

## 1. Resistance to ocean acidification in upwelling-associated phytoplankton communities

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Atmospheric carbon dioxide (CO<sub>2</sub>) concentrations have rapidly risen to levels that have not been observed in 800,000 years. Increased CO<sub>2</sub> dissolving in seawater results in a decline in pH and shift in carbonate chemistry commonly referred to as ocean acidification. In particular, coastal upwelling regions are acidifying at rates double that of the global average with an anthropogenic signal superimposed on existing high natural variability. Recent laboratory studies suggest that acidification may reduce iron bioavailability and expand existing iron limitation in upwelling environments. Here we show that upwelling-associated phytoplankton communities are resistant to ocean acidification via trace metal clean incubations in the California Current Ecosystem. Natural communities were subjected to 400, 800, and 1200 ppm pCO<sub>2</sub> and examined for changes in growth, nutrient uptake, community composition, and gene expression. Despite the dramatic decline in pH, communities dominated by diatoms and the picoeukaryotes *Ostreococcus* and *Pelagomonas* were unaffected. These results suggest that phytoplankton in upwelling regions are accustomed to low pH and that high levels of primary production will likely continue in upwelling environments under future acidification scenarios.

## 2. A growth ceiling exists when *Prochlorococcus* cultivates in artificial seawater media?

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As one of the most abundant phytoplankton in the oligotrophic ocean, *Prochlorococcus* contributes nearly half of primary productivity in the vast open ocean ecosystems. Here, we observed what appeared to be a growth ceiling in *Prochlorococcus* cultivated in artificial seawater (ASW) based media. Nutrient depletion was not the cause of growth arrest, but rather *Prochlorococcus* cells lysed when cell density reached the ceiling. As shown previously, co-culture with marine heterotrophic bacterium helped *Prochlorococcus* survive at low inoculation cell density, but the inoculation cell density did not affect the maximum biomass of *Prochlorococcus*. Moreover, the presence of heterotrophic bacteria or not did not change the maximum biomass of *Prochlorococcus*. During semi-continuous cultivation with periodic dilution by 50% with either Pro99 media or ASW (without nutrients) showed that the 'age' of the previous generation negatively affected the height of the growth ceiling in the new culture. Dilution of old media with ASW (without nutrients) could temporarily abolish the inhibition effect of old media. These results suggest that *Prochlorococcus* may secrete some infochemicals that negatively regulate its own cell density.

## 3. Programmed cell death in coccoid green microalga *Ankistrodesmus densus* Korshikov (Sphaeropleales, Selenastraceae)

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Reports of programmed cell death (PCD) in unicellular chlorophytes raises intriguing questions on its ecological and evolutionary roles. Here, we have reported responses to rapidly changing light, temperature and fluctuations in macronutrients in the common selenastracean green microalga *Ankistrodesmus densus* (Chlorophyta, Chlorophyceae, Sphaeropleales). Specifically, the stimuli of darkness, nitrogen deprivation, heat and cold shock were tested since these occur naturally. PCD phenotypes were examined by way of ultrastructural changes, phosphatidylserine (PS) externalization and DNA degradation. Flow cytometric Annexin-V analysis of PS externalization revealed that the darkness and nitrogen deprivation treatments were significantly different than the control cultures ( $p < 0.05$ ) while heat and cold cultures did not affect significantly the PS externalization ( $p = 0.44$  and  $p = 0.99$ , respectively). Transmission electron microscopy (TEM) images revealed that darkness induced high cytoplasmic vacuolization, among other ultrastructural changes. Nitrogen deprived cells showed less vacuolization but presented chromatin condensation and marginalization. Heat and cold treatments resulted in necrotic-like features. DNA laddering was not detected. We suggested that vacuolar cell death, a special type of plant autophagic-like PCD, might play a role in cell death in Selenastraceae. Yet, autophagy might provide a mechanism whereby nitrogen may be recycled and exported to kin during nitrogen limitation conditions.

#### **4. Mesophotic diversity of Rhodymeniales (Rhodophyta) in Hawai‘i: species new to science?**

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Macroalgal communities dominate Hawai‘i’s mesophotic coral ecosystems and much about the diversity of these communities remains unknown. Due to advances in molecular technologies, such as DNA barcoding, discovering new species has been made more tractable. This project focuses on uncovering the diversity found in the Hawaiian mesophotic for the order Rhodymeniales. DNA sequences were generated for common red algal molecular markers such as the COI barcode region, LSU, and rbcL markers. Phylogenetic comparisons indicate that there are at least four possible new species in this order based upon molecular data; these samples most closely match the genera *Leptofauchea* and *Halopeltis*. These genera have 19 species, none of which have been previously found in Hawai‘i. Morphological work will be conducted on these samples over the coming months to determine whether they match characters present in these genera, and whether they differ from characters of congeners. Thousands of samples have

been collected from the mesophotic zone in the Main Hawaiian Islands as well as in the Papahānaumokuākea Marine National Monument, and future work will entail searching for additional diversity in the Rhodiales from these collections.

## **5. Temperature but not carbon dioxide stimulates growth in southern ocean phytoplankton**

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Southern Ocean phytoplankton have been shown to overcome the low light and low iron (Fe) environment through genomic and physiological adaptations. Together, these adaptations allow the efficient use of light and Fe to photosynthesize optimally in this cold polar region. Through biological and physical processes, the Southern Ocean (SO) accounts for approximately 40% of global carbon fixation. Model projections indicate that light, temperature, Fe and CO<sub>2</sub> (thus pH) in the SO are likely to change simultaneously in the future due to changing climate. Although prior investigations have constrained the response of SO species to changes of individual environmental variables, multiple species responses to concurrent changes is unclear. This study adds to a growing research focus which aims to understand how marine biota will respond to climate changes over the coming century by culturing two SO phytoplankton species under a matrix of light, temperature, Fe and CO<sub>2</sub> treatments. We measured growth, photophysiology and cellular chlorophyll, carbon and nitrogen quotas and show that species respond differently to the combination of environmental treatments. We hypothesize that increased CO<sub>2</sub> and temperature individually and combined alleviate photoinhibition at higher irradiances in the diatom *Chaetoceros flexuosus*, but increased CO<sub>2</sub> had a negative impact on growth of both *C. flexuosus* and the haptophyte *Phaeocystis antarctica* at high light, regardless of temperature or Fe concentration.

## **6. Revealing the hidden taxonomic, trophic, and functional diversity of conspicuous coral reef benthic cyanobacterial mats**

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Little is known about the community composition or functional potential of coral reef benthic cyanobacterial mats, which remain generally ill-defined. Here, we used shotgun metagenomic sequencing to characterize the community composition and functional potential of a coral reef benthic cyanobacterial mat sampled from the Caribbean island of Bonaire, Netherlands. Read-based taxonomic profiling revealed a diversity of non-cyanobacterial members of the sampled mat community, including diatoms, fungi, Archaea, viruses, and bacteria. Mat samples were co-dominated by reads belonging to the phylum Cyanobacteria and diverse classes of the phylum Proteobacteria. We found numerous gene families for regulatory systems and for functional pathways (both aerobic and anaerobic). These gene families were involved in community coordination; photosynthesis; nutrient scavenging; and the cycling of sulfur, nitrogen, phosphorous, and iron. We also report bacteriophage and prophage sequences associated with this subtidal coral reef cyanobacterial mat, which could contribute to cellular lysis, horizontal gene transfer, intra-mat nutrient cycling, and bloom dynamics. Overall, our results suggest that

subtidal coral reef cyanobacterial mats are taxonomically rich communities that possess broad metabolic potential for intra-mat nutrient scavenging, recycling, and retention. Such community coordination, similar to archetypical microbial mats, likely contributes to the contemporary success of cyanobacterial mats on reefs.

## **7. Culturable cyanobacterial diversity from Harike Wetland (Ramsar Site), Punjab, India**

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During present study, samples were collected from Harike Wetland, Punjab to isolate, purify and identify cyanobacterial species/strains using culture based approach. Harike Wetland is situated at 31°09'00.6"N latitude and 74°57'04.7"E longitude on 'T' point of river Sutlej and Beas. Water and algal samples were collected from 4 sampling sites covering entire wetland in the month of April, 2019. Total 45 cyanobacterial isolates were isolated comprising 14 unicellular, 26 non-heterocystous filamentous and 5 were heterocystous filamentous forms. These isolates were identified on the basis of microscopic observations of their phenotypic characters i.e. cell shape, cell dimensions, presence/absence of sheath, presence/absence of heterocyst etc. These isolates were represented by 24 species of 17 genera (*Synechococcus*, *Microcystis*, *Aphanocapsa*, *Chroococcus*, *Cyanosarcina*, *Oscillatoria*, *Phormidium*, *Komvophoron*, *Pseudanabaena*, *Limnothrix*, *Lyngbya*, *Leptolyngbya*, *Porphyrosiphon*, *Plectonema*, *Nostoc*, *Rivularia* and *Nodularia*) belonging 11 families of class cyanophyceae. Nitrogen content in the water favors the growth of non heterocystous forms both unicellular and filamentous while absence or lower amounts of nitrogen favors the growth of heterocystous cyanobacteria which has the ability to fix the atmospheric nitrogen. It is also clear from the results that the non heterocystous filamentous forms dominant the cyanobacterial community in the wetland which also depict nitrogen and phosphorus rich habitat. pH of the 3 sites H2, H3 and H4 is between the desired ranges of Indian Standards for drinking water except site H1 having pH 9. The concentrations of calcium, magnesium, chloride, sulphate and nitrate are also within the prescribed values of IS.

## **8. Synthetic, episome-based regulatory systems for controlling gene expression in diatoms**

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Diatoms hold great promise for a biotechnological chassis enable the light-driven production of high-value chemicals or fuels. Unlike model organisms (*E. coli*, yeast, and *Arabidopsis*), manipulation and optimization of diatom metabolism have been constrained by lack of quantitatively characterized genetic components. We engineered chemically inducible gene expression machinery into an artificial chromosome within the model diatom *Phaeodactylum tricorutum*. We designed and evaluated six inducible expression systems that have been proven effective in other eukaryotic organisms. These are based on naturally occurring, heterologous chemically responsive transcription factors and cognate inducible promoters. We found two inducible expression systems which are suitable for controlling gene expression in *P. tricorutum*. We demonstrate that our transcriptional control systems are tunable and reversible in a dose-and time-dependent manner. Addition of chemical inducers in cells expressing inducible genetic

circuits, activate accumulation of reporter protein (YFP) with a dynamic range of up to ~450-fold. The described system is the first example of synthetic gene control in the SAR supergroup of eukaryotes and its application will facilitate gene discovery efforts and the tailoring of diatom metabolism for the production of economically important metabolites.

## **9. Phenotypic plasticity and growth responses of marine cryptophytes to varying spectral irradiance**

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Light is a critical resource for phototrophs but the spectral quality of light available in water varies among habitats. Cryptophytes, unicellular eukaryotic microalgae, contain cryptophyte-phycoerythrins (Cr-PEs) or cryptophyte-phycocyanins (Cr-PCs) as accessory pigments which allow them to exploit a diverse range of environments. The Cr-PEs have a narrow absorption spectrum that harvests green light most efficiently. Cr-PCs have a broader spectrum that absorbs yellow to orange light optimally. We measured fitness, as growth rate, of two cryptophytes (*Hemiselmis rufescens*, which contains Cr-PE 555, and *Chroomonas mesostigmatica*, which contains Cr-PC 645), at two time points (1 and 6 months) in four light environments: full spectrum, blue, green, and red light. After 6 months, *H. rufescens* had its highest growth rates in blue ( $0.46 \pm 0.03 \text{ d}^{-1}$ ) and green ( $0.4 \pm 0.02 \text{ d}^{-1}$ ) light. In red light, *H. rufescens* showed a 44% increase in growth rate over the experimental period ( $0.16 \pm 0.04$  to  $0.23 \pm 0.08 \text{ d}^{-1}$ ). In contrast, *C. mesostigmatica* had similar growth rates across all light treatments ( $\sim 0.2$  to  $0.4 \text{ d}^{-1}$ ) with no evidence of acclimation over the experiment period. Further work will determine whether phenotypic plasticity differs between Cr-PE-containing and Cr-PC-containing cryptophytes.

## **10. Using simulated coal-fired power plant emissions to rapidly grow nutritious microalgae with enhanced settleability**

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Favorable microalgal nutrition from waste, and efficient harvesting, would offset costs for systems that treat pollution and produce valuable animal feed. Co-benefits include avoidance of CO<sub>2</sub> emissions, a possible additional revenue stream as carbon markets develop. To sustainably achieve these goals at scale, barriers to microalgal production such as tolerance for waste streams and dramatic improvement in biomass dewatering must be overcome. Presently, it is largely assumed that nutritious microalgae, including *Scenedesmus obliquus*, would be inhibited by SO<sub>x</sub> and NO<sub>x</sub> in emissions and settle slowly as discrete particles. Studies conducted with a 2-L photobioreactor, sparged with simulated combustion emissions, demonstrated that both biomass productivity and settling rates were increased. The average maximum biomass productivity,  $700 \pm 40 \text{ mg L}^{-1} \text{ d}^{-1}$ , significantly exceeded that of the control culture. Thirty-minute trials of modeled bulk settling showed rapid coagulation, likely facilitated by extracellular polymeric substances, and compaction when the cultures were grown with simulated emissions. Control cultures did not show any settling progress within 30 minutes. Sparged SO<sub>2</sub> was captured as either SO<sub>4</sub><sup>2-</sup> in the medium or fixed in the biomass. The stress of simulated-emissions exposure

decreased microalgal protein contents and altered the amino acid profiles but did not decrease the fraction of methionine, a valuable amino acid in feed.

### **11. Foes with benefits: Evolution of conflict and cooperation between *Prochlorococcus* and *Alteromonas***

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*Prochlorococcus* is the most abundant photosynthetic organism in the world, covering 1/3 of Earth's surface to a depth of more than 200 m and contributing as much as 1/8 of total planetary primary production. Yet in culture *Prochlorococcus* is extremely fragile, requiring "help" from heterotrophic bacteria such as *Alteromonas* to grow robustly. The relationship between *Prochlorococcus* and *Alteromonas* appears outwardly mutualistic – *Prochlorococcus* "pays" *Alteromonas* with fixed carbon in return for protection from reactive oxygen species — but it is possible that this cooperation is a mere side-effect of reductive "Black Queen" evolution occurring in parallel with more traditional competition. Here we show results from a 500-generation evolution experiment pairing these two organisms under either modern or year 2100 pCO<sub>2</sub> conditions. At the beginning of the experiment, the mutualism between the two organisms broken down at year 2100 pCO<sub>2</sub>, resulting in dramatically reduced growth rates and survival of *Prochlorococcus*, but this problem no longer existed after 500 generations. However, this change was likely caused by mutations in the *Prochlorococcus* genome rather than changes in the "helping" relationship. Indeed, evolved strains of *Alteromonas* reduced growth rates of the ancestral *Prochlorococcus* even further, suggesting they had evolved to be superior competitors with *Prochlorococcus* rather than cooperators. Nevertheless, evolved *Prochlorococcus* retain their dependence on *Alteromonas*, as axenic cultures still experienced dramatically reduced growth rates compared to co-cultures of the two organisms together. Collectively these results imply a complex tug-of-war between conflict and cooperation between these two ubiquitous and important marine microorganisms.

### **12. Calcification does not necessarily protect coralline algae from herbivores**

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Calcification is widely thought to be an adaptation to reducing the impact of herbivory. Recent work has shown that ocean acidification may negatively impact calcification of marine organisms, including coralline red algae, which could theoretically increase the susceptibility of corallines to benthic grazers. By manipulating calcium carbonate content of three articulated coralline algal species, we demonstrated that calcification has a variable and species-specific effects on urchin grazing. For two species, *Corallina vancouveriensis* and *Corallina officinalis* var. *chilensis*, reductions in calcium carbonate content did not cause a significant increase in urchin grazing, raising questions about the benefit of calcification in these species. For *Calliarthron tuberosum*, reduced calcium carbonate content caused an increase in urchin grazing rates but only after calcium carbonate had been reduced by more than 20%, suggesting that only dramatic shifts in *Calliarthron* physiology would make it susceptible to urchin grazing. We hypothesize that the herbivory-reducing benefits of calcification likely depend upon coralline

thallus morphology and vice-versa. Moreover, negative impacts of ocean acidification on calcification in coralline algae may not necessarily increase herbivory rates.

### **13. *Haraldiophyllum hawaiiensis* sp. nov. (Ceramiales, Rhodophyta), a new delesseriacean alga from the Hawaiian Archipelago**

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*Haraldiophyllum hawaiiensis* (Delesseriaceae, Rhodophyta) is a new mesophotic algal species from the Papahānaumokuākea Marine National Monument; with specimens collected from Kure Atoll, Salmon Bank and Pearl and Hermes Atoll. Phylogenetic analyses supported *H. hawaiiensis* as a distinct lineage within the genus *Haraldiophyllum*, as well as a new genus record for the Hawaiian Islands. The Hawaiian specimens were shown to be identical in DNA sequence, but unique among other species of the genus and also the recently established genus *Neoharaldiophyllum*, which comprises half of the species that were previously classified as *Haraldiophyllum*. The vegetative morphology of *H. hawaiiensis* sp. nov. resembles *N. udoense* (formerly *H. udoensis*); however, no female or post-fertilization structures were found in our specimens that would allow a more thorough investigation. Therefore, the Hawaiian specimens are placed within the genus *Haraldiophyllum* and described as a new species. This new record for the Hawaiian Islands highlights the novel biodiversity from mesophotic depths, reaffirming the need for further investigation in these ecosystems. This result represents one of several ongoing studies to characterize the algal biodiversity and will contribute to investigations of how algal communities are ecologically associated with Mesophotic Coral Ecosystems from the Hawaiian Archipelago and in the Pacific.

### **14. Reproductive Phenology of an Invasive Alga in a “Pristine” Marine National Monument**

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Pearl and Hermes Atoll (PHA) is in the Northwestern Hawaiian Islands (NWHI), a 1,931 km chain of uninhabited, remote, and pristine atolls in the Pacific. The NWHI is part of the Papahānaumokuākea Marine National Monument, composed of an intact food web structure. In July 2019, expansive mats of an undescribed, red macroalgal species in the genus *Chondria* were discovered to be highly abundant across PHA from 1 to 21 m depths. The invasive algal mats smothered native corals and algae and appeared to reduce the diversity and abundance of other benthic organisms on the scale of thousands of m<sup>2</sup>. Collections of 25 individuals were made at five locations across PHA to determine the reproductive phenology of this alga. Individuals were identified as either vegetative, male gametophytes, female gametophytes, or tetrasporophytes based on the absence or presence of reproductive structures microscopically. Determining the reproductive phenology of a newly documented invasive alga provides an understanding of the alga’s proclivity for acclimation and adaptation (i.e., is sex occurring) and will hopefully lead to

better management practices regarding its optimum habitat preferences that may be present at other locations within the NWHI.

### **15. The chemistry between an amphipod and its macroalgal host**

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Inter- and intraspecific interactions between organisms can either be a form of communication, environmental sensing, or defence and are often mediated by chemicals such as secondary metabolites. Sessile marine organisms such as macroalgae commonly produce chemical defenses against grazers, pathogens, as well as biofoulers. *Plocamium cartilagineum* is a finely branched red understory alga that is common in Antarctic macroalgal forests. It supports a very high abundance of amphipods of which most are not able to feed on the heavily chemically defended *P. cartilagineum* except for *Paradexamine fissicauda*. Different *P. cartilagineum* individuals produce differing mixtures of halogenated secondary metabolites which are referred to as chemogroups. Around Palmer Station between 2016 and 2018 a total of 16 different chemogroups were identified. A subset of these chemogroups were used to identify whether the feeding rate of *P. fissicauda* differs between individuals that vary in secondary metabolite production. The same subset was used to assess differences in growth rate and reproductive output of *P. fissicauda* when held on a chemogroup-specific diet. These data determined whether there is a fitness cost associated with feeding on particular chemogroups and whether secondary metabolite variation impacts the grazer's feeding rate.

### **16. Identification of a cryptogenic seaweed displaying invasive characteristics at Pearl and Hermes Atoll, Papahānaumokuākea Marine National Monument**

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Survey cruises by NOAA in 2016 and 2019 yielded specimens of an undetermined red alga that rapidly attained alarming levels of benthic coverage at Pearl and Hermes Atoll, Papahānaumokuākea Marine National Monument (PMNM), Hawai'i. By 2019 the seaweed had covered large expanses on the northeast side of the atoll with mat-like, extensive growth of entangled thalli. Specimens were analyzed using light microscopy and molecular analyses, and were compared to morphological descriptions in the literature for closely related taxa. Analyses confirmed its genus-level placement within *Chondria*, yet a species match could not be made. Thus, this cryptogenic seaweed is proposed as a new species: *Chondria tumulosa* A.R. Sherwood & J.M. Huisman sp. nov. *Chondria tumulosa* is distinct from all other species of *Chondria* based on its large, robust thalli, mat-forming tendency, large axial diameter in mature branches which decreases in diameter with subsequent orders of branching, terete axes, and bluntly rounded apices. This seaweed is not closely related to any known Hawaiian native species and is of particular concern given its sudden appearance and rapid increase in abundance in the PMNM, a UNESCO World Heritage Site that remains an uninhabited, remote, and pristine portion of the Hawaiian archipelago, positioned to the northwest of the Main Hawaiian Islands.



**17. *Porphyra dioica* J.Brodie et L.M.Irvine; a first look to a mass cultivation of a European species**

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The use of macroalgae for human nutrition is constantly expanding, particularly in Europe. In particular, the species of the genera *Porphyra* and *Pyropia* that are economically important. (FAO 2018). Was considered for this study *Porphyra dioica*, present in all of Northern Europe (Holmes and Brodie 2004) is considered a species suitable for aquaculture (Pereira et al. 2004). The aim of the present research was to study the influence of different environmental parameters on thalli growth to improve the knowledge on mass cultivation methods for *P. dioica*. For this study thalli of *P. dioica* were collected along the coasts of Galicia. The blades were cultured at 14°C. The main target was to test the effects on biomass yield of photoperiod (12L: 12D, 16L: 8D and 8L: 16D) and irradiance (250, 140 and 70  $\mu\text{E m}^{-2} \text{s}^{-1}$ ). Furthermore, we tested the "free-living" growth conditions on the *conchocelis* phase, traditionally cultivated on a calcareous substrate. To support the obtained data, the health status of the gametophytes was evaluated by the Fv/Fm index. The highest growth of thalli was obtained at the photoperiod 16:8 and the light intensity of 140  $\mu\text{E m}^{-2} \text{s}^{-1}$ . The further increase of light intensity caused a reduction in the growth due to a high light stress, as shown by the Fv/Fm index. The cultivation of the *conchocelis* phase in free-living conditions present excellent results.

**18. Diversity of Kallymeniaceae (Gigartinales, Rhodophyta) associated with the mesophotic reefs of Hawai‘i with description of *Psaromenia laulamaula* sp. nov. and *Meredithia hawaiiensis* sp. nov.**

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Small algal red blades of varying morphology have been moderately well-collected from Hawaiian reefs, but poorly classified. In surveys of the Papahānaumokuākea Marine National Monument (PMNM) and Main Hawaiian Islands (MHI), we discovered two undescribed small red blades that molecularly and morphologically matched *Psaromenia* and *Meredithia*, respectively; neither genus has been previously recorded in the Hawaiian Islands. Accordingly, these specimens are described here as new species within the family Kallymeniaceae and new records to the Hawaiian marine algal flora. *Psaromenia laulamaula* sp. nov., exclusively found at mesophotic depths (83–94 m) in PMNM, is easily distinguished from other members of the genus by its comparatively large, procarpic carpogonial branch system and solitary obovate pink to magenta blades. Conversely, *Meredithia hawaiiensis* sp. nov., occurring in both shallow (0–17 m) and mesophotic depths (55 m), has high morphological plasticity, with characters that overlap with other *Meredithia* species, and can only be distinguished based on DNA sequences. This

study provides additional evidence of the extent of diversity in the Family Kallymeniaceae from mesophotic depths, which are poorly characterized, and provides further evidence that even small, inconspicuous members of the macroalgal flora contain undescribed biodiversity.

### **19. Sugar kelp, *Saccharina latissima*, population genetics in Northeast US, for guiding a breeding program**

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The cold-water sugar kelp, *Saccharina latissima* has a circumboreal distribution and in the Northeast US is at its southern distributional limits in Long Island Sound. An understanding of genetic diversity of natural kelp populations is critical for making recommendations for breeding and cultivation efforts of the growing seaweed aquaculture sector in the US. An important component of the ARPA-E's MARINER project is selectively breeding several kelp species in order to improve overall productivity for biofuels, feeds and food. We made collections of 15 wild *Saccharina* spp. populations via SCUBA along the New England coast. Microscopic gametophytes were isolated and the parental populations were used to make over 500 hybrid crosses that were planted at several farm locations over several years. We then used genome-wide single nucleotide polymorphism data to explore the genetic structure of the kelp throughout this region. An assessment of the sequence diversity revealed distinct genetic variation between the Gulf of Maine and Southern New England ( $F_{ST} > 0.25$ ), confirming that Cape Cod acts as a barrier to *S. latissima* gene flow. Furthermore, based on the analysis of molecular variance (AMOVA), we found the largest variance (58%) within sites. We also observed admixture among five sub-populations and isolation by distance. Future steps include skim sequencing the haploid microscopic gametophytes to identify trait heritability and phenotypic diversity observed for both morphological traits and tissue composition. Furthermore, in the future, we plan to place our sequence data into a larger context to include samples from sites in Europe and Asia.

### **20. Screening the Plankton Soup-Utilization of Imaging FlowCytobot**

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Harmful algal blooms (HABs), defined as the rapid increase in algal population, have adverse impacts on the environment. The consequences of HABs vary greatly by algal species, ranging from the reduction in food quality to animal mortality. Traditionally, the identification of bloom species has relied upon microscopy; however, microscopic identification requires an extensive amount of time and labor. Over the past two decades, the occurrence of HABs has become more

frequent, and therefore, technology that allows for real-time monitoring is needed. A combination of the Imaging FlowCytobot (IFCB) and the computational artificial neural network (ANN) model has been applied to achieve real-time plankton identification in the York River, Chesapeake Bay, VA. The IFCB combines flow cytometry and photography to capture high-resolution images of suspended particles. These images are manually sorted into algal groups to build a reliable ANN classifier for real-time identification. We deployed the IFCB to determine the bloom dynamics of *Dinophysis* spp., a producer of diarrhetic shellfish poisoning toxins, and its prey, *Mesodinium* spp., over the seasonal progression

## 21. JGI Algal Genomics Resources

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The US Department of Energy Joint Genome Institute (JGI) provides access, at no cost, to high-throughput genomics and functional genomics capabilities including DNA and RNA sequencing, synthesis, metabolomics and data analysis through Community Science Program (CSP) Annual and semi-annual Calls for proposals (<https://jgi.doe.gov/user-programs/program-info/how-to-propose-a-csp-project/>). The JGI algal genomics started with the first genome of diatom *Thalassiosira pseudonana* published in 2004, followed by several first of its kind algal genomes including model green algae *Chlamydomonas reinhardtii*, haptophyte *Emiliania huxleyi*, and others. Recently with development of new sequencing platforms and analytical tools algae became a new strategic focus for JGI to explore algal biology, diversity and evolution by scaling up genome sequencing and bringing additional functional and multi-omics genomics capabilities. The sequenced algal genomes with transcriptomes and other data are integrated into the JGI algal multi-omics resource PhycoCosm (<https://phycocosm.jgi.doe.gov>), which currently includes over 50 algal genomes across the eukaryotic tree of life and continues to grow. The data is equipped with interactive web based analytical tools for in-depth exploration of algal genomes, comparative genomics, and community annotation.