Nannochloropsis gaditana* can have up to 65% lipid content of total dry weight (TDW) under specific conditions, and its lipid profile mostly composed of palmitic (C16:0) and palmitoleic (C16:1) acids which facilitate the appropriate hydrocracking process of bio-jet fuel production. *Ettlia Oleoabundans* has 27% lipid content of TDW, and its lipid profile is compatible with bio-jet fuel operations. Significant amount of eicosapentaenoic acid (C20:5, EPA) was detected during nitrogen-replete cultivation of *Nannochloropsis gaditana*, thus multivalORIZATION of microalgae biomass needs to be discussed in order to compete with economic viability of conventional jet fuels.

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TECHNO-ECONOMIC ASSESSMENT OF SUSTAINABLE AVIATION FUEL PRODUCED IN AN INTEGRATED ALGAL BIOREFINERY

The need for sustainable energy sources for transportation sector is increasing every day. Today, civil aviation is responsible for 2% of the global carbon dioxide emissions and is expected to reach 3% by 2050. Sustainable aviation fuels (SAF) from third-generation, non-food biomass feedstocks such as microalgae, stands out as a strong candidate to combat GHG emissions. The objective of this study was to assess the techno-economic viability of SAF production in an integrated biorefinery. Candidate microalgae species were selected as *Ettlia oleabundans*, *Nannochloropsis gaditana*, *Botryococcus braunii* and *Chlamydomonas nivalis*. Microalgae were cultivated in open raceway pond reactors, harvested and dewatered by centrifugation to be ready for extraction. Hydroprocessed esters and fatty acids (HEFA) were converted to SAF and blended with Jet A-1 to be used in civil aviation. The capital (CAPEX) and operational expenditures (OPEX) were calculated where downstream and upstream equipment costs were found to be 54% and 19% of the CAPEX while construction costs were accounting for 27% excluding land cost. The commercialization of SAF, like any other alternative bio-product, depends on the price competition with the conventional products. Although algal SAF is not viable to be used on its own, blending with Jet A-1 enables the blend to compete with fossil-based jet fuels. Furthermore, the adoption of the integrated biorefinery concept, production of by-products and minimize the waste material from the production of bio-jet fuel is a promising step for commercialization.

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MONITORING CHANGING INTERTIDAL FUCOID COMMUNITIES USING UNMANNED AERIAL VEHICLE IMAGING AND DEEP LEARNING ALGORITHMS

In Nova Scotia, the invasive brown seaweed *Fucus serratus* is becoming more widely distributed both geographically and ecologically. At several sites on the Atlantic coast this species can occupy up to 40% of the area of the intertidal zone and it can be a dominant species in shallow subtidal water. To best quantify its spatial distribution and abundance, we use unmanned aerial vehicle (UAV) surveys and a U-Net deep learning algorithm to efficiently and automatically quantify cover of *Fucus serratus* in these new locations. The U-Net is a deep learning algorithm developed for applications in medical imaging that can return robust results with small amounts of training data, which makes it uniquely suitable for our study. Here we summarize the methodology and give preliminary results from selected field sites. We fly a Mavic 2 Pro recreational UAV ten to twenty meters above the shore at multiple sites on the Atlantic shore to collect high quality images at low tide. Images are currently being used to train a U-Net algorithm to differentiate between *Fucus serratus* and co-occurring seaweeds, in particular *Ascophyllum nodosum* and *Fucus vesiculosus*. The final trained U-Net is expected to have applications in long-term monitoring of *Fucus serratus* encroachment in Nova Scotia and ongoing assessment of economically important seaweeds in Nova Scotia.

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COMMUNITY METABARCODING OF THE EUSTIGMATOPHYCEAE (AND BEYOND) TARGETING THE *RBCL* LOCUS

Sequences from the stramenopile class Eustigmatophyceae are rarely reported in metabarcoding studies. When they have been reported, there are very few haplotypes. We hypothesized that the paucity of eustigmatophyte species detected in these studies may be a result of the metabarcoding techniques used, which have primarily employed universal ribosomal RNA gene regions. We examined environmental DNA samples from 22 sites in Southwestern Virginia, some of which had previously been studied using ribosomal RNA metabarcode analysis. We targeted the plastid *rbcL* gene with new primers that were designed to produce a 370 bp amplicon from all lineages of the Eustigmatophyceae in a reference collection. The amplicons were then analyzed with software that produce amplicon sequence variants (ASVs). Our results revealed 184 *rbcL* haplotypes that can be tentatively assigned to the Eustigmatophyceae, representing much higher diversity than has been detected by ribosomal DNA based studies. Our primers also produced amplicons from other algal groups, such as chrysophytes, xanthophytes, some diatom lineages and even cryptomonads. This method using our *rbcL* primers has good potential in applications of metabarcoding for diversity and ecological studies. We invite phycologists studying chromophytes or other groups to interact with us to see if our amplicons include sequences from their favorite algae. We can attempt to perform these assessments on the fly during the poster session.

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RISK ASSESSMENT OF THE ANTIBIOTIC AMOXICILLIN ON TOXIN PRODUCING AND NON - TOXIN PRODUCING STRAINS OF *MICROCYSTIS*

There is a growing concern over the ecological effects of broad-spectrum antibiotics on non-target organisms like cyanobacteria. The present study aimed to investigate the risk assessment (RQ) and physiological effects of AMX on *Microcystis aeruginosa* EAWAG 198 (non-toxin producing = NTP), *Microcystis aeruginosa* LE3 (toxin-producing = TP), and *Microcystis flos aquae* UTEX-LB 2677 (toxin-producing = TP). Our study showed differences in the RQ of the drug to the tested organisms – demonstrating *Microcystis aeruginosa* EAWAG 198 < *Microcystis aeruginosa* LE3 < *Microcystis flos aquae* UTEX-LB 2677. The calculated EC₅₀ values show that AMX was more toxic to the toxin-producing strains than the non-toxin producing strain. AMX caused a significant ($p < 0.05$) decrease in the cell densities, chlorophyll-a, and total carotenoids of the three strains. A significant ($p < 0.05$) rise in the levels of intracellular hydrogen peroxide (H₂O₂) of the treated cultures at 96 h post-exposure was observed – demonstrating that AMX caused oxidative stress in the strains. Lipid peroxidation and the activity of the antioxidant enzymes – peroxidase (POD) and glutathione-S-transferase (GST) – of the cultures were significantly ($p < 0.05$) different. This study revealed that environmentally relevant levels of AMX pose an adverse risk and could alter the population dynamics, photosynthesis, biochemical composition, and the general physiology of *Microcystis* species/strains in aquatic ecosystems.

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TEMPORAL TRENDS OF HEAVY METAL CONCENTRATIONS IN BROWN MACROALGAE FROM COASTAL ENVIRONMENTS

Heavy metals are one of the major drivers of ecological changes in coastal ecosystems. Macroalgae are primary producers of great relevance for ecosystem structure and functioning in these environments, and play a key role in the trophic transfer of these contaminants in the food web. Here, we present the most extensive assessment until now (>3500 records) of heavy metal concentrations in brown macroalgae (Class Phaeophyceae) sampled between 1933 and 2020 worldwide. The study compiles this information from 420 peer reviewed articles to be used as a proxy of global long-term changes in metal concentrations. We report the first detailed multi-decadal time series of Cd, Co, Cr, Cu, Fe, Hg, Mn, Pb and Zn in algae using generalized additive models (GAMs), confirming a significant decrease in metal contamination in the world's coastal environments since ca. the 1970s for Pb (84% reduction), Zn (79%), Cd (77%) and Cu (72%), since the 1980s for Mn (75%) and Hg (65%), and since the 1990s for Cr (66%), Fe (64%) and Co (60%). Important environmental consequences for the whole aquatic ecosystem, even for human health, may be expected from these changes. The present results provide a building block for the overall evaluation of the status and trends of marine metal contamination, and will help researchers and policy makers to promote new legal regulations and environmental goals against pollution.

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GROWTH-ENHANCING EFFECT OF AMPEP IN *NEOPYROPIA YEZOENSIS*

Neopyropia yezoensis is one of the most important seaweed species worldwide, and cultivated in China, Korea and Japan. Acadian Marine Plant Extract Powder (AMPEP), derived from *Ascophyllum nodosum* is a biostimulant, enhancing growth of land plants. This study was to examine the effects of AMPEP in growth enhancement and thermal tolerance in *N. yezoensis*. *Neopyropia yezoensis* samples were exposed to 0 ppm (Control) and 1 ppm (A1 treated) at 10 °C for 10 days. After exposure, the samples were transferred to 20 °C and the release of neutral spores were induced. After reproduction, juvenile blades from Control were exposed to 0 ppm (Control) and 1 ppm (A2 treated) at 10 °C for 10 days. The samples from A1 and A2 samples were cultivated at 10 and 20 °C for 20 and 30 days, respectively after exposure. Specific growth rates, pigments, reactive oxygen species and protein contents were measured. A1 and A2 treated samples showed no thermal tolerance, but a higher growth than the control was observed at 10 °C. In protein contents, no effect of AMPEP was observed. The reactive oxygen species showed no significant effects of AMPEP in A1 treated, but showed lower contents in A2 treated samples than control at 20 °C. Chlorophyll *a* was higher at control at 20 °C than A1 treated and higher at the control than A2 treated at 10 °C. For phycoerythrin content, A1 treated was higher than that of control at 10 °C. For phycoerythrin and phycocyanin contents in A2 samples, A2 treated was higher than control at 10 °C. These results suggest that growth enhancement by AMPEP may pass on to the next unfertilized blades in *N. yezoensis*.

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LAGUNA SALADA AS A POTENTIAL RESERVOIR FOR THE BROWN TIDE ORGANISM, AUREOUMBRA LAGUNENSIS, IN A SOUTH TEXAS ESTUARY

Blooms of the “brown tide” organism, *Aureoumbra lagunensis*, have occurred regularly since 1990 in Texas’ Laguna Madre and Baffin Bay, yet the source population for the blooms is unknown. Field sampling from 2013-2016 showed persistently high abundances in one tributary (Laguna Salada) of Baffin Bay, even when the bloom had dissipated in the rest of the bay. Here we present results from a study that aimed to characterize the environmental conditions, as well as phytoplankton dynamics, in Laguna Salada. Results show that chlorophyll in Laguna Salada is at times tenfold higher than Baffin Bay proper, averaging $136 \mu\text{g}^{-1}$ vs. $15 \mu\text{g}^{-1}$ and with *A. lagunensis* abundance averaging one million cells ml^{-1} . During the study, dissolved organic nitrogen (DON) and dissolved inorganic nitrogen (DIN) concentrations in Laguna Salada were high ($200 \mu\text{M}$ and $30 \mu\text{M}$, respectively) compared to Baffin Bay proper ($62 \mu\text{M}$ and $4 \mu\text{M}$, respectively). DIN:DIP ratios were similar (10.9 and 14.3) for Laguna Salada and Baffin Bay, suggesting nitrogen limitation of algal growth. Additional findings will be presented to highlight the characteristics of Laguna Salada that are favorable to *A. lagunensis* persistence.

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A REINFORCEMENT LEARNING APPROACH TO MODELING PLANKTON SWIMMING BEHAVIOR – A TEST CASE WITH *KARENIA BREVIS*

Behavioral models require extensive tuning of parameters and development of equations that are often species specific. Reinforcement learning (RL) uses interactions of agents with their environment in order to learn behaviors that will maximize a reward signal (e.g. growth). An individual-based model (IBM) using RL was developed and compared to a previously published IBM focused on *Karenia brevis*, a HAB dinoflagellate. The development process was split into two parts: a chlorophyll model and a swimming model. The chlorophyll model was created by training a neural network using environmental conditions (e.g. temperature, light) and outputting the amount of carbon and nutrients the cell acquired. Training data was compiled from published growth rates of cultured cells under various conditions. This model was then coupled to a second neural network that learned swimming behavior through RL. A positive reward was received if the cell acquired enough carbon and nutrients to divide and a negative reward was received if the cell died. By having the cell randomly move throughout the water column, the cell learned to swim upward if more carbon was needed and swim downward if needing more nutrients. A simulated 30-day growth experiment produced similar results between the two model types: the RL model produced 4.6 ± 0.5 cell divisions (~ 0.153 div / day) while the original IBM approach produced 4.0 ± 0.0 cell divisions (~ 0.133 div / day). The flexibility of this approach provides a framework to easily extend this model to other species for which extensive growth data may not exist.

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LOW-COST PRODUCTION OF HIGH-PURITY C-PHYCOCYANIN FROM *DESERTIFILUM THARENSE*

Phycobiliproteins are photosynthetic proteins that are mainly found in cyanobacteria and red algae, and serve as light harvesting complexes. Blue-colored C-Phycocyanin (C-PC), one of the phycobiliproteins, gained significant attention in the recent years due to its anticarcinogenic, antioxidant, anti-inflammatory, antiviral, hepatoprotective and neuroprotective effects. In addition to these benefits, C-PC is also used as a natural and non-toxic coloring agent alternative to conventional dyes in food, cosmetic, textile and similar industries. Meanwhile, simple extraction and purification techniques for C-PC still remain a labor-intensive and costly process. This study aimed to optimize a low-cost C-PC purification methodology coupled by activated carbon and chitosan extraction from a local filamentous cyanobacteria *Desertifilum tharense*. Cultures were grown in 2L reactors with BG-11 medium for 11 days under light flux of $37 \mu\text{E s}^{-1}\text{m}^{-2}$ at ambient temperature. Harvested culture was lyophilized and treated with Na-P extraction buffer (0.01M) after homogenization. Purification was done using 0.02 g/ml activated carbon and chitosan 0.02% (w/v) dissolved in 1% acetic acid. Preliminary data showed that a purity increase from 0.71 to 2.48 (above food grade) is possible. The results showed that low-cost production of high purity C-PC is possible as an alternative to traditional processes such as salt precipitation, dialysis, ion-exchange chromatography and/or other chromatographic techniques.

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BIOCRUST COMMUNITY COMPOSITION AND IMPLICATIONS FOR CARBON FLUX UNDER TIMED LIGHT INCUBATION

Biocrusts are living soil aggregates hosting diverse communities of cyanobacteria, eukaryotic algae, lichens, bryophytes, and other microorganisms in the uppermost millimeters of dryland soils. Biocrusts array along a gradient of structural complexity, each biocrust type distinguished by the dominant photoautotrophic community member. Consequentially, each type hosts a unique microbial community with different biogeochemical. This project aims to assess the carbon fixing capacity of biocrust types under varying incubation times and light intensities, and link maximal fixation rate of each crust with microbial community composition and biomass. Five biocrust types (light cyanobacterial, dark cyanobacterial, cyanolichen, chlorolichen, and moss crust) were collected from four locations in the Chihuahuan Desert. Carbon fixation rates were quantified using a LI-6400XT portable photosynthesis system. Measurements were taken after biocrust wetting and light incubation at five different time periods. Microbial biomass and community composition were assessed using phospholipid fatty acid assays. Preliminary data showed that, generally, carbon fixation and respiration increased in thicker crusts, and net fixation increased over time. Additionally, it was observed that biomass increased with increasing structural complexity and this pattern was observed across all sites. This project will provide new insights into the dynamics of carbon flux within biocrust communities in the context of their respective microbial communities.

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EXTRATERRESTRIAL CYANOBACTERIA AND DIATOMS IN THE ORGUEIL (CI1) AND MURCHISON (CM2) CARBONACEOUS CHONDRITES

The Orgueil (CI1) and Murchison (CM2) primitive meteorites contain cosmic dust, presolar nanodiamonds, refractory element composition of the solar photosphere, extraterrestrial water, carbon and

complex organics. Lack of chondrules and aqueously altered minerals shows extensive periods of liquid water on the CI1 parent body, suggesting they are fragments of cometary nuclei. They contain indigenous extraterrestrial water, 8 of the 20 protein amino acids, 3 of 5 nucleobases and ancient degradation products (pristine, phytane, porphyrins) of chlorophyll. The missing amino acids, nucleobases and DNA show that these stones are not contaminated by modern, post-arrival terrestrial biology. However, Scanning Electron Microscopy studies since 1996 in the US and Russia have provided images of well-preserved fossils of aquatic microalgae embedded in the meteorite rock matrix. Morphotypes of extinct acritarchs and helical coiled *Obruchevella* sp. along with uniseriate and multiseriate Oscillatoriales (cf. *Phormidium*, *Oscillatoria*, *Lyngbya*, *Microcoleus*); heterocystous Nostocales (cf. *Nostoc*, *Rivularia*, *Calothrix*) and diatoms (cf. *Pinnularia segariana* and unidentified pennates) have been found. Energy Dispersive X-ray Spectroscopy data show Nitrogen is below the EDS detection limit and C/N, C/O and C/S ratios are inconsistent with modern life forms. Therefore, these recognizable cyanobacteria and diatoms are interpreted as indigenous, ancient and extraterrestrial fossils of microalgae with direct implications to the Origin of Life on Earth and the Distribution of Biospheres.

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WORLDWIDE LITERATURE SURVEY OF MARINE MACROPHYTIC HABITATS AND EPIFAUNAL ASSEMBLAGES: TRENDS AND GAPS IN RESEARCH

Biogenic habitats provided by macrophytes maintain high biodiversity that extends to essential ecosystem functions and trophic roles in marine and coastal areas. A common method of measuring biodiversity of epifaunal and macrophytic assemblages involves collecting the habitat itself and sorting both the macrophytes and epifauna. However, it is unclear if there are areas that are well-studied/understudied or analyzed evenly on a global scale. This literature review aims to compile and determine gaps in research related to marine macrophytic habitats for epifaunal assemblages worldwide. We hypothesize that the majority of studies were conducted in temperate regions and emphasize brown algae and seagrasses. A literature search was conducted towards observational survey studies that sampled epifaunal assemblages on macrophytic habitats. We currently found 131 papers that fit our criteria. 60% of studies occurred in temperate bioregions, while 35% and 5% occurred in tropical and polar systems respectively. Within our sample of temperate-based studies, most occurred in temperate northern Atlantic (68%) or temperate Australasia (22%) bioregions, while the tropical Atlantic accounted for 77% of tropical studies. In terms of habitats surveyed, we found 40% of macrophytes were ochrophytes, 25% rhodophytes, 18% seagrasses, 12% chlorophytes, and 8% mangroves. This study provides evidence of obvious gaps in research related to epifaunal assemblages in macrophytic habitats, and that further studies should include other environments besides temperate areas or brown macroalgal habitats.

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EVALUATION OF TRAIT DRIFT AND EVOLUTION OF FIELD-ADAPTED NANNOCHLOROPSIS CULTURE IN OUTDOOR OPEN RACEWAY PONDS

Maintenance of desired trait of a strain is a challenge in field cultures. Trait drift and evolution might occur, through time, in response to drivers including changing weather conditions, pest invasions and

other selection pressures specific to each environment. In this work, to track trait drift and evolution across field environments, we established a field-adapted strain of *Nannochloropsis* in each of four different field sites in outdoor raceway ponds for almost 6 months. In a common garden experiment, we characterized the phenotype of the strain. Biomass productivity, robustness, and biomass composition were compared across field cultures from different sites with a full or reduced microbiome; comparisons were also made to an initial cryopreserved strain. Field cultures with and without microbiome did not show significant difference in performance when compared to the cryopreserved strain, except for one site. Higher chlorophyll fluorescence, chlorophyll *a* content and total carotenoids content were determined for one field strain in comparison to the other strains. As for biomass biochemical composition, proteins were the major biomass fraction regardless of the field site. This study will contribute to estimating the magnitude and the timescale of trait shift in microalgae outdoors cultures.

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EFFECTS OF LEAD (Pb) EXPOSURE ON THE GROWTH, PIGMENT CONTENTS AND OXIDATIVE STRESSES IN THE RED ALGA, *AGAROPHYTON VERMICULOPHYLLUM*

Agarophyton vermiculophyllum is one of common species around the coastal environment of Korea. Lead (Pb) is one of the major heavy metals in industrial effluents and can be leaked into marine environment. Because of the non-biodegradable characteristics, Pb accumulates and may have a negative effect on marine organisms and even humans. To investigate the effects of Pb in *A. vermiculophyllum*, specific growth rate (SGR), pigment contents (chlorophyll *a*, carotenoids, phycoerythrin and phycocyanin) and oxidative stresses (ROS, catalase, LPO) were examined in this study. *Agarophyton. vermiculophyllum* was cultivated at different concentrations of Pb (0, 20, 200 and 2000 ppb) at 18°C with von Stosch enriched (VSE) medium for 3 weeks. There were no significant differences in SGR, pigment contents. However, the ROS level was increased with increasing Pb concentration. No significant differences in LPO levels was observed at different Pb concentrations. This study shows that high concentration (> 200 ppb) of Pb may enhance antioxidant activity in *A. vermiculophyllum* but the growth capacity was not inhibited even at 2000 ppb.

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LOST IN THE TROPICS: *CHONDRUS* SP. NOV. (RHODOPHYTA) ON EAST HAWAII ISLAND

Members of the genus *Chondrus* are well-known from temperate and cold waters. Abbott reported *Chondrus* from Hawaii Island (19° N latitude) in 1999 as a new record, although specimens had "been collected many times over many years." Lack of reproductive material made identification of this member for the Gigartinales "hazardous," but Abbott identified specimens as *C. ocellatus* based on vegetative and tetrasporangial characteristics. Recent successful efforts to analyze DNA sequences from seven genes (nuclear: 18S, EF2 and ITS1-5.8S-ITS2 spacer; plastid: psbA, rbcL, and 23S/UPA; and mitochondrial: cox1) indicate that this Hawaiian *Chondrus* is a distinct, new species which raises interesting questions about macroalgal biogeography.

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COMPETITIVE INTERACTIONS AS A MECHANISM FOR CHEMICAL DIVERSITY MAINTENANCE IN *NODULARIA SPUMIGENA*

Nodularia spumigena is a bloom-forming diazotrophic cyanobacterium inhabiting brackish waters worldwide. This species produces non-ribosomal peptides (NRPs), including the hepatotoxin nodularin, often referred to as cyanotoxin. Several known classes of NRPs have various biological activities, although their modes of action are poorly understood. In the Baltic *N. spumigena*, there is a high NRP chemodiversity among strains, allowing their grouping in specific chemotypes and subgroups. Therefore, it is relevant to ask whether the NRP production is affected by intraspecific interactions between the co-existing strains. Using a novel approach that combines culture technique and liquid chromatography-tandem mass spectrometry for the NRP analysis, we examined *N. spumigena* strains under mono- and co-culture conditions. The test strains were selected to represent *N. spumigena* belonging to the same or different chemotype subgroups. In this setup, we observed physiological and metabolic responses in the test strains grown without cell contact. The changes in NRP levels to co-culture conditions were conserved within a chemotype subgroup but different between the subgroups. Our results suggest that intraspecific interactions may promote a chemical diversity in *N. spumigena* population, with higher NRP production compared to a single-strain population. Studying allelochemical signalling in this cyanobacterium is crucial for understanding toxicity mechanisms and plankton community interactions in the Baltic Sea and other aquatic systems experiencing regular blooms.

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MICROALGAL EXTRACTS INCREASE FLUCONAZOLE SENSITIVITY IN *CANDIDA ALBICANS* BIOFILMS

Extracts from numerous species of algae have been screened for antifungal activities. However, the increased incidence of fluconazole resistance in yeast infections, especially in hospital settings, has encouraged a shift in focus toward alternative approaches for fungal control including resistance mechanism targeting and anti-virulence therapies aimed at the biofilm formation and dynamics of fungal pathogens. This study examines the application of microalgal extracts to increase fluconazole sensitivity in biofilms of the model nosocomial fungal pathogen, *Candida albicans*. Biofilm formation and biofilm sensitivity to fluconazole were examined as a consequence of extract treatment in *C. albicans*. Preliminary results demonstrate increased fluconazole sensitivity of *C. albicans* biofilms treated with extracts from *Botryococcus braunii* and *Nannochloropsis oculata* and only limited impacts on *Candida* biofilm formation by most extracts tested. A semi-quantitative analysis of the antioxidant properties and main chemical classes present in the extracts is also reported.

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A DNA BARCODE APPROACH OF *COLPOMENIA* (ECTOCARPALES, PHAEOPHYCEAE) SPECIES FROM SOUTH AND SOUTHEASTERN AUSTRALIA

Macroalgae are difficult to identify to the species level due to their morphological simplicity, presence of widespread phenotypic variation, and rampant incidence of homoplasies. Consequently, the use of molecular tools to species identification has become widely used, particularly DNA barcoding and single-marker species delimitation methods. *Colpomenia* is a common intertidal brown algal genus in Australia, which are morphologically cryptic and often lack reproductive structures. Consequently, *Colpomenia* species identification is challenging. The objective of this study was to assess the diversity of *Colpomenia* species in southern and southeastern Australia using DNA barcode techniques. We generated 44 new COI-5P DNA sequences of specimens from nine different populations across three Australian states, (South Australia, Victoria and Tasmania) and applied 13 variations of species delimitation methods: ABDG, SPN, PTP and GMYC. Our results support the presence of four *Colpomenia* species in the region: *C. sinuosa*, *C. expansa*, *C. claytoniae*, and *C. peregrina*. *Colpomenia sinuosa* is the most widely distributed species in Australia. *Colpomenia peregrina* and *C. claytoniae* presented high levels of intraspecific genetic divergence. We did not find *C. ecuticulata* and although there are no previous records of *C. expansa*, our results confirmed its occurrence for the first time in Australia. Future research including more widespread sampling are required to assess *Colpomenia* species diversity across the entire country.

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COMPARING QUANTITATIVE METHODS FOR ANALYZING SEDIMENT DNA RECORDS OF CYANOBACTERIA IN EXPERIMENTAL AND REFERENCE LAKES

Sediment DNA analyses are emerging as powerful tools for the reconstruction of environmental change. While there are an increasing number of studies using molecular genetic approaches to track changes over time, few studies have compared the coherence between quantitative PCR methods and metabarcoding techniques. We compared the performance of droplet digital PCR (ddPCR) and high-throughput sequencing (HTS) for the quantification of target genes of cyanobacteria in lake sediments and tested whether the two techniques reveal similar patterns through time. Absolute concentrations of cyanobacterial 16S rRNA genes were compared between ddPCR and HTS using dated sediment cores collected from two experimental (eutrophied Lake 227 and acidified Lake 223) and two reference lakes (Lakes 224 and 442) in the Experimental Lakes Area, Canada. Relative proportions of *Microcystis* 16S rRNA genes were also compared. Moderate to strong correlations were found between the molecular approaches but results from ddPCR were more consistent with the known history of lake manipulations. A 100-fold increase in ddPCR estimates of cyanobacterial gene abundance beginning in ~1968 occurred in Lake 227, in keeping with experimental addition of nutrients and increase in planktonic cyanobacteria. No significant rise in cyanobacteria associated with lake fertilization was observed with HTS. Both ddPCR and HTS approaches are suitable for sediment DNA analysis, but studies aiming to quantify absolute abundances from complex environments should consider using ddPCR due to its high tolerance to PCR inhibitors.

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SPATIAL DIVERSITY OF SEAWEEDS FROM ELEPHANT AND VEGA ISLANDS, ANTARCTICA: NEW RECORDS AND CONNECTIVITY FACING CLIMATE CHANGES

This study aims to compare the macroalgal community of distinct oceanographic cells, focusing on new records, and trying to discuss their possible causes for richness changes. Elephant Island (transitional zone between SSI and Weddell Sea), and Vega Island (Weddell Sea) were sampled during the austral summer of 2014 and 2017, respectively. Macroalgae sampled along intertidal and shallow subtidal zone were analyzed using stereoscopic and optical microscopy. A total of 23 taxa were identified, being 11 Rhodophyta, 7 Chlorophyta and 5 Phaeophyceae. Elephant showed higher richness (20 spp.) in comparison to Vega (8 spp.). The similarity index between islands was 0.36 (Sorensen) and 0.22 (Jaccard). Five new records (*Rhodochorton purpureum*, *Porphyra plocamiestris*, *Monostroma hariotii*, *Acrosiphonia arcta* and *Ulothrix australis*) were registered to Elephant; and eight (*Cladophora vagabunda*, *U. australis*, *U. flacca*, *Urospora peniciliformis*, *Gononema* sp., *Desmarestia anceps*, *Pyropia endivifolia* and *Palmaria decipiens*) to Vega. Among these taxa, only *P. decipiens* and *P. endivifolia* were previously listed to Weddell Sea (Hope Bay and Melchior archipelago), being the other 6 spp. also new occurrences for the entire area. The SST ranged from 0.24°C to -1.41 °C (NOAA), being lower at Vega. These new occurrences including opportunistic species, improves seaweed Antarctic database. Temperature anomalies, as well biogeographic distribution changes of some taxa, suggest biotic and abiotic changing patterns, and the urgent need for further and continuous monitoring, including molecular data.

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COMPETITIVES INTERACTIONS IN MARINE MACROALGAE: A REVIEW

In marine coastal systems, the competition among macroalgae is considered as one of the main processes that structure and determine patterns in the entire environment. Therefore, this work aimed to identify and quantify competitive processes in macroalgae, in order to understand the patterns regarding competition processes, which species and competitive interactions are the most studied. For this purpose, a literature search was performed on the Web of Science database. It was searched articles published from 1934 to 2019, using the following combination of Boolean operators and keywords: “Seaweed OR macroalgae OR macroalga, AND ecolog *, AND competiti *”. From this research, 278 scientific articles were obtained, from 1991 to 2019, and based on a careful reading, those that did not fit on the proposed theme were excluded. After the selection, a total of 135 articles were obtained. Information from these articles were compiled into a dataset for analysis. The results showed the participation of 96 distinct macroalgae genus in studies about competition processes, in witch 202 species were recorded: 41% belonged to the class Phaeophyceae; 29% to the phylum Rhodophyta and; 16% to Chlorophyta. The most studied genus were *Dictyota* (7%), *Sargassum* (7%), and *Ulva* (5%). Furthermore, competition for space was responsible for most of the studies (33%). In conclusion, we have summarized the knowledge regarding the patterns of competitive interactions on marine macroalgae.

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VARIATION IN THE COVERAGE AND MORPHOLOGY OF SEAGRASSES IN A REEF LAGOON OF THE MEXICAN CARIBBEAN DUE TO POSSIBLE EFFECTS OF SARGASSUM DRIFT

There are few studies on the effect of Sargassum drift on coastal ecosystems. One of the most obvious changes since this, are the increase in turbidity and nutrients, however it has not been studied how this is affecting seagrass communities and what changes they can induce in their composition and coverage that can indicate the state of health in the ecosystem, so this work tries to determine the relationship of transparency in the morphology of seagrass, in the reef lagoon of the area of El Castillo, Xcalak, Quintana Roo. five consecutive 50 m transects were measure, separated by 5 meters of distance perpendicular to the coast. In each transect, 25 x 25 cm quadrants were placed every 5 m to obtain coverage and morfometric data. Monospecific meadows and the largest sizes and lengths (58.9 cm) of *S. filiforme* were found at a transparency of 40% transparency. While in the most remote areas, with less than 20% no meadow were present at all, and with 95% transparency, specimens had shorter lengths (30 cm) and were intermingled with *Thalassia testudinum*. When usually the lagoon were characterized by being predominant of *Thalassia* and in less proportion *S. filiforme*. with smaller sizes (20-40 cm). It is considered very probable that the turbidity caused by drifts of *Sargassum* is a cause of the increase of sizes and the type of monospecific meadows, being these indicators of change in the meadows of the reef lagoon.

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DEFINING OPTIMUM: GROWTH CONDITIONS AFFECT HEAT STRESS RESISTANCE IN THE ANTARCTIC EXTREMOPHILE *CHLAMYDOMONAS* SP. UWO241

Antarctica is home to many unique and endemic species that thrive under extreme conditions. Isolated 17 m below a permanent ice sheet at Lake Bonney (Antarctica) the psychrophilic green alga *Chlamydomonas* sp. UWO241 (hereafter UWO241) natural habitat is perennially stable with temperatures (~5°C), low light irradiance (>11 $\mu\text{mol}/\text{m}^2\text{s}^1$), and high salinity (700 mM). Despite its life at such extreme conditions, it has been shown that UWO241 grows faster and has greater photosynthetic efficiency at higher temperatures (10-15°C), salinities 70 times lower than it experiences in nature (10 mM) and light intensities a magnitude brighter (100 $\mu\text{mol}/\text{m}^2\text{s}^1$). This work challenges the classically held belief that organisms are at their optimum when they are experiencing the fastest growth rates. It proposes instead that an organism's ability to resist external stresses must also be included when determining optimal conditions. We examined UWO241's heat stress resistance and suggest that UWO241 is better adapted to low light and high salinity conditions. Algal cultures grown under 4°C conditions and subsequently transferred to 24°C (lethal temperature) survived the longest when grown under the combined conditions of low light (13 $\mu\text{mol}/\text{m}^2\text{s}^1$) and high salinity (700 mM) despite having very slow growth rates. The mechanism behind this unexpected response is still being investigated. Glycerol is known for its cryoprotectants an osmoregulant properties and this work shows that it accumulates in both light and salt stress conditions.

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ENDOPLURA JEJUENSIS SP. NOV. AND E. KOREANA SP. NOV. (RALFSIALES, PHAEOPHYCEAE) FROM KOREA BASED ON MOLECULAR AND MORPHOLOGICAL ANALYSES

A crustose brown algal genus, *Endoplura*, has been known as a monotypic genus characterized by its intercalary plurilocular reproductive organs composed of 2–4 separate parallel filaments capped with 2–5 sterile cells and by containing several to many chloroplasts per cell. In this study, *E. jejuensis* sp. nov. and *E. koreana* sp. nov. from Korea are newly described based on molecular and morphological analyses. Our phylogenetic analyses of *rbcL* and COI-5P genes reveal that *E. jejuensis* sp. nov. and *E. koreana* sp. nov. are placed in the same clade with “*E. aurea*” from Japan with a strong bootstrap supporting value.

Endoplura jejuensis is characterized by small and light to dark brown crust thalli of less than 1 cm, tuft of hairs arising from the basal disc, plurangia composed mostly of two separate parallel reproductive filaments capped with 2–4 sterile cells, and sessile unangia with one paraphysis. *Endoplura koreana* is distinguished by olive or yellowish-brown crust thalli of up to 3 cm, tuft of hairs arising from the basal disc and apical of erect filaments, plurangia with 2–5 separate reproductive filaments, with 2–8 terminal sterile cells, and sessile unangia with 1–2 paraphysis. Our studies also show that “*E. aurea*” specimens from Japan may be recognized a different species from other *Endoplura* species.

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ARE METALS REALLY INSIDE THE CELLS OF BROWN ALGAE?

Knowing the cellular location of metals in algae improves the understanding of their toxicity, as the nature and the intensity of the effect caused will depend on the cellular compartment in which they are located. Several studies investigated the cellular location of metals finding higher intracellular levels. However, they only considered the extracellular and intracellular fractions, including remaining fractions (intercellular and adhered to particulate matter) in the latter. Moreover, they did not test whether the extracellular extractant used displaced ions efficiently or altered membrane permeability. This may have led to misleading results, difficult to explain from a biological standpoint, as the algae have no reason to actively accumulate these toxic elements inside their cells. In the present work we tested the efficiency of different concentrations of EDTA and $\text{Pb}(\text{NO}_3)_2$ as extracellular extractants, and then performed the Sequential Elution Technique (SET) to find out the cellular location of two metals, Cadmium and Cooper. EDTA, the extractant used in most studies, did alter the permeability of the membrane, meanwhile $\text{Pb}(\text{NO}_3)_2$ did not. Thus, the SET was carried out using the latter as extracellular extractant, and it revealed that a relevant fraction of the metals studied remained in the extracellular compartment.

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PHYLOGEOGRAPHIC ANALYSIS OF ALSIDIUM TRIQUETRUM AND A. SEAFORTHII FROM THE MEXICAN ATLANTIC

Alsidium seaforthii and *A. triquetrum* are red seaweed species distributed sympatrically on the Mexican Atlantic, both with potentially economic importance but so many biological aspects unknown in Mexico. The objective of this study was to analyze phylogeographic patterns in *A. seaforthii* and *A. triquetrum* populations from Gulf of Mexico and Mexican Caribbean, as well as to determine their systematics within

the Rhodomelaceae family. From 137 individuals coming from 17 localities, measures of genetic variation, distances, genetic structure and haplotype networks, were determined by *rbcL* Rhodomelaceae sequences. As from this, a phylogenetic analysis was performed in addition to *rbcL* Rhodomelaceae sequences. Intraspecific analysis of *A. seaforthii* determined four haplotypes so as low genetic diversity, mostly concentrated in Campeche, while in *A. triquetrum* were determined six haplotypes and higher diversity, mostly in Sisal, Yucatán. Moreover, restricted to this locality, a differentiated haplotype from both species was revealed. Interspecific analysis yielded a phylogenetic hypothesis which confirms *Alsidium* monophyly and its relationship with sister genus *Digenea* within Alsidiae tribe, while interspecific distances showed a specific variation range. Both variation and genetic structure, as well as haplotype distribution concentrated in Northwestern Yucatan and Campeche, supports previous hypotheses concerning this high diversity area as a genetic break, mostly determined by ocean currents. The haplotype detected by intraspecific analysis suggests an ongoing speciation process.

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THE ROLE OF MACROALGAL MICROBIOMES IN THE CYCLING OF MERCURY THROUGH COASTAL ECOSYSTEMS

Macroalgae has been shown to have high accumulation potential for excess nutrients and metals that enter coastal ecosystems. Although higher concentrations of metals can be toxic to macroalgae, some groups have been shown to have a higher tolerance to these pollutants. Additionally, recent work has suggested that the algal microbiome may either facilitate metal uptake or act as a buffer when toxic concentrations are present. The objective of this study was to investigate the role of the *Ulva sp.* microbiome in the accumulation of mercury. *Ulva sp.* were collected at three coastal and three estuarine locations and exposed to mercury over a six-day period in a laboratory setting. The microbiome was treated with surfactants both before and after exposure to mercury, and the accumulation of mercury in the *Ulva sp.* tissue was analyzed after the six-day exposure. Additionally, *Ulva sp.* samples from each of the six locations were analyzed to determine the bacterial species present in the microbiome. Initial results show the microbiome accounted for 71% of mercury present in *Ulva sp.* (n=12), suggesting an important role in mercury accumulation and potential implications for bioremediation processes.

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SULFATED POLYSACCHARIDE PRODUCTION, COMPOSITION, AND BIOLOGICAL ACTIVITY FROM FOUR STRAINS OF THE MARINE RHODOPHYTE PORPHYRIDIUM (NÄGELI)

Sulfated polysaccharides (SPS) are long-chain carbohydrates that have potential biomedical and pharmaceutical applications with their hygroscopic and antimicrobial properties. Species of *Porphyridium* (Rhodophyta), a type of unicellular microalga, secrete layers of SPS as a defense against bacteria and related pathogens. To determine the maximal production of SPS, four strains of marine *Porphyridium* (*P. cruentum* UTEX 161, *P. sp.* UTEX 637, *P. purpureum* LB UTEX 2757, and *P. sp.* ZZ1203) were grown under five different concentrations of $MgSO_4 \cdot 7H_2O$, ranging from 5 – 80 mM, for two weeks. Cultures were sampled after 7 and 14 days for SPS isolation. SPS samples were separated into high molecular weight (HMW; > 500 kDa) and low molecular weight (LMW; < 500 kDa) fractions using stirred-cell ultrafiltration and precipitated using isopropyl alcohol to determine yields (g/cell/L). The HMW and

LMW fractions were then analyzed using LC-MS/MS to determine monomer composition and degree of sulfation. Bioactivity was tested using rehydrated SPS and ampicillin standards against DH5 α *E. coli* incubated on LB plates in the dark at 37 °C, and zones of inhibition were compared with antibiotic controls. SPS yields, monomer composition, degree of sulfation, and antimicrobial activity results will be reported.

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INFERENCE OF TRANSCRIPTIONAL REGULATORS REVEALS GENOME-WIDE REGULATORY RELATIONSHIPS IN SYMBIODINACEAN DINOFLAGELLATES

Understanding dinoflagellate mechanistic responses to changing ocean conditions is essential to expand our understanding of coral symbiosis. Transcriptional regulation ubiquitously controls responses in eukaryotic organisms, yet it is poorly understood in dinoflagellates, particularly regarding transcription factors (TFs). Here we used an integrative genomic approach to identify and characterize TFs in model symbiodiniacean dinoflagellates, and TF regulatory relationships in these dinoflagellates were inferred by deploying network analysis on transcriptomic data. A total of 1189 and 898 putative TFs and transcriptional regulators were found in *Fugacium kawagutii* and *Brevolium minutum*, respectively. An examination of the abundant TF domain families in the putative TFs, free living dinoflagellates, and other protists indicated functional evolution of the C2H2-type zinc finger and HMG (high mobility group) box TFs which allowed for *F. kawagutii* to regulate non-canonical functions. Furthermore, transcriptomic data provided evidence that *F. kawagutii* and *B. minutum*, respectively, utilize 38 and 44 TFs transcriptional regulators; some of which plausibly regulate processes necessary for the maintenance of coral symbiosis such as transmembrane lipid transport, transmembrane ion transport, photosynthesis, and heat stress responses. This study lays a foundation in understanding dinoflagellate transcriptional regulation and provides a promising approach to further investigate regulatory mechanisms that influence coral symbiosis.

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MORPHOLOGICAL AND MOLECULAR SYSTEMATICS OF THE TAXONOMICALLY CONFUSED FRESHWATER DINOFLAGELLATE HEMIDINIUM, BASED ON THE FIRST OBTAINED NORTH AMERICAN ISOLATES

Hemidinium is an unusual freshwater dinoflagellate with confused taxonomy. It has been alternatively placed in the orders Peridiniales and Phytodiales, based on contradictory descriptions in the All previous descriptions were based on observation of field material; clarification of these discrepancies been hampered by a lack of available cultures. In the present research, we isolated two strains of Hemidinium from North Carolina mountain bogs and brought them into clonal culture as the first isolates ever reported outside of Eurasia. Live cells were examined by light and electron microscopy for important morphological characters. Both imaging and staining determined the absence of cellulosic thecal plates and the presence of a horseshoe apical groove that is a morphological synapomorphy of the dinoflagellate order Gymnodiniales. No “*G. montanum*-like” cells were ever observed in either strain. Average cell sizes between our isolates differed significantly, and one isolate consistently formed resting cysts, unlike the other. Novel rDNA sequences were obtained from each strain that differed from, but consistently formed a monophyletic clade together with the few previously reported sequences for Hemidinium. All

observations suggest our isolates represent two different Hemidinium species. Overall, morphological and molecular data support movement of Hemidinium into the order Gymnodinales, with the description of new species.

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SHORT-TERM PHYSIOLOGICAL RESPONSES OF THE KELP *ECKLONIA ARBOREA* DURING *IN SITU* BIOASSAYS AT DIFFERENT DEPTHS

Seaweeds can be used as efficient bioindicators of anthropogenic (e.g., aquaculture) and natural (e.g., upwellings and internal waves) inputs of nutrients, by performing *in situ* bioassays of variable duration and at variable distance from the nutrient source. Macroalgae can show physiological acclimation to factors such as temperature and light availability that vary through the bathymetric gradient, which in most cases are not assessed. These physiological responses can alter their nutrients acquisition capacities, which ultimately can confound the results of the bioassays. This work examined the physiological acclimation to depth of the kelp *Ecklonia arborea* during its use as a potential bioindicator of nitrate advection by internal waves (San Juanico, Baja California Sur, Mexico). Short-duration bioassays (3 days) were performed *in situ* by transplanting adult sporophytes from shallow waters (< 1m) to three different depths (1, 7 and 15 m). Photobiological descriptors, nutrients content and nitrate uptake kinetics were analyzed. Photosynthetic efficiency and blade absorptance increased with depth, while NPQ (i.e., thermal dissipation of light energy) decreased. Although nitrate concentration was similar among depths, nitrate uptake rates and N-content were also drastically reduced in the deepest plants, likely due to the limited assimilation capacity of inorganic-N under low irradiance conditions. This condition can confound the nitrogen signal of the seaweed when it is employed as bioindicator of nitrogen inputs.

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GROWTH OF *CHLORELLA KESSLERI* UNDER HIGH NITRATE CONDITIONS

Due to various anthropogenic activities, nutrient enrichment in water bodies has become a major issue all around the world in which nitrate is one of the major contributors. To determine, whether algae can be used to solve the nutrient enrichment problem, the effect of different concentrations of nitrate on the growth of *Chlorella kessleri* was investigated. Two different kinds of growth media were used, namely, TAP medium and Chlorella medium for the estimation of nitrate removal by the algae. It was observed that *Chlorella kessleri* can grow from 1 mM concentration of sodium nitrate up to 200 mM. *Chlorella kessleri* did not show much growth once nitrate concentration was reached 200 mM in the medium. At high nitrate concentration, these algae still grow but, they start to form palmelloids structure. Also, the nitrate removal was observed to be higher in Chlorella medium in comparison to TAP medium. The

results from this study suggest that *Chlorella kessleri* can tolerate high nitrate conditions and can be used for further high nitrate conditions related investigations.

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EFFECT OF HERBIVORY ON MORPHOLOGY OF CRUSTOSE ALGAE

Crustose Coralline Algae (CCA) are commonly found in tropical marine environments where they are important reef calcifier and some species can induce coral settlement. Calcification ability and crustose shape of CCA are considered defense mechanisms against herbivores such as parrotfishes. Field observations indicate that crustose morphology of some species (e.g., *Mesophyllum* spp.) might be a direct response effect of herbivory pressure. We evaluated this hypothesis by growing *Mesophyllum* spp. in limestone tiles (10x10 cm) conditioned in mesocosms until individuals reach foliose (rose-like) shape. After nine months in the mesocosm, tiles with crustose and foliose shape were exposed to herbivores. Feeding assays were conducted in coral reefs with high abundance of parrotfish. In approximately 45 minutes, all (100% of tiles with rose-like shape) were consumed by herbivores while crustose individuals were barely touched (<5 bites). The main rose-like CCA eater was the browser herbivore, red-band parrotfish (*Sparisoma aurofrenatum*). Our results indicate that the shape of CCAs, at least partially, controlled by herbivory pressure.

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NEW GREEN CHEMISTRY: A BIOTECHNOLOGICAL APPROACH TO PRODUCE GLYCOLATE IN *CHLAMYDOMONAS REINHARDTII*

The aim of the "New Green Chemistry" concept is the excretion of glycolate by green algae to replace biomass for starch production in a biotechnological approach. In doing so, biomass production is prevented as far as possible while glycolate excretion is to be increased as much as possible. In the best case, harvesting and refining can be avoided by using the glycolate-enriched medium directly for fermentation. In this study, *Chlamydomonas reinhardtii* cells are converted into a continuous glycolate-producing factory. An increase in glycolate production can be achieved by exploiting the oxygenase function of Rubisco. This process requires three steps. First, an adjustment of the CO₂ / O₂ ratio. Furthermore, it requires the inactivation of the carbon concentrating mechanism (CCM) and the inhibition of a key enzyme of glycolate metabolism (glycolatedehydrogenase (GYD)). This can be done, for example, by adding an inhibitor such as ethoxzolamide (EZA). However, EZA interferes with the subsequent use of the glycolate-enriched medium for direct fermentation or chemical conversion. To optimise the process, genetic modification of the cell can be used instead. Instead of creating transgenic lines, a classical crossing approach was used to generate new strains deficient in CCMs and GYD. The double mutants thus generated with functional defects in the CCM master regulator gene (*cia 5*) and in the gene coding for GYD show high biotechnological potential for process optimisation of glycolate formation.

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INHIBITION OF DRUG-RESISTANT BACTERIA BY SULFATED POLYSACCHARIDES FROM *PORPHYRIDIUM PURPUREUM* (RHODOPHYTA)

Approximately 35,000 people die every year in the U.S. due to infections from drug-resistant Gram-negative (G-) and Gram-positive (G+) bacteria that have high mutation rates and become resistant to commonly-used antibiotics. *Porphyridium* is a unicellular red microalga which is known to synthesize sulfated polysaccharides (SPS) as components of their cell wall, and secrete SPS to create a protective extracellular matrix. The antimicrobial activity of extracellular SPS from *Porphyridium purpureum* UTEX LB 2757 was tested against *Staphylococcus aureus* (G+), *Bacillus subtilis* (G+), *Pseudomonas aeruginosa* (G-), and *Acinetobacter baumannii* (G-) to assess growth inhibition in bacterial cultures. Different concentrations of SPS (10, 50, 100, and 500 µg/mL) were added to pre-incubated cultures in the middle of exponential phase to determine the minimum inhibitory concentration (MIC) for each bacterium. Results for SPS experiments were compared to treatments with tetracycline (positive control), and tryptic soy broth (TSB) and water (negative controls). Culture density was measured using a plate reader spectrophotometer at 600 nm set at 37 °C with constant mixing; measurements were taken once every 30 min over 8 hours. The growth of bacteria decreased significantly, or was halted completely, after the addition of SPS; growth inhibition in SPS treatments was dose-dependent for all bacteria tested. Ten µg/mL was the MIC of SPS that inhibited the growth of *S. aureus*, *B. subtilis*, and *A. baumannii*, whereas 50 µg/mL was the MIC that inhibited the growth of *P. aeruginosa*. Ten µg/mL of tetracycline was found to be equivalent to 20 µg/mL of SPS for the inhibition of *S. aureus*. These experiments demonstrate the antimicrobial properties of SPS from *Porphyridium purpureum* and the feasibility of using microalgal natural products to help combat drug-resistant bacteria.

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THE BACTERIAL COMMUNITY OF *SACCHARINA LATISSIMA* AND SALINITY STRESS

Saccharina latissima is host to a community of microbes, including bacteria. The composition of *S. Latissima's* bacterial community is closely linked with *S. latissima* health because bacteria provide essential services, such as nitrogen fixation, antibiotic production, and resistance to abiotic stress. In return, the bacteria receive benefits from *S. latissima* in the form of sugars. Studies in other kelp species, have shown that under abiotic stress, there is high bacterial taxonomic turnover, which co-occurs with degrading host condition (thallus blistering and lower photosynthetic pigment concentration). However, these studies were conducted under laboratory conditions. For my study, I am sampling the bacterial community of the *S. latissima* meristem at four sites every low-tide cycle during the 2021 Spring Freshet along with other *S. latissima* health indicators and water parameters. These data will serve to test the hypothesis that there is a taxonomic and functional turnover in the bacterial community of *S. latissima* and that this turnover is associated with specific environmental thresholds and host condition. Once the data are collected (end of the Spring Freshet period), I will sequence the V4 subregion of the 16S gene to identify the bacterial taxonomy and functional groups associated with *S. latissima* at different timepoints throughout the study.

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EFFECT OF DESICCATION ON GROWTH, PIGMENT AND BIOCHEMICAL RESPONSES IN *AGAROPHYTON VERMICULOPHYLLUM*

To determine the effect of desiccation on growth, pigment and biochemical responses of *Agarophyton vermiculophyllum*, this alga was daily exposed to air for 0 (control), 30 min (23±5% water loss) and 60 min (40±5% water loss), for 8 days. *Agarophyton vermiculophyllum* was cultivated in von Stosch enriched (VSE) medium at 20°C, 12:12 L:D photoperiod and 100 µmol m⁻² s⁻¹. *Agarophyton vermiculophyllum* was exposed to air at noon every day. Thalli were placed on a 0.4 mm mesh. Tissue samples were collected after one hour of rehydration on day 2, 4 and 8. SGR was higher at control than other conditions on day 2. At 30 min desiccation, SGR was significantly lower than control on day 2, and no significant difference was found between 30 min desiccation and control on day 4. SGR at 60 min desiccation was significantly lower than that in control. Desiccation and time did not affect pigment contents (Chl *a*, carotenoid and biliproteins). Reactive oxygen species (ROS) was significantly higher at 30 and 60 min desiccation on day 2. However, ROS was decreased on day 4. The activation of antioxidant enzymes (catalase, GST, glutathione reductase and GPx) was significantly higher at desiccation conditions than at control on day 2, but no significant differences were observed on day 4. These results suggest that mild desiccation (e.g. 30 min) may stimulate increase the activation of antioxidant enzymes of *A. vermiculophyllum* within two days *Agarophyton vermiculophyllum* may recover from the desiccation stress in 2 days.

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GOING WITH THE FLOW: PHYTOPLANKTON MORTALITY AND COMMUNITY DYNAMICS

Phytoplankton communities consist of a dynamic assemblage of organisms, existing in an ever-changing environment. Both abiotic (light, temperature, nutrients) and biotic factors (grazing, species interactions) have been considered to regulate phytoplankton growth, but other factors may be at play that we know much less about – loss processes and cell mortality. Traditionally, losses are thought to be due to sedimentation or grazing, with little consideration of environmental factors and their influence on cell mortality. Knowing that phytoplankton communities undergo changes in composition throughout the seasons, we studied the phytoplankton community and cell death in a small urban pond in southeastern Wisconsin for three years. Using flow cytometry, phytoplankton groups were resolved using red and orange fluorescence, and cell mortality was determined using the mortal stain, Sytox Green®. Of eleven populations tracked, five were intermittent, ranging from undetectable to over 200 cells/L, while six populations were persistent and stable with populations in the range of 200-1,200 cells/L. The proportion of dead cells generally varied with abundance, from < 10% in dominant groups to almost all cells dead in rare species at their lowest populations. Abundance and cell death poorly correlated with most abiotic factors but some populations exhibited correlations with others, suggesting possible biotic interactions (e.g. allelopathy) may be driving community dynamics.

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ASPARAGOPSIS TAXIFORMIS AND A. ARMATA (RHODOPHYTA, BONNEMASSONIACEAE) TWO PRODUCTIVE SPECIES OF ANTI-METHANOGENIC MOLECULES FOR APPLICATIONS IN CATTLE FARMS

Methane is a potent greenhouse gas (GHG) considered one of those responsible of global warming; for this reason, the world of research and industry is looking for a natural anti-methanogen agent. Those compounds are naturally present in macroalgae of the family Bonnemassoniaceae (Rhodophyta). Among them, *Asparagopsis* species produce halo-organic compounds in specialized “gland cells”, as a natural defense against diseases and marine herbivory (Paul et al. 2006, 2013) The aim of present study was to test two red algae, *Asparagopsis taxiformis* and *A. armata*, collected from the Strait of Messina, Italy, as a source of anti-methanogenic compounds in cattle diet. DNA barcoded samples (BOLD #REAPP006-21, #REAPP004-21) were lyophilized and used at dietary inclusion levels (0, 2, and 4% as-fed basis) in an *in vitro* study to examine GHG production and volatile fatty acid (VFA) profiles. *A. taxiformis* contained higher levels of bromoform, iodine and crude protein, than *A. armata*, which contained higher levels of acid and neutral detergent fibers. When lyophilized algae were supplemented in the diets total gas, butyrate and valerate production increased, while production CH₄, acetate (A), propionate (P), A/P ratios and *in vitro* dry matter digestibility were reduced. Therefore, it may be possible to suppress methanogenesis both directly and indirectly by addition of *Asparagopsis* species which modified rumen fermentation profiles. To efficiently use seaweeds as feed ingredients with nutritional and environmental benefits, more research is required to determine the mechanisms underlying seaweed and dietary substrate interactions.

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THE ROLE AND REGULATION OF HEAT SHOCK PROTEINS IN THE ANTARCTIC ALGA CHLAMYDOMONAS SP. UWO241

Chlamydomonas sp. UWO241 is a psychrophilic alga found 17 m below the ice-covered surface of the Antarctic Lake Bonney, where it experiences a myriad of extreme environmental conditions such as low temperature, low light, and high salinity. While this habitat is extreme, it is also very stable, so this alga rarely experiences changes in its environment. Heat shock proteins (HSPs) are a ubiquitous family of chaperone proteins that perform important housekeeping roles. In general, HSP expression is induced during abiotic stress to regain protein homeostasis, a process regulated by heat shock transcription factors (HSFs). Previous work has shown that UWO241 constitutively accumulates high protein levels of HSPs in steady-state conditions but fails to induce additional HSP accumulation during heat stress. It is hypothesized that UWO241 has lost the ability to regulate HSPs in its extreme but unchanging environment. In this study, a single HSF was identified in UWO241 genome. Comparative sequence analysis with related species revealed conservation in all the domains characteristic of a functional HSF. Next, we performed targeted analysis of the UWO241 transcriptome in heat-stressed cultures. We show that ~40% of UWO241 HSPs were differentially expressed during heat stress; however, the HSF1 transcript was not. Additionally, we have not been able to experimentally detect a full-length HSF1 transcript. More work needs to be done to fully elucidate the regulation of HSPs in UWO241.

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PROTECTING THEIR HOME: EELGRASS MESOGRAZERS' TOP-DOWN CONTROL OF EARLY LIFE STAGES OF ULVA SPP.

Macroalgal blooms pose a threat to coastal ecosystems worldwide, especially in highly eutrophic environments. Excess nutrients often facilitate the proliferation of opportunistic algae, but in some systems grazing activity counterbalances its effects. The regulating role of mesograzers associated with eelgrass (*Zostera marina*) was evaluated in Elkhorn Slough, a eutrophic estuary where *Ulva* spp. blooms are frequent during the upwelling season. Recruitment and transplant success of *Ulva* spp. were monitored along transects placed across the edge of the largest *Z. marina* bed. Changes in abundance of *Ulva* spp. on transplants differed spatially and seasonally, and were significantly correlated with density of both small and large invertebrate groups. Of the large mesoinvertebrate groups, sea slugs had the strongest regulating effect on *Ulva* spp. Taylor's sea hare (*P. taylorii*), found almost exclusively on eelgrass, accounted for the majority (>90%) of individuals within this taxonomic group at the study site. Grazing affected not only adult *Ulva* spp. but also its early developmental stages, leading to decreased *Ulva* spp. abundance on transplants and minimal recruitment inside the *Z. marina* bed.

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10 YEAR VARIATION IN CARBON AND NITROGEN RATIOS IN KELP POPULATIONS ACROSS THE PACIFIC RIM WITH A SPECIAL FOCUS ON CALIFORNIA

Globally, kelp forests and the ecosystems they support are in danger due to several intensifying threats brought on by anthropogenic climate change (Krumhansl et al, 2016). The roles of nutrient availability, especially carbon and nitrogen uptake kinetics in maintaining kelp forest health have been well studied at small scales (Edwards et al, 2010, Koweeck et al, 2017) but more research is needed to understand how these factors influence kelp persistence across large spatial scales and oceanographic gradients. Studies at this large scale are often prohibitively costly and are therefore, rare. Here, I present an opportunity to analyze carbon and nitrogen tissue concentrations and their isotope ratios, in a rare sample set that spans nearly the entire Pacific Rim. The KelpWatch Program consecutively sampled kelp populations during 2013-2016 to track radiation from Fukushima Daichi meltdown in 2011. These samples offer an opportunity to address the persistence and resiliency of kelp forests through time. My overarching objective is to identify patterns in kelp Nitrogen (i.e. terrestrial versus oceanic) and Carbon (CO₂ versus HCO₃⁻) signatures across this broad geographic region, and to identify patterns associated with regional oceanographic gradients. I will also compare the KelpWatch sample set with historic and contemporary samples of the same populations for insights into how shifts river inputs, human populations, and upwelling strength have changed isotopic signatures in California populations over a 20 year period.

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CYANOBACTERIAL AKINETE DISTRIBUTION, VIABILITY, AND CYANOTOXIN RECORDS IN SEDIMENT ARCHIVES FROM THE NORTHERN BALTIC SEA

Cyanobacteria of the order Nostocales, including Baltic Sea bloom-forming taxa *Nodularia spumigena*, *Aphanizomenon flos-aquae*, and *Dolichospermum* spp., produce resting stages, known as akinetes, under unfavorable conditions. These akinetes can persist in the sediment and germinate if favorable conditions return, simultaneously representing past blooms and possibly contributing to future bloom formation. The present study characterized cyanobacterial akinete survival, germination, and potential cyanotoxin production in brackish water sediment archives in order to understand recent bloom expansion, akinete persistence, and cyanobacteria life cycles in the northern Baltic Sea. Results showed that cyanobacterial akinetes can persist in and germinate from Northern Baltic Sea sediment up to >40 and >200 years old, at coastal and open-sea locations respectively. Akinete abundance and viability decreased with age and depth of vertical sediment layers. The detection of potential microcystin and nodularin production from akinetes and revived cultures was minimal. Phylogenetic analysis of culturable cyanobacteria from the coastal sediment core indicated that most strains likely belonged to the benthic genus *Anabaena*. Results of germination experiments supported the notion that akinetes don't play an equally significant role in the life cycles of all bloom-forming Baltic Sea cyanobacteria. Overall, there was minimal congruence between akinete abundance, cyanotoxin concentration, and the presence of cyanotoxin genes in either sediment core.

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CULTIVATION OF SNOW ALGAE SPECIES IN OPEN RACEWAY PONDS FOR BIO JET FUEL PRODUCTION IN A BIOREFINERY CONCEPT

Algae remain one of the promising candidates in the production of alternative jet fuel for aviation. However, outdoor production in large quantities around the whole year is still a challenge and valorization of side-products is a must for economic viability. Cooler temperatures are important parameters to limit algal growth, therefore, we explored snow algae strain candidates in open raceway pond (ORP) cultivation during cold seasons for their performance of inner cell lipid storage and performed nutritional profiling. *Chlamydomonas nivalis* UTEX 2428 were first grown indoor tubular 12L photobioreactor (PBR), then transferred outdoor, where cultivation volume was gradually increased to 100L, 1000L and 3000L. ORPs were grown in wintertime, exposed to snowfall and sub-zero temperatures. At the end of the cultivation, dry weight reached to 0.40 ± 0.04 g/L. Lipid profile were determined, and carbohydrate, total lipid and hydro-soluble protein percentages were found to be 21.7 ± 4.8 , 4.1 ± 1.5 and 68.4 ± 5.4 , respectively. Testing the effects of temperature range in springtime and nutrient deficient conditions are currently underway. To the best of our knowledge, this is the first time that this strain is used for outdoor ORP cultivation in large volume. Preliminary analyses indicate that *C. nivalis* can be a good candidate as a biorefinery input source, both for bio jet fuel production through hydrothermal liquefaction process, and for valuable materials through downstream process.

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EARLY SUMMER PHYTOPLANKTON COMPOSITION IN A TEMPERATE LAKE ALTERED BY BODY WASH MICROPLASTICS IN A MESOCOSM EXPERIMENT

Microplastics alter the development, physiology, and behavior of various aquatic organisms including algae; however, very limited data are available on how they interact with phytoplankton assemblages in

lakes. We tested the effects of two types of microplastics, polystyrene (PS) calibration beads and polylactic acid (PLA) plastic body wash scrub particles, and one type of plant-derived body wash scrub particle on a natural phytoplankton assemblage through an incubation experiment in a temperate, mesotrophic Otsego Lake in upstate New York, USA. The calibration beads and the plant-derived particles generally did not alter the taxonomic composition of the phytoplankton in the mesocosms, while the PLA body wash microplastics eliminated cryptophytes and increased chrysophytes. Our findings demonstrate differential effects of irregularly shaped PLA body wash microplastics vs. PS calibration beads on lake phytoplankters and provides support for the bottom-up effect of secondary microplastics on aquatic food webs.

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ESTIMATING PHYTOPLANKTON CARBON BIOMASS USING DNA

In most phytoplankton studies, species composition and their contribution to the phytoplankton community are essential. However, it is technically challenging to assess an individual species biomass in a phytoplankton assemblage. Fortunately, DNA analysis has the potential to be a proxy for estimating species composition and species-specific biomass simultaneously now. This requires an established relationship between carbon biomass and DNA content at the species level using a measurable DNA index, 18S rDNA. To address this shortcoming, species representing major phyla of micro algae are being studied. We used CTAB method for DNA isolation, qPCR to quantify 18S rDNA abundance, and EPA 440 method for carbon measurement. The results from 10 species that have been examined so far showed an apparent log-log relationship for carbon and DNA content ($R^2=0.9703$, $P<0.0001$) as well with DNA and 18S rDNA ($R^2=0.8448$, $P<0.0001$) and with Carbon and 18S rDNA ($R^2=0.8852$, $P<0.0001$), which verified the feasibility of estimating phytoplankton carbon biomass using DNA. Furthermore, this 18S rDNA-to-carbon approach will enable high-throughput sequencing (HTS) work for natural plankton assemblages in the future. If validated, an accurate and efficient determination of phytoplankton species composition and species-specific biomass will become feasible.

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SARGASSUM MITIGATION LOCATIONS IN BARBADOS

Sargassum, which is normally viewed as a species that forms a highly productive ecosystem in the open ocean, has been causing ecologic and economic problems on and around Caribbean shores. It forms thick mats which shade and suffocate other ecosystems, such as seagrass beds, as these mats travel nearshore and begin to decompose. Barbados' beaches, used for recreational and commercial purposes, have been inundated with large sums of *Sargassum* called landings. This study investigates where the most landings occurred in 2019 and where the areas of highest economic value are located. These locations are crucial for the Barbados government to know where to focus their mitigation efforts. It was found that the southwest coast of Christ Church and the southernmost coast of Saint Michael had the most *Sargassum* landings and happen to be the areas which rely the heaviest on tourism.