

Abstracts

Plenary Abstracts

THE FOSSIL RECORD OF ALGAL PRECURSORS TO THE LAND PLANTS

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Historically, the use of fossils, and, especially fossil spores, in the search for evidence of the algal-plant transition has worked backwards in time, starting with the earliest occurrences of fossil plants, which are in the Silurian, and then sampling progressively older non-marine deposits. This work commenced during the later half of the 20th century based on the recovery of trilete spores from the lower Silurian, which have unambiguous affinities with extant embryophytes. A second phase of discovery came with the recognition that permanent spore tetrads and dyads, some of which did not retain unambiguous morphological homologs to extant plants, also belonged to early land plant lineages. These sporomorphs were labeled "cryptospores" in 1984, and, since 1996, their occurrence in the middle Ordovician (Darriwilian) of Saudi Arabia has stood as the placeholder for the origin of the embryophytes, in large part, because their occurrence in isomorphic, tetrahedral tetrads can be construed as homologous with sporogenous development in extant bryophytes.

The more recent recovery of spore-like palynomorphs (cryptospores *s.l.*) from lower Ordovician and Cambrian strata has begun a third phase in tracing land plant origins backwards through time. These forms no longer possess character traits that unambiguously link them to embryophytes. Instead they show novel characters that can be construed as in between the charophytes and the embryophytes. These include multiple wall layers and lamellations, irregular clusterings of enclosed dyad pairs, and irregular topologies of attached spore-like bodies. Starting with the late Cambrian *Agamachaetes* Taylor & Strother 2009, we have begun to explore the idea that the zygotes of aeroterrestrial charophytes underwent multiple rounds of DNA endoreduplication and cytokinesis to produce resistant-walled spores, rather than flagellated zoospores as "meiotic" products. More recently described microfossils of middle Cambrian age also show spore development in which ploidy is not well constrained - an observation that seems to be consistent with reviews of meiosis in extant charophytes. Morphological models of land plant origins, originating in the antithetic hypothesis of Bower, begin with the constraint that spores originated prior to the vegetative sporophyte generation. The "spores before sporophytes" scenario is well supported in studies of sporogenesis in extant bryophytes in which heterochrony in sporopollenin deposition and cytokinesis can accommodate a *Coleochaete*-like ancestor to the land plants. This is supported by studies of Cambrian cryptospore morphology as well, but with the caveat that embryophytic style of meiosis was not attained until the middle Ordovician and thus, the timing of land plant origins as middle Ordovician is, in reality, the origin of embryophytic-style (meiotic) sporogenesis. This opens up the possibility that lower Paleozoic fossils may include morphological remains of subaerial charophytes which were evolving vegetative structures that were later incorporated into the embryophytic sporophyte. Indeed, sheets of spore-like cells from the lower Ordovician Kanosh Formation, which are organized into orthogonal sets of dyads, appear to show vegetative division patterns that mimic extant algae, such as *Prasiola* and *Coleochaete*. Thus it remains a possibility that the evolution of the plant sporophyte included the co-option of developmental division

patterns that were long established in prior algal lineages. The non-marine fossil record of the lower Paleozoic now indicates that character evolution in the algal lineage leading up to the origin of embryophytes was ongoing by middle Cambrian time, plant-like meiotic sporogenesis was achieved by the middle Ordovician, and axial upright sporophytes evolved by the middle Silurian.

Special Symposia

Non-aquatic/ Terrestrial Algae

TRANSITIONS TO A TERRESTRIAL LIFESTYLE IN THE HAWAIIAN ALGAL FLORA

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The tropical environment of the Hawaiian Islands is associated with abundant and diverse terrestrial and subaerial algae. Representatives are known from multiple lineages of algae, including the cyanobacteria, green algae, red algae, diatoms, and xanthophytes, and numerous (putative) endemic species have been described from these members of the Hawaiian algal flora in recent years. Members of two Hawaiian lineages of the green algal Class Ulvophyceae, *Spongiochrysis hawaiiensis* and *Pseudorhizoclonium* spp., represent particularly interesting case studies of the transition to a terrestrial lifestyle in the Archipelago. Described in 2006, *Spongiochrysis hawaiiensis* is a green-to-golden colored unicellular or pseudofilamentous alga that is a prominent member of coastal tree bark biofilm communities on the windward sides of the Hawaiian Islands. Phylogenetic analyses resolve the sister taxon of this lineage as a marine cladophoralean alga. Similarly, two closely related species of the newly described cladophoralean genus *Pseudorhizoclonium* are being described from the Hawaiian Islands (one endemic); again, phylogenetic analyses of representatives collected thus far suggest that the terrestrial lifestyle of these two species may be most recently derived from marine lineages. These examples hint towards evolutionary transitions by algae from marine to terrestrial habitats, possibly without a freshwater transition phase.

SUBAEROPHYTIC CYANOBACTERIA FROM WET ROCKWALLS IN UTAH

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Subaerophytic environments pose unique challenges to inhabiting cyanobacteria, requiring specific genetic, physiological and biochemical adaptations. Despite these many constraints previous studies revealed a high diversity of cyanobacteria in such environments. Yet most of the studies have been conducted in Europe and much remains to be discovered for North America. I will present findings from a study of strains isolated from wet walls of the Grand Staircase-Escalante National Monument in Utah. I characterized a filamentous group of the Synechococcales using the polyphasic approach including 16S rRNA phylogeny, secondary structures of the 16S-23S intergenic spacer gene region, p-distances and morphological descriptions. In addition, phylogenetic characterization was supported by *rpoC1* gene phylogeny. The study facilitated the description of a new family with 7 new genera and 14 species. The advent of modern techniques now utilized in prokaryotic taxonomy encourages revisiting previous floristic studies. Revisits such as our study allowed for a more precise description of the diversity, finer and more robust taxonomic resolution, and detection of cryptic species.

GREEN ALGAE OUT OF THEIR ELEMENT (OR ARE THEY?)

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Green algae play a significant role as producers in aquatic ecosystems. However, an ever-growing body of research shows their diverse presence in terrestrial habitats across the globe from some of the world's driest, hottest environments to even some of the coldest. The class Chlorophyceae, and even more so the class Trebouxiophyceae, are of special interest because of their wealth of terrestrial taxa. Every year, new taxa of terrestrial green algae are described, not only through taxonomic splitting of existing species and genera, but also through discovery of distinct evolutionary lineages. Phylogenetic studies suggest that terrestriality, including desert-dwelling lifestyles, evolved many times in Chlorophyceae and Trebouxiophyceae, and some lineages subsequently diversified on dry land. As more data about biodiversity of terrestrial green algae emerge, so do questions about their fundamental biology, ecology, physiology and evolution in terrestrial environments. For instance, even though green algae use flagellated gametes for sexual reproduction, sex does not seem to be absent from terrestrial, even desert green algae, at least according to genomic data. Further, new genomic and transcriptomic data provide insights into synthesis of protective pigments and other pathways likely associated with terrestriality.

SOIL EUSTIGMATOPHYCEAE

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Eustigmatophytes are frequently reported as components of soil and biotic crust algal communities. Only one or two species of the genera *Eustigmatos* and *Vischeria* are typically reported in these studies. These results give the impression that the soil eustigmatophyte diversity is rather low, with just a few species that are widely distributed in many habitats. However, recent studies have shown that some extreme environments harbor new

species of *Eustigmatos/Vischeria* and suggest that the diversity of soil and crust Eustigmatophyceae may be greater than previously suspected. We will present an overview of current knowledge of the diversity and taxonomy of the Eustigmatophyceae and a summary of the taxa that are known from soil, crust and subaerial habitats. We will also present the results of our work with the *Eustigmatos/Vischeria* group. This work focuses on multi-locus DNA sequence analyses coupled with morphological evaluation to better describe the diversity of these “ubiquitous” organisms and progress toward a more meaningful species-level taxonomy.

ILLUMINATING THE DIVERSITY OF SOIL CYANOBACTERIA FROM NORTH AMERICA

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Terrestrial Cyanobacteria embody crucial ecosystem components in drylands contributing to a large portion of the photosynthetic biomass. Particularly, Cyanobacteria found in biological soil crusts (short biocrusts) are globally recognized for their essential ecological roles and contribution to ecosystem health. A recent review on the diversity of biocrust cyanobacteria reported 26 genera and 51 species from North American biocrusts. This estimate was based on historical data spanning the 1960's to late 90's identifying taxa by morphology only. However, modern technological and taxonomic approaches have brought a proliferation of taxonomic revisions and descriptions of new soil cyanobacterial taxa. Polyphasic approaches including DNA sequence data especially have led to the discovery of many cryptic new taxa. It becomes apparent that cyanobacterial diversity has been underestimated. My talk will present a review of recent advances in the understanding of cyanobacterial diversity from dryland soils. I will compare historical with current data as well as will discuss challenges and knowledge gaps. We live in an era during which it is very exciting to be a cyanobacterial taxonomist aspiring towards a better understanding of alpha level taxonomy. Current and future work on cyanobacterial taxonomy and diversity from North American soils will allow us to take the next steps and ask inspiring ecological and biogeographical questions.

THE FIRST STEPS TOWARDS THE REVISION OF THE POLYPHYLETIC GENUS: *PLEUROCAPSA* (CYANOBACTERIA)

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The Pleurocapsales is an order of coccoid cyanobacteria that is defined by its ability to produce baeocytes. The order currently contains 25 genera in four families. However, it is apparent from the literature that the group is taxonomically confusing. Confusion arises due to inconsistencies

in morphological character states between genera, their rare occurrence and abundance in nature, and the lack of sequence data of all representative genera. A particular problematic taxon is the type genus *Pleurocapsa*. Many strains identified as *Pleurocapsa* that are available in culture collections of the world have been sequenced. Interestingly, in phylogenies these strains are intermixed with strains assigned to *Chroococciopsis*, *Hyella*, *Myxosarcina*, *Stanieria*, *Xenococcus*, and *Dermocarpella*. Others form their own unique clades. Thus, to achieve monophyletic genera in the Pleurocapsales, we have to 1) establish a phylogenetic benchmark clade for *Pleurocapsa sensu stricto*, 2) assign some of the sequenced *Pleurocapsa* taxa to other existing genera, and 3) assign others to new genera. A challenge to revisionary work is that some of the most abundantly sequenced and clearly polyphyletic genera have not had their generitype species sequenced. In our present work, we propose to establish epitypes for the generitype, *P. fuliginosa*, and a long-established species, *P. minor*, based on sequenced strains that closely conform to morphological descriptions for each species. Furthermore, we establish a clade of strains which we designate *Pleurocapsa sensu stricto*, which includes the two species mentioned as well as a new species isolated from desert soils in the southern hemisphere, *P. ercegovicii*. Finally, we make recommendations for designating reference strains and sequences for four additional genera: *Xenococcus sensu stricto*, *Stanieria sensu stricto*, *Chamychalyx sensu stricto*, and *Foliisarcina sensu stricto*.

Bold Award Talks

TO BUILD A CORALLINE: THE EFFECT OF MORPHOLOGY AND MATERIALS ON BENDING IN CONVERGENT ARTICULATED CORALLINES

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Flexible macroalgae bend over and reconfigure in flow, minimizing projected surface area and taking on a streamlined shape to mitigate drag. Coralline algae are mostly rigid due to calcified cell walls; however, most upright corallines have uncalcified joints, or genicula, that separate calcified intergenicula, resulting in overall flexibility. Articulated corallines evolved from crustose ancestors multiple times, resulting in three phylogenetic groups: corallinoids, amphiroids, and metagoniolithoids. Recent work has shown material similarity among the three lineages – genicular tissues are often stronger and more extensible than fleshy algae - but comparative bending performance remains unexplored. Although genicula allow for flexibility, they are also subject to amplification of bending stress, which increases risk of breakage. The morphology of genicula may represent a balance between increasing flexibility and decreasing stress. Furthermore, genicula in the three articulated lineages differ in both cellular construction and development, which may result in different constraints on morphology. By studying the interaction between flexibility and morphological variation in multiple species, we show that there are many different ways to generate flexibility in upright corallines. We also show that genicula at the most risk of stress amplification are typically the strongest, mitigating the trade-off between flexibility and stress reduction. By putting both morphology and materials in a phylogenetic context, we show that there is more than one way to build a coralline.

PLASTIDS FORCE A PARADIGM SHIFT IN RED ALGAL PARASITISM

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Parasitism is a life-strategy that has independently evolved more than 100 times among red algae, with parasitic red algae exclusively infecting other red algae. Parasites that infect close relatives have been termed adelphoparasites, while those more distantly related to their hosts are called allopasites. Current dogma states that red algal parasites begin as adelphoparasites and over time diversify, becoming allopasites. To date, all investigated adelphoparasites maintain their own mitochondrion, but have lost their plastid, instead incorporating a dedifferentiated host plastid when packaging spores. Recently, a reduced plastid genome was sequenced from the allopasite *Choreocolax polysiphoniae*, indicating that not all parasites pass through an adelphoparasite stage. Here, we present sequence data from the organellar genomes of three additional allopasites, *Harveyella mirabilis*, *Leachiella pacifica*, and an undescribed parasite of *Polysiphonia paniculata*. These data, in combination with that from *C. polysiphoniae* provide support for a single evolutionary event, giving rise to a clade of allopasites in the Rhodomelaceae, with parasites adapting to infect different hosts. Like *C. polysiphoniae*, the allopasites in this study retain their native plastid and mitochondrion. Insights on organellar genome evolution in red algae that have transitioned from photosynthesis to a parasitism will be discussed. Furthermore, we propose characteristics that may be a more appropriate for distinguishing types of red algal parasites.

PLASTID GENOMICS AND GENE EXPRESSION ANALYSIS OF *LYMPHA MUCOSA* GEN. ET SP. PROV. EXPOSED TO HIGH AND LOW LIGHT

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Red algal plastids retain features reminiscent of Cyanobacteria, such as unstacked thylakoids and phycobiliproteins that make up the light-harvesting phycobilisome. Wavelengths of visible light captured by red algal phycobilisomes allow them to occupy light-depleted environments. Most red algae are marine, but ~5% occur in freshwater environments that experience dynamic seasonal fluxes in light availability. Proposed hypotheses for their acclimation to these light dynamics include changes in phycobiliprotein ratios and phycobilisome abundance per cell. To explore potential transcriptional regulation for photoacclimation in freshwater red algae, plastid genomics and gene expression assays were performed for *Lympha mucosa* gen. et sp. prov. Specimens were collected either from the river midsection (i.e., sun-adapted) or along edges under the tree canopy (i.e., shade-adapted). Samples were divided equally into two light treatments (i.e., high or low light) for three days. A draft plastome assembly (~183,695 bp) provided sequence data for four genes encoding alpha-subunits of the phycobilisome proteins and photosystems, and one gene for electron transfer. A nuclear-encoded apoprotein (RedCAP), known only in the red lineage, was included for analysis. Relative transcriptional abundance was measured with qRT-PCR and compared among treatments to discern genetic regulation for photoacclimation. These data serve as the first expression dataset for a freshwater red alga.

QUANTITATIVELY ESTABLISHING THAT HIGHLY CONSERVED ITS 16S-23S RRNA DOMAIN SECONDARY STRUCTURES ARE TAXONOMICALLY INFORMATIVE AT THE SPECIES LEVEL

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Species concepts within the cyanobacteria have been subject to much debate. The monophyletic species concept has been proposed as a standard for cyanobacterial systematics, requiring the description of an apomorphy to test phylogenetic hypotheses. With relatively depauperate morphological features from which to choose, coupled with issues of phenotypic plasticity and cryptic diversity, describing and elucidating cyanobacterial species has been problematic. When morphological traits cannot distinguish closely related taxa, differences in ITS secondary structures have been used as surrogates, becoming a standard component for describing novel cyanobacterial taxa and a powerful tool for phylogenetic studies. However, the efficacy of these markers across the entirety of the cyanobacterial lineage have not been assessed quantitatively. This study conducted multivariate statistical analysis of 37 independent measures of ITS secondary structures from newly and previously sequenced cyanobacteria representing all orders. Additionally, characteristic ITS domain Compensatory base changes were determined and statistically evaluated for taxonomic import at the species level. The results demonstrate to what extent and which ITS secondary structure characters are taxonomically informative at both the genus and species level. Comparing ITS secondary structures from a range of cyanobacterial taxa has generated the first comprehensive data set of folded ITS motifs organized phylogenetically. This will provide future researchers a plethora of structural motifs against which new data can be measured, allowing for more efficient identification of novel or phylogenetically challenging taxa.

PHYSIOLOGICAL AND SYSTEMS LEVEL OBSERVATIONS OF *SYNECHOCYSTIS* PCC 6803 GROWING IN A RAPIDLY FLUCTUATING LIGHT ENVIRONMENT

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Microbial autotrophs have evolved under light regimes that bear little resemblance to those of mass cultivation where light is supplied in a highly irregular fashion. We used computational fluid dynamics to model the light environment experienced by cells grown in a bench-top photobioreactor. Incident light fluxes mimicked a natural day. The daily integrated light exposure experienced by a single cell was $184 \mu\text{mol photons m}^{-2}\text{s}^{-1}$, and cells experienced rapid fluctuations (~ 6 s) between 2000 and $<1 \mu\text{mol photons m}^{-2}\text{s}^{-1}$. This was due to vertical mixing and self-shading. The photosynthetic capacity remained high across the day and we could not detect any in situ non-photochemical quenching or photo-damage. An ex situ experiment showed that 30% of electrons derived from PSII were diverted to alternative electron transfer in this

rapidly fluctuating light regime. We monitored the transcriptome and proteome across 24 hours with 12 and 6 time-points, respectively. Collectively, 2256 out of the 3290 genes changed on a diurnal basis, compared to 481 out of 1291 detected proteins. A majority of gene transcripts associated with photosynthesis peaked in the morning (4 - 20 fold higher than the night) and then decreased in abundance during the afternoon. The transcriptome was a poor predictor of the proteome, which was comparatively stable across the day. Changes in the proteome at night coincided with the cessation of cell division, suggesting major changes are associated with the switch to heterotrophic metabolism.

SINGLE-CELL DIATOM POPULATION GENOMICS ACROSS THE WORLD'S LARGEST LAKES, AND ACROSS THE WORLD

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Little is understood about the population genetics of dominant freshwater planktonic diatoms, though such information is vital to understanding and modeling the response of lake communities to environmental change. The Laurentian Great Lakes and Lake Baikal are geographically a world apart; while each harbors unique planktonic diatoms, they also share cosmopolitan species. We obtained population-level data for a species of the genus *Aulacoseira* common to both lakes, as well as data from *Aulacoseira* species unique to each location. Some species were difficult-to-culture, which necessitated creation of a single-cell protocol, adapting molecular tools to get high quality DNA for ddRAD (double digest restriction associated DNA) library preparation, next-generation sequencing, and production of genome-wide SNP datasets. Using comparative population genomics, we characterized the population genetic structure of multiple *Aulacoseira* species, while testing species-specific temporal and geographic hypotheses. Our results show varying levels of population genetic structure among species, even those inhabiting the same lake. Our findings indicate that complexities of environment and life history play, perhaps, a larger role than dispersal ability in defining population structure in freshwater planktonic diatoms.

Phylogeny and Systematics

MORPHOLOGY AND MOLECULAR SYSTEMATICS OF THE DASYPTILEAE, A NEW TRIBE IN THE CALLITHAMNIACEAE (CERAMIALES) CONTAINING *DASYPTILON* AND *PLUMARIOPSIS*

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Dasyptilon pellucidum was originally described from New Zealand as *Ptilota pellucida* by Harvey in 1855. Similarly, *Plumariopsis eatonii* was described from Kerguelen as *Ptilota eatonii* by Dickie in 1876. Both *Dasyptilon* and *Plumariopsis* have consistently been placed in the tribe Ptiloteae ever since. The chief reason for this ascription is the regular alternate-distichous branching from successive segments, in which the apical cell divides obliquely producing a

major branchlet from the high side followed by a minor branchlet on the opposite side. Our morphological studies demonstrate that the fertilized carpogonium transfers the diploid nucleus to the base of the auxiliary cell in *Dasyptilon*, which then divides into a gonimoblast initial and a foot cell that contains a diploid nucleus and the remnant haploid nucleus, as in Callithamniaceae. *Ptilota* is very different in that the fertilized carpogonium cuts off a minute connecting cell containing a highly condensed nucleus that fuses with the auxiliary cell at its anterior end. The diploidized auxiliary cell divides into a gonimoblast initial containing the diploid nucleus and a foot cell containing only the haploid nucleus, which divides several times. Molecular analyses resolve a strongly supported *Dasyptilon* and *Plumariopsis* clade further supporting the proposed tribe, Dasyptileae.

PHYLOGENETIC ANALYSIS OF *DUNALIELLA* (CHLOROPHYTA) EMPHASIZING NEW BENTHIC AND SUPRALITTORAL ISOLATES FROM GREAT SALT LAKE

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Many species of the ubiquitous halophile *Dunaliella* have been described, but many are rarely reported, poorly documented, unavailable in culture collections, and/or misidentified or unidentified ("*Dunaliella* sp."), precluding reconciliation of morphological and phylogenetic entities. Sampling bias toward planktonic isolates misses potentially vast benthic and supralittoral diversity. We report a new phylogeny incorporating multiple new isolates, mostly benthic/supralittoral, from Great Salt Lake (GSL), Utah, USA. These and previous subaerial isolates provide a more comprehensive molecular phylogeny and possibly novel strains for morphological, physiological and biotechnological characterization. Our new GSL isolates reveal considerable molecular (ITS-2) diversity, in some cases lacking close phylogenetic affiliation with any named species. They comprise five widely divergent clades, with low to moderate sequence variation within clades and no clear geographical pattern. However, each of the five clades contains isolates only from either the more saline north arm or the less saline south arm of GSL, suggesting local environmental selection. Moreover, benthic and planktonic isolates from the north arm are phylogenetically distinct. We also document persistent sarcinoid morphology (cells embedded in an expanded glycocalyx) in benthic/subaerial isolates, which may be the norm rather than the exception. We were unable to induce dispersal of cell clusters.

COMBINING PHENOMES AND GENOMES TO FILL ANALYTICAL GAPS USING: DATA MANAGEMENT IN PHYCOLOGY

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Algal species have been observed and described for centuries, but modern molecular methods of identification and analysis have only been available for the past several decades. This temporal mismatch, in combination with the difficulty of working with microscopic organisms, has led to the severe under-representation of microbial eukaryote taxa in gene sequence databases. Modern

reliance on molecular methods excludes the vast majority of taxa from analyses, for example, only 7% of described *Gymnodinium* have a sequence available in GenBank. Much additional work is needed to find and sequence missing species, but funding for this type of taxonomic gap-filling is scarce. What if we could use the non-molecular data we have to fill this need? We present a workflow that successfully placed a *Gymnodinium* species in a phylogenetic tree using morphological and physiological traits. Multiple methods of placement will be discussed and a brief overview of the data infrastructure that enables these types of analyses, including pipelines for publishing, maintaining, and sharing many types of algal data, will be given.

THE ENIGMATIC RED ALGAL GENUS *WALDOIA* W.R. TAYLOR (RHODOMELACEAE; CHONDRIEAE): MOLECULAR SYSTEMATICS ELUCIDATE THE GENUS AND NEW SPECIES

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Waldoia W.R. Taylor (Rhodophyta; Rhodomelaceae; Chondrieae), with generitype *W. antillana* W.R. Taylor, was described from Tobago, Lesser Antilles (Caribbean Sea). Since then it's only been mentioned in checklists or as a new distribution record, and has remained a little known red alga. The phylogenetic position of recent deep-water Gulf of Mexico collections of *W. antillana*, inferred from rbcL-based sequence analysis reveals three distinct clades: *Chondria* C. Agardh, *Waldoia*, and a third that represents a new genus, *Coelochondria*. *Waldoia antillana* is nested within a clade of species that includes some that would have previously been considered to belong in a broadly defined *Chondria*. The genus *Waldoia* is redefined to include species characterized by acute or blunt branch apices, trichoblasts originating from central cells, and a lack of cell wall thickenings. It contains 10 species, including 9 now described on the basis of molecular and morphological analyses. Of the 9 new species, 3 represent first records of the genus in the Western and South Pacific, and 1 is from the Western Atlantic (WA), 1 from Caribbean Sea (CS), 1 in both WA and CS, 2 in Gulf of Mexico (GMx), and 1 from both WA and GMx. Distribution of *W. antillana*, known from the Western Atlantic, Caribbean and Eastern Atlantic is extended to the northwestern and southeastern Gulf of Mexico. Two other species, one from the Philippines and another from Western Australia, are of uncertain generic placement.

ORGANELLAR GENOMES AND INSIGHTS INTO THE ORIGIN OF LINEAGES IN THE HETEROKONT TREE OF LIFE

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Heterokonts comprise an incredibly heterogeneous and diverse group of organisms. Members of this assemblage (e.g., Diatoms) generate approximately 40% of the world's oxygen and comprise one of the most productive and ecologically critical assemblages in marine ecosystems. Moreover, classes in this assemblage represent some of the last lineages in the Eukaryotic tree of life to evolve complex morphologies (e.g., brown algae). However, we are just beginning to understand diversification patterns of its various clades and resolve the backbone of the heterokont tree of life. Numerous organellar genomes now becoming available represent excellent opportunities to use these genomes to gain insights into diversification patterns and time evolution of the clades in the heterokont tree of life. This talk highlights progress made in mining these genomes and using those genes to time origination of clades in the heterokont tree of life. For example, phylogenomic analyses based on 17 plastid genomes selected across the SI, SII and SIII clades and two haptophyte outgroups resulted in an alignment of fifty-two chloroplast protein coding genes. These genes were used to build a concatenated dataset of 13,508 AAs. Phylogenomic and molecular clock analyses enabled dating of the origination of the S1 through PX clades. Similar analyses were accomplished with extracted genes from available mitochondrial genomes providing many exciting insights and dating of clades in the heterokont tree of life.

RESOLVING THE TWO REMAINING OLDEST AVAILABLE NAMES FOR GENICULATE CORALLINES IN THE NORTH PACIFIC, *CORALLINA ARBUSCULA* AND *C. PILULIFERA*
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The four oldest available names for geniculate coralline species in the North Pacific were published in the magnificently illustrated Postels and Ruprecht (1840) *Illustrationes algarum....* *Corallina tuberculosa* and *C. frondescens* have been resolved as *Calliarthron tuberculosum* and *Bossiella frondescens*, respectively. Of the remaining two, *Corallina pilulifera* (type locality: Siberia transbaicalensis [possibly Sea of Ochotsk]) has been applied nearly worldwide from cold temperate to tropical waters in both hemispheres, whereas *C. arbuscula* (type locality: Unalaska Island) was reported only from the type locality and from Bering Island, Russia by Kjellman (1889). We have obtained partial *rbcL* sequences from holotype fragments of *C. pilulifera* housed at LE and from isotype material of *C. arbuscula* housed at S. The sequences were identical, demonstrating that these two species are conspecific. Corresponding sequences from field-collected or herbarium material demonstrated that this species occurs at widely spaced localities in the Northeast Pacific including, Nanaimo, British Columbia, Strait of Georgia, Canada, where we hypothesize that it was introduced on oysters from Japan; Calvert Island, central coast of British Columbia; the Alaskan Peninsula (Kinzarof Lagoon), west through the Aleutian Archipelago. It is more common in the Northwest Pacific where it is confirmed from

the Commander Islands, Russia and Hokkaido, Japan. Reports of this species from all other localities need to be confirmed by DNA sequences.

PHYLOGENETIC DIVERSITY OF SNOW ALGAL COMMUNITIES

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Blooms of snow algae are seasonally abundant and are commonly referred to "watermelon snow". Pink snow is a community of microorganisms that includes algae, bacteria, and fungi, and is a likely carbon source for snow dwelling herbivorous arthropods. The known diversity of these algal communities, based on microscopy, ranges from 2 to 40 species dominated by *Chlamydomonas nivalis*, or *Chloromonas nivalis*, two closely related species of single celled Chlorophyte green algae but also include members of the Stramenopiles and Alveolata. However, microscopic identifications almost always underestimate the full diversity of algal species because there are few features to quantify. Recent molecular surveys of snow algae communities from the Arctic, Antarctic, European Alps, and in the United States have also lead to varied results. Here we describe a phylogenetic investigation of snow algae including isolate in culture and field-derived samples using 18S rDNA amplicon sequencing. Our samples are focused on snow collected in alpine regions of the Pacific Northwest but include samples from California, Montana, and Peru. We discuss local diversity by comparing geographically close samples in the context of global diversity of the group.

JEFF THING

GOMPHONEMOPSIS MEDLIN, POSSIBLE SISTER GROUP TO THE MODEL DIATOM *PHAEODACTYLUM TRICORNUTUM* BOHLIN.

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Comparison of the genome of *Phaeodactylum tricornerutum* Bohlin to that of *Cyclotella nana* Hustedt (as *Thalassiosira pseudonana* Hasle and Heimdal) has yielded significant insight into the molecular ecology of diatoms, and has generated compelling hypotheses about diatom molecular evolution that beg testing. Whereas the phylogenetic position of *C. nana* as the sister to other euryhaline *Cyclotella* species, rather than a true *Thalassiosira*, has been robustly established, our understanding of the evolutionary significance of *Phaeodactylum*'s genome is limited by uncertain placement of *P. tricornerutum* in the phylogeny of raphid diatoms. The morphological simplicity of *P. tricornerutum*, partly due to its incompletely formed valve, suggests several equally plausible hypotheses. Molecular approaches, even the use of the entire chloroplast genome, has not yet provided a more robust result, suggesting that the problem is not simply one that can be solved with more data. However, increased taxon sampling of raphid pennates, particularly of cultured material of the raphid pennate, *Gomphonemopsis* sp. from the Red Sea, has yielded a much more robust placement of *Phaeodactylum* than heretofore possible.

SOME NEW HALYMENIACEAE, KALLYMENIACEAE AND RHODYMENIACEAE FROM THE MESOPHOTIC ZONE COLLECTED ON THE 2016 BERMUDA NEKTON CRUISE OF THE R/V *BASELINE EXPLORER*

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As part the R/V *Baseline Explorer* Bermuda Nekton cruise in the summer of 2016, technical divers and submersibles collected a number of benthic marine algae from 56-178 m on mainland deep nearshore reefs and two offshore seamounts, the Argus and Challenger Banks. COI-5P and *rbcL* assessments of the collections revealed six species in the Halymeniaceae (Halymeniales) and Kallymeniaceae (Gigartinales) that are largely aligned with Southern Hemisphere species, some in genera not previously known north of the equator, adding to an interesting biogeography shared between Bermuda and the Australia/New Zealand region. These include *Galene*, *Austrokallymenia* and *Psaromenia*. A new species of *Nothokallymenia* is the first collected outside of the eastern Atlantic/Mediterranean region. A second species of *Halopeltis* (Rhodymeniaceae, Rhodymeniales) from Bermuda was collected at a depth of 90 m, the same species collected alongside *H. pellucida* by dredging and U.S. Navy lockout divers in 1960, and identified at the time as *Leptofaucha* sp.

Ecology

A BIODIVERSITY ASSESSMENT OF KELP FOREST AND CORALLINE ALGAE HABITATS IN SOUTHWESTERN GREENLAND.

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Non-geniculate coralline algae, both crustose and free-living forms (maerl), are some of the most prominent reef builders in the shallow marine environment. In the Arctic, corallines structure reef habitats in both crustose reef flats (Alaskan Arctic) and in large maerl beds (North Atlantic). Both communities are known to be biodiversity hotspots in this extreme environment, however

many geographic regions remain to be investigated. In Greenland kelp forests and maerl beds were surveyed using video transects, quadrats, and biodiversity grabs. The amount of CaCO₃ within *Clathromorphum compactum* beds was estimated to evaluate how important his habitat is as a blue carbon repository. Results highlight that the dominant species in these two habitats are not mutually exclusive, which is exemplified by kelp swaths and estimated percent cover of coralline algae from transects. One kelp species, *Agarum clathratum*, can be particularly abundant in maerl beds and crustose coralline algae (CCA) is very common on the hard substrate, underneath invertebrates and algae in kelp forests. Furthermore, habitats are alternatively more diverse depending on the scale of measurement (transect and quadrat vs. grab) indicating that kelp forests and maerl beds are important to specific species and life history stages. This is a baseline for region and we hope to continue investigating vulnerable coralline habitats and their ecosystem services in the North Atlantic.

FOSSIL ALGAE PROVIDE EARLY WARNINGS OF IMPACTS FROM EUTROPHICATION, INVASIVE SPECIES AND CLIMATE CHANGE IN THE GREAT LAKES

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Multiple stressors need management options in the Laurentian Great Lakes and diatom-based paleolimnology provides tools to track changing conditions and predict future impairments. We can provide early data reflecting aquatic impacts before they are realized in higher trophic levels, thereby predicting future conditions. Here are two examples of how paleolimnology is being used to inform management decisions for the Great Lakes. (1) The remedial plan for the St. Louis River (Duluth/Superior) requires removal of beneficial use impairments associated with nutrients. Sediment cores were analyzed for physical, chemical and biological remains and long-term changes in fossil algae provided evidence that some areas have improved since nutrient abatement. However, nearshore areas show increasing nutrients and algal abundance, likely due to stressors that are not fully understood (climate change, sediment nutrients). Recommendations for delisting and future studies are forthcoming. (2) A diatom-based paleolimnological study has revealed the first biological effects of climate change on the base of the food webs in all five Great Lakes: an increasing relative abundance of *Cyclotella sensu lato*. Atmospheric warming is the strongest correlate with these changes, and recommendations are made regarding the eventual impacts on food webs throughout the Great Lakes system.

EXPLORING DIATOM ECOLOGY ON THE CORAL REEFS OF THE SAUDI ARABIAN RED SEA COASTLINE IN THE DEVELOPMENT OF A DIATOM-BASED, COST-EFFECTIVE BIOMONITORING TOOL

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Due to their diversity and quick response to changing environmental conditions, diatoms have been successfully utilized to monitor aquatic environments and provide early warning of possible harmful or undesired water quality affects, or as monitoring tools to help provide objective goals for efforts to mitigate water quality issues in a cost-effective fashion. One environment where diatoms have not been used in this fashion, however, are vulnerable coral reef habitats, such as those found along the Saudi Arabian Red Sea coastline. This has largely been due to a general lack of knowledge of tropical benthic diatom taxonomy and ecology. We have created an international collaboration to overcome these obstacles, building a database of benthic marine diatoms and their habitats, in one of the first studies of marine benthic diatom tolerance and distribution in relationship to coastal pollution in a tropical region. In February 2015 and May 2016, we collected benthic diatoms by SCUBA diving from a diversity of coral reef-associated substrates from five locations with different levels of human impact along the Saudi Arabian Red Sea coastline. In this presentation, we will discuss the results from the 2015 sampling, both in terms of diversity and community structure.

SEEING THE FOREST FOR THE TREES: RECENT AND LONG-TERM SHIFTS IN TROPICAL NEARSHORE ALGAL ASSEMBLAGES IDENTIFY AGENTS OF CHANGE

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Long-term quantitative datasets in tropical areas are rare, yet needed for comparisons to present community states to identify temporal patterns and potential agents of change. The southwest region of Oahu has undergone substantial changes in watershed use, and local residents are concerned about the perceived decline of algal species used for consumption and cultural practices. To better understand intertidal dynamics in a tropical setting, 13 sites in the nearshore benthic community along southwest Oahu, Hawaii have been sampled repeatedly since 2006. A survey done in 1991, at three of the thirteen sites, allowed for a comparison between past and more recent assemblages. All surveys describe a lush and diverse algal-covered shore shaped spatially by subtle changes in shore topography and sand. Yet, 1991 shores were dominated by

the opportunistic species *Ulva* sp. and *Hypnea musciformis*, which are known to bloom with nutrient enrichment. Both species were rare (<3%) in more recent assemblages dominated by foliose and turf forms. This shift coincided with the end of sugar cultivation and an upgrade in sewage handling. Assemblages from 2006 were fairly stable until 2014, when algal diebacks coincided with high temperature anomalies. Surveys also captured a local invasion of the green alga *Avrainvillea* sp. that continues to increase at multiple sites. This long-term dataset shows that tropical intertidal assemblages are therefore shaped by local conditions and susceptible to bottom-up forcing, invasive species, and climate events.

INVESTIGATING THE CHEMICAL AND BIOLOGICAL LANDSCAPE OF *NANNOCHLOROPSIS SALINA* CULTURES TO MITIGATE POND CRASHES

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Open ponds are likely to succumb to unpredictable, devastating crashes as a result of algal predation by one or several deleterious species. We are interested in identifying signature chemicals, to aid in predator identification and treatment, and microbiota, to aid in algal protection from predatory species to prevent pond crashes. We investigated the production of algal volatile organic compounds by *Nannochloropsis salina* in the presence of active predation. Using highly-sensitive GCMS assays, we identified various chemicals that will aid in specific predator detection and treatment. Additionally, we have isolated microbial consortia that have all shown specific, but unexplained, protection against rotifer predation. From these consortia, 200 bacterial isolates were selected testing and identification using 16S Sanger sequencing analysis. We have also used MiSeq amplicon sequencing to identify several members of the predator-killing consortia. With these data, we plan to design a microbial consortium within which cultures of *N. salina* can survive predation from multiple predators. Currently, we are analyzing secreted secondary metabolites using HPLC-MS analysis in order to identify the chemical components responsible for killing algal predators. Collectively, our data will contribute to the growing knowledge of chemical and biological components that define pond communities, help algae thrive, and allow survival in the presence of predators.

KELP LOSS AND THE CASCADING EFFECTS ON BIODIVERSITY AND NET ECOSYSTEM PRODUCTION IN THE ALEUTIAN ARCHIPELAGO

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Kelp forests provide habitat and food for numerous other species, moderate physical environment within their boundaries, and regulate carbon and nutrient cycling in nearshore environments. Consequently, their loss can have far-reaching impacts on ecosystem functioning. This may be especially important in the Aleutian Archipelago where the kelp forests have largely disappeared due to overgrazing by herbivorous sea urchins, and expansive urchin barrens have formed. We used diver surveys and benthic respiration chambers to study how this impacted

biodiversity and net ecosystem production (NEP) at five islands in the central and eastern Aleutians. Our results clearly show that the transition from kelp forests to urchin barrens coincided with reduced biodiversity and lower rates of NEP. Specifically, we found that NEP was reduced by 2/3 in the urchin barrens compared to the kelp forests. Further, we used shipboard incubations to examine how losses of individual algal taxa, and increases in invertebrate taxa, contributed to the reduced rates of NEP. Most notably, hydroids, sponges and sea urchins were all more abundant in the urchin barrens and contributed the greatest to ecosystem respiration, with the abundant sea urchins showing exponential increases in respiration with body size. Together, the transition of the kelp forests to urchin barrens resulted in up to a 30% reduction in the ecosystems ability to take up CO₂ from the surrounding seawater, and up to a 99% reduction in the ecosystem's ability to store carbon.

INTER-ANNUAL AND SEASONAL GROWTH PATTERNS OF THE SUBTIDAL KELP *NEOAGARUM FIMBRIATUM*

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Neoagarum fimbriatum is a large subtidal kelp that forms primary habitat along rocky reefs in Howe Sound, British Columbia. Since 2013, *N. fimbriatum* has faced increased grazer pressure from the urchin *Strongylocentrotus droebachiensis* since the loss of top predator sea stars. To understand long-term implications of higher grazer abundance on persistence of the local habitat, we quantified the role of light and temperature in the seasonal and inter-annual growth patterns of *N. fimbriatum* to establish a baseline variation in kelp bed productivity. Fifteen blades of kelp were tagged and a Hobo™ temperature-light logger was installed at three reefs minimally disturbed by urchins in 2015. Growth measurements were made monthly through October. New blades were tagged in January 2016 and monitored through November. Growth rate of *N. fimbriatum* was higher in 2015 with growth peaking at 6.62 cm/wk, compared to 3.39 cm/wk at the same site in 2016. Average light intensity and temperature extremes – daily minimum or maximum temperature – best explain seasonal growth patterns. Reduced growth during spring bloom each year can likely be linked to reduced light availability on the seabed, while increased temperature early in 2016 was an important factor in growth peaking a month earlier. Inter-annual variability in *N. fimbriatum* growth is expected to impact the seasonal persistence of kelp particularly when late season warming and extended plankton blooms reduce growth through to summer.

PHYSIOLOGICAL EFFECTS OF NITRATE, LIGHT, AND INTERTIDAL POSITION ON THE RED SEAWEEDS *MAZZAELLA FLACCIDA* AND *MAZZAELLA SPLENDENS*

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California's intertidal zone is home to three species of *Mazzaella*: *Mazzaella flaccida*, *Mazzaella splendens*, and *Mazzaella linearis*, which reside in different intertidal zones. The yellow-green *M. flaccida* is found in the high and mid-intertidal while the brown-purple *M. splendens* and *M. linearis* are found in the mid and low-intertidal. These differences in intertidal position and blade color, in addition to minute differences in morphology, are typically used to differentiate these species in the field. A reciprocal transplant study by M. Foster (1982), however, found that not

only can *M. flaccida*, and *M. splendens* reside in each other's zone, but *M. splendens* can also alter its coloration to the yellow-green of *M. flaccida*. Furthermore, morphological differences between the two species were not always consistent. Thus, he hypothesized that these two species may be conspecifics; presently, genetic evidence supports the separation of these species. Little progress has been made towards understanding the cause, mechanism, and impact on physiology this color change has had. This study serves to improve our knowledge in these areas through both field transplant and laboratory experiments. Here, photosynthetic pigment concentration, growth rate, and survival were measured as a function of intertidal position, nitrate concentration, and light availability. Preliminary data indicate significant differences in pigment concentration and survival between sites, species, and treatments.

BRILLIANT AND INTENSE: WHAT DO WE KNOW ABOUT STRUCTURAL COLOUR IN MARINE ALGAE

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Structural colour is well-documented in nature where its function may include a method of visual communication, mate attraction or camouflage. It is widespread in the marine environment and the appearance of iridescent blue tips in the gametophyte phase of the red alga *Chondrus crispus*, for example, will be a familiar sight in rock pools in the intertidal in the North Atlantic.

Structural colour is reported for red and brown algae, yet the phenomenon is largely unexplored. In the red algae two structural mechanisms are responsible for structural colour, either iridescent bodies or multi-layered cuticles, whereas in the brown algae, only iridescent bodies have been observed. The functional purpose of structural colour in these algae is unexplored experimentally, but studies from leaves of flowering plants have speculated that such colour may function as photoprotection or as predator deterrents. Here, we will explain how structural colour is produced in the algae and discuss possible evolutionary relationships with terrestrial plants. By reviewing their distribution and ecology we will also explore the functional relevance in the brown algae where structural colour is confined to species of the Fucales and Dictyotales. We will also explore the hypothesis that structural colour in algae is predominantly for a non-communicative purpose, most likely protecting the seaweeds from radiation damage, e.g. harmful UV light and discuss this in relation to climate change.

HIGH RESOLUTION TIME-SERIES PROFILING REVEALS SEASONAL AND GEOGRAPHICAL TRANSITIONS IN PHOTOSYNTHETIC STRAMENOPILE COMMUNITY STRUCTURE

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Eukaryotic phytoplankton are a suite of highly diverse organisms that play key roles in regulating productivity and material export in ocean ecosystems. Knowledge of their diversity, distribution and ecology is limited by data types and analyses. Here, we use an analytical

strategy that maximizes phylogenetic accuracy to study plastid-encoded 16S rRNA gene diversity in long-term oceanographic time-series data in the northwestern Sargasso Sea and the northeastern Pacific Ocean. Photosynthetic stramenopiles were abundant in amplicon sequencing data and exhibited pronounced patterns across a trophic gradient in the surface Pacific Ocean, ranging from diatoms in nutrient-rich coastal waters to pelagophytes in a mesotrophic region, and dictyochophytes in oligotrophic waters. We observed similar shifts in stramenopile community composition across seasonal transitions in the Sargasso Sea, suggesting that offshore upwelling influences and seasonality in the open ocean may shape eukaryotic phytoplankton community structure by similar mechanisms. Unexpectedly, dictyochophytes were the most important grouped plastid bearing taxa based on relative amplicon abundances in the open ocean surface and during stratified periods, raising questions about their trophic strategy and contributions to carbon export from stratified ocean systems. In contrast, pelagophytes had higher relative abundances than other stramenopiles in the subsurface chlorophyll maximum. These studies illustrate variations in fine scale aspects of community composition that are robust across different marine ecosystems.

ECOPHYSIOLOGY OF *SARGASSUM HORNERI* IN THE SOUTHERN CALIFORNIA BIGHT
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Non-native species introductions negatively impact native species assemblages, food web dynamics, and ecosystem functioning. Detecting and controlling invasions by marine macroalgae is complicated by dispersal during microscopic life history stages. However, understanding how each stage responds to abiotic conditions can help predict invasion success in recipient ecosystems. *Sargassum horneri* is an invasive rockweed spreading through nearshore habitats in the Southern California Bight. The objective of this study was to assess the invasibility of *S. horneri* by its physiological responses during embryonic and juvenile life stages to environmental conditions representative of both invaded and uninvaded ecosystems within this region. We manipulated seawater temperature (10, 15, 20, and 25 C), PAR (50 vs. 500 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$), and nutrient availability (ambient vs. F/2-enriched seawater) in fully factorial three-week-long laboratory culture trials. We measured growth weekly and photosynthetic efficiency after three weeks using photosynthesis versus irradiance curves. Separate trials conducted using individuals from Santa Catalina Island and San Diego compared responses among populations from different abiotic regimes. Results suggest that seawater temperature is the best single predictor of physiological performance in juvenile *S. horneri*; however, other factors interact to affect growth and photosynthesis. We conclude that bottom-up controls influence the spread of this species, and can be used by managers to predict high-risk habitats and prevent further invasion.

PHYTOPLANKTON STUDY IN THE LAKE TANGANYIKA LITTORAL ZONE
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This survey was conducted in littoral zone on the north-eastern coast of Lake Tanganyika on the Burundi side. The study objectives were to show the phytoplankton spatial distribution and to assess human activity impact in water quality. Sampling was done from July 1993 to July 1994

at 3 sites around the Ntakangwa River mouth, Mugere River mouth and one bay without river mouth out of Bujumbura. The Ntakangwa River crosses Bujumbura, while the Mugere River takes much sediments and the bay is as pristine. Results showed spatial variation in phytoplankton densities. At Ntakangwa River mouth, more than 53,000 cells/ml were observed. At 100m from mouth: 2,000 cells/ml at depth of 5 to 10m, while at 300m: 1,000 cells/ml at depth of 20m. *Chlorella* sp. was abundant in above samples. This led us to conclude that the Ntakangwa River flows under the lake. Beyond 100m from shore no remarkable difference in density between samples of 3 sites; so, no eutrophication in lake. Rivers effects are too low. Human activity impact is powerless. Density peak at 50m from Ntakangwa River mouth due to nutrients and cells carried were quickly diluted. Domestic and industrial waste cause eutrophication in this river. Upper water layers of lake had high cell densities. At more than 30m depth, mostly beyond 60m densities decline for missing light. At 60m depth in Mugere site, cells are died; the bottom is near. Cell density in Mugere mouth is less than in bay, because sediments loading don't favour light. Phytoplankton spatial distribution and composition change according to depth and distance from shore. Diatoms, Chlorophyta and Cyanobacteria are dominant.

Evolution and Biodiversity

PHYLOGENETIC-BASED CHARACTERIZATION OF MICROBIAL EUKARYOTE DIVERSITY AND COMMUNITY STRUCTURE WITHIN A DYNAMIC ESTUARY IN THE SALISH SEA

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Coastal estuaries are highly dynamic environments. Due to a multitude of environmental variables, microbial communities in these systems are generally complex and difficult to predict. A majority of studies in estuaries have focused on relating environmental factors to changes in community response through indirect measurements (e.g., biomass, chlorophyll). Though these studies are important and necessary, they treat community members as a “black box” by focusing on broad environmental inputs and biological outputs of the system. However, community composition and diversity dictates how cohabitants respond to both environmental stimuli and each other, which in turn affects their community-level response. We used metabarcoding of the 18S SSU RNA gene to phylogenetically characterize the diversity of microbial eukaryotes in a Northeastern Pacific Ocean coastal estuary, and describe spatial and temporal patterns in community structure. Sampling was carried out daily to biweekly for 4 years during the 2013-16 summer seasons. While diatoms and dinoflagellates were the most abundant taxa, there was a diverse assemblage of rarer taxa that showed spatial and temporal patterns. We also found that our assessment of stability in this system varied based on timescale. Our results highlight the importance of repeated sampling to characterize microeukaryotes in dynamic environments, and the importance of including small and/or rare taxa in future ecological studies of these systems.

CYANOPRO - AN INTERACTIVE DATABASE FOR CYANOBACTERIAL DIVERSITY

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Although a number of existing databases include entries of cyanobacteria, such as GBIF, EOL, etc., only few contain images or allow for direct data uploading on herbarium specimens or live reference culture material. CYANopro is designed to accept all of this information. It also offers entry functions of comprehensive information on habitat, specimen collection, and genetic data. With the addition of these functions tracking of essential data from the moment of specimen collection from natural populations to the time of genetic or genomic characterization is now possible. The structure of CYANopro provides five different primary source options: data import for herbarium specimens, cultured material, field observations from natural populations, records from published literature, as well as records from another source (e.g. from a different database). It is also possible to upload other types of data such as images of habitat, photographs depicting macrocolony and microcolony morphology, morphological descriptions, taxonomic notes and DNA sequence data. The database is searchable by species, genus, locality, etc. Lists of species, photos, ecological information and other data reports can at any point be downloaded and used according to the terms of creative commons license. CYANopro currently contains data from two herbaria and two culture collections representing more than 3500 records. All data entries from CYANopro are shared with GBIF, EOL, Algaebase. Overall, CYANopro is a modern, easy to use tool for integrative biodiversity data management of cyanobacteria research.

THE CURIOUS CASE OF COMPLEX LIFE CYCLES: THE UNTOLD STORY OF MATING SYSTEM VARIATION AND RANGE EXPANSIONS

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Baker's Law predicts uniparental reproduction will facilitate colonization success in novel habitats. While evidence supports this prediction among colonizing plants and animals, few studies have investigated shifts in reproductive mode in haplo-diplontic species, in which there are both prolonged haploid and diploid stages. In these life cycles, asexual reproduction can yield the dominance of either haploid or diploid individuals. Using *Mastocarpus* sp. and *Gracilaria vermiculophylla* as examples, I will highlight patterns of mating system variation and range expansions across spatial scales. Asexuality results in the loss of the crustose life history stage in *Mastocarpus* sp. The maintenance of these patterns of geographic parthenogenesis do not appear to be driven by the same mechanisms that underlie these patterns in higher plants or animals. Rather, the loss of a free-living stage likely enables range expansions along tidal and latitudinal gradients. In the case of *G. vermiculophylla*, the ecological shift from attached to unattached thalli, ostensibly necessitated by the invasion of soft-sediment habitats, correlated with shifts from sexual to asexual reproduction during the Northern Hemisphere invasion. A labile mating system likely facilitates colonization success and subsequent range expansion, but the long-term eco-evolutionary impacts will depend on which ploidy stage is lost and the degree to which asexual reproduction is canalized.

THE RISE AND FALL OF CORALLINE ALGAE: EVOLUTIONARY TRANSITIONS BETWEEN CRUSTOSE AND ARTICULATED MORPHOLOGIES

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Coralline red algae (Corallinales, Sporolithales, Hapalidiales) produce calcified thalli in marine ecosystems worldwide. “Crustose” corallines grow mainly prostrate whereas “articulated” corallines produce flexible, upright thalli with alternating calcified and uncalcified segments. Fossil evidence suggests that articulated corallines evolved from crustose corallines millions of years ago. Moreover, developmental and molecular data show that articulated corallines evolved from crusts at least three separate times in three distinct subfamilies. Repeated examples of convergent evolution suggest a shared response to similar selective pressures – but the identity of those selective pressures is unclear. Several articulated species develop reduced fronds consisting of only a few segments, representing an evolutionary reduction in stature and suggesting that fronds need not be large to be successful. Moreover, recent molecular work has demonstrated that the crustose genus *Crusticorallina*, which includes four species, evolved from articulated ancestors, representing a complete evolutionary reversal and a return to the crustose state. Additionally, we show the genus *Bossiella* contains both articulated and crustose species. That articulated fronds are repeatedly gained and lost throughout coralline evolution complicates our ability to maintain adaptive arguments, and the existence of both morphologies in the same genus suggests that transitions can occur rapidly. I will discuss the roles of selection and mutation in this widening perspective on coralline evolution.

Harmful Algal Blooms

THE ROLE OF NUTRIENTS IN *PSEUDO-NITZSCHIA* BLOOMS ON THE OREGON COAST: A NONPARAMETRIC APPROACH

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The idea that domoic acid (DA) production is associated with nutrient depletion or metabolic instability at the end of phytoplankton blooms may explain the intermittent production of DA by some species of *Pseudo-nitzschia* (P-N), but time series of bloom progression, toxicity, and nutrient availability are not widely available. We use a novel non-parametric approach to address this question using data from MOCHA (Monitoring Oregon Coastal Harmful Algal Blooms), a seven-year monitoring survey off the Oregon Coast. All Stations where sampling included simultaneous measurement of P-N abundance, particulate and dissolved DA, and nutrients were included. These cover 27 different east-west transects and 138 different physical locations from Washington to Northern California. Most are from 44-46° on the central Oregon coast; those used for correlation analyses and time series analyses are from surface tows (N=

570). Correlation analysis show a strong relation between P-N abundance, binned by abundance levels, and DA concentration, particularly with a “wide” sub group presumed to be *P. australis*. N:P ratios for upwelled source water are relatively constant over the entire sampling period and support an assumption that primary production is nitrogen-limited during upwelling in this region. Sequential analysis of several bloom events showed that DA peak concentrations followed depletion of macronutrients, consistent with the idea that DA production is somehow associated with metabolic imbalance at the end of a bloom terminated by macronutrient starvation.

DETERMINING CYANOTOXIN (MICROCYSTIN) EXPOSURE IN STRANDED BOTTLENOSE DOLPHINS (*TURSIOPS TRUNCATUS*) IN NORTHEAST FLORIDA

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Water sampling for cyanotoxins in the St. Johns River (SJR) and surrounding freshwater tributaries has confirmed the presence of multiple cyanotoxins year-round. The most prevalent are microcystins/nodularins (MCs/NODs) that are hepatotoxins. The lower basin of the SJR provides year-round habitat for a resident bottlenose dolphin population. Analyses of dolphin mortality have shown deaths occurring upstream from critical SJR habitats suggesting possible exposure to toxin producing cyanobacterial blooms. Dorsal fin photos from stranded dolphins during 2013-2017 were compared to Northeast Florida Dolphin Research Consortium catalogs and categorized as resident (N=17) or coastal (N=10) dolphins. MCs/NODs exposure and concentration (bound and unbound) present in liver tissues was determined via the MMPB (2-methyl-3-methoxy-4-phenylbutyric acid) technique. This process has been modified for quantitative determination of total MCs/NODs in biological matrices. Preliminary results indicate that both populations are exposed to MCs/NODs. To date, 24 samples have been analyzed with three residents and three coastal animals testing positive for MCs/NODs. Five individuals tested between the method detection limit (1.3ng/g) and the method quantification limit (MQL;3.9ng/g), and one tested above the MQL (14.3±5.6ng/g). Moreover, five positive animals had incidence of other ailments, including dermal lesions or dermal fungal mats, morbillivirus, or angiomas. Additional ELISA testing will be conducted for samples that tested positively for MMPB for confirmatory analyses.

A DNA-BASED APPROACH FOR STREAM ALGAL BIOASSESSMENT: A CASE STUDY IN SOUTHERN CALIFORNIA

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Global increases in harmful algal blooms (HABs) have been attributed to various anthropogenic factors including climate change, nutrient loading, and water residence time. Perennial monitoring campaigns help track the health and composition of California’s stream algal communities and identify the environmental drivers of harmful bloom events. In this presentation, we will highlight a six-month (Feb-Aug) monitoring program in the Santa

Margarita River watershed (San Diego county) that examined algal community dynamics using high-throughput DNA sequencing coupled to nutrient and geochemical monitoring. We compared the performance of DNA and morphology-based approaches to algae taxonomy, with a special focus on known toxin-producing algae and their bloom timing. We found an improved resolution of algal species diversity using DNA barcode sequencing, including the identification of cyanotoxin-producing species within the *Anabaena*, *Microcystis* and *Dolichospermum* genera that were overlooked with a morphology-based approach. We also identified critical gaps in global DNA reference databases for common California taxa. Additionally, our study helped link nutrient concentrations and ambient conditions to periphyton species diversity, revealing the complex bloom timing of closely-related taxa. The results of this study provide a comprehensive view of algal community composition across spatial and temporal scales and further emphasize the importance of rapid, scalable routine monitoring approaches to improve our understanding of nutrient cycling and algal bloom dynamics.

USING HYPERSPECTRAL IMAGING FOR LOW-LEVEL DETECTION OF HARMFUL ALGAE AND PREDICTING TOXIN STATUS

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The purpose of this research is to assist US Army Corps of Engineer resource managers in controlling cyanobacteria blooms in the early stages. To fulfill this need we are developing a hyperspectral imaging technique to improve detection and identification of harmful algae coupled with better prediction of toxic events. Initially we obtained hyperspectral signatures for various cyanobacteria and algae. We then identified stressors associated with/predictive of toxin status in *Microcystis aeruginosa* and *Anabaena* sp. To induce stress we tested several different N:P ratios (100≤2.5:1) and concentrations (N: 0.176-17.6mM; P: 1.75-583μM) in batch culture. Preliminary experiments revealed a change in spectral signature and toxin production that may be dependent on the N₂ fixation status. For example, when compared to high N:P ratios, *Anabaena* cultures with low N:P ratios (2.5-5:1) produced more microcystin but displayed no change in growth. In contrast, high N:P ratios (≥10:1) supported more growth in *Microcystis* but had no impact on toxin status. To validate these results we are currently performing laboratory mesocosms while investigating other stressors (metals, UV and temp). This information is being used to compile a database for the rapid identification of algae in field samples. With this system we will also acquire the relative abundance of each genus/species, as brightness is related to absorbance. Therefore, hyperspectral imaging has the potential to surpass current algal monitoring technology in that it provides greater sensitivity in conjunction with identification information in a rapid, mesoscale platform.

INVESTIGATING ABIOTIC DRIVERS FOR VERTICAL AND TEMPORAL VARIABILITY OF CYANOBACTERIA BLOOMS USING A LONG TERM IN-SITU MONITORING STATION

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Harmful Algal Blooms (HAB) are a ubiquitous ecological and public health hazard. HAB are made up of potentially toxic freshwater microorganisms called cyanobacteria. The occurrences of toxic HAB are unpredictable and highly spatially and temporary variable in freshwater ecosystems. To study the abiotic drivers for toxic HAB, a floating research station has been deployed in a eutrophic lake from June-October 2016. This research station provides full depth water quality (hourly) and meteorological monitoring (5 minutes). Water quality monitoring is performed by an autonomously traversed water quality sonde that provides chemical, physical and biological measurements; including phycocyanin, a photosynthetic pigment distinct to cyanobacteria. The research station data collection is coupled with discrete samples, including: phytoplankton enumeration and composition, toxins, and nutrients. This investigation illuminates how physical lake conditions, i.e. mixing conditions, temperature stratification stability, light, wind speed and nutrients transport, mediate temporal and vertical variability in HAB formation and cyanobacteria composition. Seasonal and lake scale analysis shows that temperature stratification, Schmidt number, drives the stratification of both bulk cyanobacteria biomass and individual cyanobacteria taxa. These results will help identify the abiotic environmental processes that drive HAB formation, accumulation and composition, which can direct timely toxic HAB prediction and prevention efforts.

HOW WILL GLOBAL CLIMATE CHANGE WITH ELEVATED CO₂ AFFECT THE PHYSIOLOGY OF TOXIC MARINE AND FRESHWATER CYANOBACTERIA?

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Global climate change and anthropogenic nutrient input are responsible for the increasing frequency of cyanobacterial bloom occurrence. Cyanobacteria produce over 48 classes of bioactive secondary metabolites, which threaten the health of human and animals. Co-occurrence of cyanotoxin was well-documented in natural bloom samples; however, there is no laboratory study on the combination of elevated CO₂ and reduced pH levels affecting cyanotoxin co-production. This study investigated the effects of elevated CO₂ and reduced pH levels on two cyanobacterial strains isolated from TX—marine *Synechocystis* sp. and freshwater *Microcystis* sp. Cyanobacterial strains were semi-continuous cultured in media at ambient concentrations. The presences of cyanotoxins were qualified and quantified using high performance liquid chromatography (HPLC)/triple-quadruple mass spectrometry (MS). Pigments were determined using HPLC/diode array detector and fatty acid composition was determined using gas chromatography (GC)/tri-axis MS to evaluate the physiological responses of cyanobacteria to the changes of CO₂ and pH levels.

Genomics and Transcriptomics

CHARACTERIZATION OF THE GENE REGULATORY MECHANISMS INVOLVING SMALL NON-CODING RNAS IN RED ALGAE

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Small RNAs (sRNA) are short (18-26 nt long) RNA molecules that guide regulatory processes at the DNA or RNA level. Although endogenous sRNAs and proteins involved in sRNA biogenesis have been reported for species of green, brown and red algae, regulatory mechanisms involving sRNAs in algae remain mostly uncharacterized. The goal of our research is to assess the sRNA repertoire in red algae, especially focusing on miRNAs, and investigate whether these sRNA participate in the relationship between eukaryotic parasites and their hosts. Small RNA libraries from 2 different tissues ('clean' *Gracilaria andersonii* and isolated *Gracilariophila oryzoides*) were prepared using TriLink Small RNA prep kit and sequenced on a HiSeq 4000. Using the publicly available eukaryotic Argonaute (AGO) and Dicer-Like (DCL) protein sequences (essential part of the sRNA machinery) we have identified both AGO and DCL in the free-living *G. andersonii* genome and the parasitic *G. oryzoides* in different isoforms, suggesting that a complex regulation by sRNAs is likely in the host and in its parasite. Preliminary analysis of the sRNA sequenced data indicates that the size distributions of sRNAs are consistent with that described in the general literature for eukaryotes. Further analysis of comprehensive annotation and quantification of genes producing regulatory sRNAs are currently being conducted. The results of this work open a new and wide range of molecular and functional studies to the understanding of post-transcriptional regulation in algae and in eukaryotic parasitic infection.

UNDER ATTACK OR A COMPLETE LACK? HOST RESPONSE TO RED ALGAL PARASITE INFECTION

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Parasites must exploit their hosts in order to complete their life cycle. Many notable parasites have been studied due in part to their harmful effects on agriculture and humans. Many of these parasites are millions of years old and are now distantly related from their hosts. Conversely, red algal parasites are closely related to their host, often infecting a sister species. This relationship enables the investigation of how a closely related parasite may impact its host throughout infection and determine if their common ancestry allows the parasite to avoid detection by the host. Earlier research used microscopy to identify the morphological characteristics of host response to infection—plastid dedifferentiation, rapid cell division, lipid deposition, and a decrease in stored floridean starch. The advancement of transcriptomics methodologies now enables the exploration of the influence of the parasite on host genome expression. Parasite spores from *Choreocolax polysiphoniae* were collected from Beavertail State Park, Jamestown, Rhode Island and used to infect lab cultured host material *Vertebrata lanosa*. Using a modified single cell transcriptomics protocol, amplified mRNA was sequenced from a series of parasite infection stages. Infected material was also collected simultaneously for microscopy to tie together morphological parasite development and host genetic expression

SCHIZOCLADIA ISCHIENSIS'S ORGANELLAR GENOMES: INSIGHTS INTO THE EVOLUTIONARY TRANSITION TO COMPLEXITY OF BROWN ALGAE

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Brown algae (Phaeophyceae) are one of the most productive and ecologically important lineages in marine ecosystems and represent one of the last lineages in the Eukaryotic tree of life to shift to multicellularity. Members of these lineages (including other heterokonts) generate approximately half the world's oxygen. However, we are just beginning to understand their organellar genomes and architectural changes that accompany their transition to complexity. This is part of a larger project initiated to understand the organellar genomes of these important primary producers and the genomic changes accompanying their shift to multicellularity. This presentation will examine the plastid and mitochondrial genomes of *Schizocladia* and discuss comparative insights gained from the project. To assure the isolation of pure genomic DNA cultures were grown with GeO₂ to inhibit diatom growth before DNA extraction. Data from a separate HiSeq and Miseq runs were collected and assembled. We report here on the size, structure, and gene content of this heterokont lineage and compare it to members of the brown algae *Schizocladia* is more brown algal like in genome size, gene content and other genome attributes. Lastly, we summarize insights gained into the evolutionary patterns in organellar genomes from heterokonts to brown algae.

PHYLOGENOMICS OF THE RED ALGAL CLADE GRACILARIACEAE (RHODOPHYTA)
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The marine benthic algal family Gracilariaceae (Rhodophyta) includes species distributed mainly in tropical regions, with decreasing poleward diversity. Some members of the family have significant economic and pharmaceutical importance, making them among the most important

agarophytes in the world. Increasing interest in the taxonomy and phylogeny of the group has enhanced our understanding of their evolution; however, considerable parts of their phylogeny demand greater attention. In particular, intergeneric relationships have not been fully resolved, and it remains uncertain if well-established genera are monophyletic. Along these lines, numerous red algae have genome sizes that are amenable to large-scale phylogenomic analyses, but such approaches have seldom been applied. In particular, there are few Rhodophyta genomes available, most of them cytoplasmatic. Here, we sequenced nuclear and organellar genomes from 38 Gracilariaceae species representing broad diversity in the family. Our multicoalescent nuclear species tree analysis inferred a strongly supported phylogeny. These results corroborate the monophyly of *Gracilaria*, and *Gracilariopsis*. The genus *Hydropuntia* was confirmed as polyphyletic. They additionally support a robust placement for the parasite *Gracilariophila oryzoides* Setchell & H.L. Wilson as a close relative of its host, *Gracilariopsis andersonii* (Grunow) E.Y. Dawson. Finally, our concatenated analyses of the plastid and mitochondrial genomes indicate a history of genealogical discordance, suggesting that we may need to reassess the phylogeny of some groups given our longstanding reliance on organellar genes for resolving Rhodophyta relationships.

USE OF *IN VIVO* METABOLIC LABELING TO EXAMINE *DE NOVO* TRANSCRIPTION IN *THALASSIOSIRA PSEUDONANA*

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Cellular RNA levels represent the integration of RNA synthesis, processing, and degradation. *In vivo* metabolic labeling can be used to measure both global and gene-specific RNA transcription and degradation rates. The technique uses sulfur-substituted molecules that are rapidly taken up by cells and incorporated into RNA. The *Thalassiosira pseudonana* genome encodes both uracil phosphoribosyltransferase (UPRT) and uridine kinase (UK), which allow for the incorporation of 4-thiouracil (4tU) and 4-thiouridine (4sU), respectively. Both 4tU and 4sU were detected in *T. pseudonana* RNA after a 5 min incubation. To examine changes in transcription in response to nitrogen availability, *T. pseudonana* cells grown in the presence and absence of nitrate were exposed to a 5 min pulse of 4tU (0.2 mM) and total RNA was extracted from cells. Newly synthesized (labeled) mRNA was separated from pre-existing (unlabeled) pools using thiol-specific biotinylation and fractionation. Fractionated mRNA was used for first strand synthesis and qRT-PCR to provide estimates of *de novo* transcription for genes involved in nitrogen assimilation. This also provided estimates of the accumulation of transcripts with the progression of nitrogen starvation. Transcriptomic analyses identified that 6.6% of the predicted protein coding genes in *T. pseudonana* were differentially expressed in N-deplete and –replete cells. Thus, *in vivo* metabolic labeling can thus be used to examine changes in gene transcription in response to nutrient availability.

Population Biology and Biogeography

BIOGEOGRAPHIC TRENDS IN FRESHWATER RED ALGAE

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Molecular systematics research has revealed new taxonomic insights for freshwater red algae. These studies examined specimens from various parts of the world and so may also inform our understanding of the biogeography of genera and species. The genera can be categorized into two groups: (1) cosmopolitan, taxa that are widespread within and among more than one continent or (2) restricted, taxa that have only been reported from a single continent and are typically geographically restricted on that continent. Examining genera for which there are data, it appears that approx. two-thirds are cosmopolitan and one-third are restricted. North America, South America, Australia, Europe and Africa each have at least one genus restricted to that continent such that no one continent has a large number of endemic genera. Most of the cosmopolitan genera are present on at least three continents. Within genera, the species may have divergent biogeographic patterns with some being cosmopolitan and restricted as defined above. In addition, there are disjunct species being common on one continent, but restricted on another or on both. For genera with more than two species, approx. one-third has a single cosmopolitan species with all other species being restricted or disjunct. The other two-thirds have species with similar geographic distributions. This current analysis provides new insights, but also highlights under-sampled taxa/regions that could be the basis for future studies.

DECREASES OF THE ABUNDANCE OF BULL KELP, *NEREOCYSTIS LUETKEANA* (MERTENS) POSTELS *ET* RUPRECHT IN CENTRAL AND SOUTH PUGET SOUND, WASHINGTON

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This study assesses changes in floating kelp canopy area through comparing historical data to recent surveys. It updates a 1990 synthesis by Thom and Hallum that found the length of shoreline with kelp forests increased substantially between 1912 and 1978, with the largest relative increases in South and Central Puget Sound. We extend the temporal comparison to 2013-2016 using boat-based canopy mapping, airphoto-based surveys, and existing studies by other scientists. We observe extensive losses in the length of shoreline with floating kelp between 1978 and 2016 in the areas we surveyed in South Puget Sound and around Bainbridge Island, with the exception of a limited number of beds which persisted throughout the time period. In Elliott Bay, in contrast, bull kelp occurs along an equal or greater length of shoreline compared to historical data sets. Overall, despite uncertainty associated with diverse data sets, our updated temporal comparison suggests strongly that the floating kelp *Nereocystis luetkeana* has decreased in South and Central Puget Sound in recent decades. This finding is supported by small area surveys and observations. The causes of the observed changes are not understood. Some candidates include competition with native or non-native vegetation, water quality degradation, substrate alteration, changes in grazer populations, and physical disturbance.

CONTRASTING PATTERNS OF GENETIC STRUCTURE AND PHYLOGEOGRAPHY IN TWO UPPER INTERTIDAL SPECIES OF *GELIDIOPHYCUS* IN NORTHWESTERN PACIFIC

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Two morphologically similar species in the Asian red algal genus *Gelidiophycus*, *G. divaricatus* and *G. freshwateri*, live in the upper intertidal zone, an extremely challenging environment that has been shaped by sea level fluctuations during the Pleistocene and by contemporary hydrological conditions. We investigated speciation in this genus using molecular inquiries into their genetic and spatial history. Three independent markers (cox1, rbcL and ITS2) from 402 specimens throughout their ranges confirmed that *G. divaricatus* is a southern species, with strong geographical structure. Analyses revealed evidence for population equilibrium over a long evolutionary timeline, followed by a short bottleneck and recent rapid expansion. By contrast, *G. freshwateri* is a northern species, occurring north of the summer 28°C isotherm, with a shallow population structure resulting from early rapid expansion and subsequent equilibrium. A few specimens from Jeju Island, Korea, which lies in the transition zone between the species, revealed discordant topologies between organelle and nuclear trees, suggesting genetic introgression via natural hybridization. Both sea surface temperature and sea level change were important factors driving the contrasting patterns of phylogeography in *G. divaricatus* and *G. freshwateri*.

THE MULTIPLICATIVE EFFECTS OF IRON, LIGHT AND TEMPERATURE ON THE REGULATION OF RUBISCO AND PHOTOSYNTHETIC PROTEINS IN SOUTHERN OCEAN PHYTOPLANKTON.

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Phytoplankton in the Southern Ocean have been shown to be iron and light limited in an otherwise high nutrient albeit cold environment. Climate model projections indicate that light, temperature, iron and pH/CO₂ in the Southern Ocean are likely to change simultaneously in the future due to the changing climate and this project seeks to understand the combined response of these variables on key phytoplankton species. Temperature, light and iron interactions were explored in the haptophyte *Phaeocystis antarctica* and the two diatom species *Proboscia inermis* and *Chaetoceros flexuosus*. Surprisingly, despite their large size and higher nutrient requirements, photophysiological measurements of the diatom species reveal faster electron transport rates from PSII to PSI compared to *Phaeocystis antarctica*. Rubisco content and kinetic measurements were undertaken for the two diatom species which could be used to argue against the heavy investment of resources into a CCM that may be observed in other regions. Unfortunately no Rubisco measurements were successful for *Phaeocystis antarctica* and more work is necessary to understand to resolve Rubisco kinetics in this species.

COMPARISON OF HAWAIIAN COASTAL AND INLAND SUBAERIAL PHOTOTROPHIC COMMUNITIES

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Visible subaerial communities dominated by free-living green algae (Chlorophyta) are found both in the interior, mountainous rainforest regions of Oahu and along coastal areas that receive high amounts wind and ocean spray. Coastal biofilms tend to be dominated either by *Spongiochrysis hawaiiensis* (Cladophorales) or a *Printzina*-morphotype of the Trentepohliales, whereas inland biofilms are dominated by either a trebouxiophyceae alga or a *Trentepohlia*-morphotype of the Trentepohliales. Five replicates from each community type were collected and sequenced for the 16S and 18S rDNA markers using modified Earth Microbiome Project protocols on an illumina MiSeq platform for 300 cycles paired-end cycles using V3 chemistry. Additionally, a survey of *Spongiochrysis*-dominated biofilms uncovered three geographically defined communities: two along the eastern coast, north and south of Kaneohe Bay, and one along the most north-western tip of Oahu at Kaena Point. Five samples each of these communities were additionally sequenced using the above protocols for a more in-depth comparison *Spongiochrysis*-dominated biofilms. Differences between community membership and diversity indices were observable based both on dominant organism and location, i.e., coastal vs. inland.

TRACKING SYMBIOTIC DINOFLAGELLATE COINFECTION DYNAMICS IN CNIDARIAN HOSTS USING DYE TRACERS

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The dinoflagellate genus *Symbiodinium* comprises hundreds of ecologically diverse but morphologically cryptic species, many of which serve as endosymbionts in a wide array of marine cnidarians. Despite their importance as foundational components of reef ecosystems, we still know very little about the cellular-level dynamics within cnidarian-algal symbioses, especially during initial infection and stress-induced disassociation (“coral bleaching”). We developed a new tool to explore such interactions within the model *Aiptasia pallida*—*Symbiodinium minutum* system. Our method efficiently stains cultured *Symbiodinium* cells with lipophilic dyes that can be observed under fluorescent microscopy. We show that cells stained different colors are not physiologically compromised and are equally capable of being taken up by the host anemone. Using this technique, we provide the first visual assessment of competitive coinfection of an aposymbiotic anemone involving two strains of the same *Symbiodinium* species. The method is inexpensive and requires no genomic manipulation, making it broadly applicable to any nonmodel algal system where visually distinguishing between otherwise identical cultures could prove useful.

Posters

DINOFLAGELLATE DIVERSITY ALONG A SUBTROPICAL PERMANENTLY OPEN ESTUARY: EMPHASIS ON POTENTIAL HARMFUL SPECIES.

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Dinoflagellates are one of the most economically and ecologically important phytoplankton groups as they are primary producers, heterotrophs and causative agents of harmful algae

blooms. Dinoflagellate abundance and diversity was investigated in a subtropical permanently open estuary (Mlalazi, South Africa) to understand the variation of species and their driving factors. 42 species, 10 of which are harmful, were recorded for a year. Species composition and abundance differed between the 3 sites [$p=0.001$, $F=2.98$] along the estuarine length and 4 seasons [$p=0.001$, $F=2.55$]. Abundance ranged from 4.00×10^1 - 6.03×10^5 Cells/L with highest and lowest values in the middle and upper reaches respectively. The harmful *Prorocentrum cordatum* was most dominant in all sites and seasons. Among sites, species richness and diversity ranged from 26-35 and 0.39-0.48 respectively. Richness was highest at the lower reach while diversity was highest in the middle reach. Other dominant species recorded were *Prorocentrum micans*, *P. triestinum*, *Scrippsiella spinifera*, *Diplopsalis lenticulata*, *Durinskia capensis*, *Gonyaulax spinifera* and *Peridinium quinquecorne*. Dinoflagellate composition and abundance in this subtropical estuary was influenced by temperature, turbidity and dissolved inorganic phosphorus and nitrogen. This study reveals the presence of harmful dinoflagellate species which have the potential to bloom with increase in dissolved inorganic nutrients, a common occurrence in our degrading estuaries.

IRISH KELP FORESTS: PRELIMINARY MEASUREMENTS OF KELP POPULATIONS AND BIODIVERSITY.

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The population structure and productivity of dominant kelps in western Ireland is understudied. Some recent investigations highlight the productivity of common seaweeds and the biodiversity of kelp holdfasts, however little is known about the subtidal kelp forest habitat. Ireland is a region expecting pressure from kelp forest harvesting and may be further threatened by invasive species such as *Laminaria ochroleuca* and *Undaria pinnatifida*. Therefore, creating a baseline for the structure and productivity of natural kelp forests is pertinent. A meta-analysis of BIOMAR surveys from the late 1990s shows highest biodiversity within *Laminaria hyperborea* forests and regional variation in dominant kelp forest fauna (north vs. south). Initial winter surveys (2017) of kelp forests on the west coast show variability in species diversity and abundance across the granite (Co. Galway) and limestone (Co. Clare) habitats. These surveys indicate that *L. hyperborea* reaches a maximum age of 4-5 years within the kelp canopy, although previous data suggest individuals can reach 8-9 years old. *L. hyperborea* fosters other kelp species and <1 year recruits in low abundance and represents approximately 5 kg fresh algal biomass m^{-2} in the winter-spring. Future seasonal measurements of biodiversity, population structure and productivity, recruitment-succession, and environmental parameters within this habitat will be useful in assessing standing stock of *L. hyperborea* for harvesting and the ecological consequences of this harvest.

VOLVOX BARBERI LIKELY USE WEAK FORCES TO AGGREGATE INTO OPTIMALLY PACKED TWO-DIMENSIONAL FLOCKS

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Volvox barberi are multicellular protists forming colonies of 10000-50000 cells. I established that typical colonies have diameters varying ten-fold from ~50 to ~500 microns, drawn from a

log-normal distribution. I measured swimming speeds up to 600 microns/second, making this one of the fastest swimming *Volvox* species. I showed that *V. barberi* aggregates actively into “flocks” of 2 to more than 100 colonies, which move and rotate collectively at high speeds. The *Volvox* centers in flocks form a packed, irregular lattice. I hypothesized that the *Volvox* were dynamically finding the optimal packing for their size distribution. To test this, I built molecular dynamics simulations of spherical particles with a log-normal diameter distribution (matching the *Volvox*), and a weak long-range attractive force with strong local repulsion (to model mutual exclusion of colonies). Such “soft-spheres” are known to form random close-packed configurations that pack nearly optimally. I found that the lattice angle distribution in these close-packed configurations was identical to that of *Volvox* flocks. This suggests that the *Volvox* achieve random optimal packing by exerting weak attractive forces on one another. My ongoing experiments test whether the forces drawing the *V. barberi* together arise from water currents produced by the rotation of colonies driven by the beating flagella of each colonies’ cells.

FACTORS DRIVING THE PRODUCTION OF DEFENSIVE SECONDARY METABOLITES IN THE ANTARCTIC RED SEAWEED *PLOCAMIUM CARTILAGINEUM*

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Inter- and intraspecific interactions between organisms are often mediated by chemicals such as secondary metabolites. Sessile marine organisms such as macroalgae commonly produce chemical defences against grazers, pathogens, as well as biofoulers. The biomass of macroalgal forests around Palmer Station on the Western Antarctic Peninsula is comparable to temperate kelp forests and provide vital functions to the ecosystem. *Plocamium cartilagineum* is a finely branched red understory alga that is common in these 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 and these unique chemical signatures are referred to as chemogroups. Around Palmer Station in 2016 a total of 12 different chemogroups have been identified from 105 individuals. Those individuals were collected from two different depth ranges at 19 sites. The 12 chemogroups fit well into two distinct genetic groups (but not different enough to be considered different species) identified by the *cox1* and *rbcL* genes. These data suggest that chemogroups are to some extent site specific, they have some correlation with depth and that there is an underlying genetic differentiation.

MIXOTROPHY IN THE PHOTOTROPHIC CRYPTOPHYTE *TELEAULAX AMPHIOXEIA* ON MARINE BACTERIA

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The cryptophyte *Teleaulax amphioxeia* is firstly reported here to be a mixotrophic species. We investigated the effects of prey concentration on the ingestion rates of *T. amphioxeia* as well as the kinds of prey microbes using epifluorescence and transmission electron microscopy. Among the prey organisms offered, *T. amphioxeia* fed on heterotrophic bacteria, *Synechococcus*, and algal preys smaller than 5 μm of equivalent spherical diameter. Larger protistan species were not consumed by *T. amphioxeia*. The ingestion rates of *T. amphioxeia* on heterotrophic bacteria and *Synechococcus* sp. rapidly increased with prey concentrations up to 8.6×10^6 cells/ml, but became saturated or slightly decreased at higher prey concentrations. The maximum ingestion rates of *T. amphioxeia* on heterotrophic bacteria and *Synechococcus* sp. were 0.74 and 0.26 cells/predator/h, respectively. The results of the present study suggest that *T. amphioxeia* is an effective protistan grazer of marine bacteria in marine planktonic food webs.

EFFECTS OF ASSOCIATED BACTERIA ON *PHAEODACTYLUM TRICORNUTUM* BIOMASS AND GROWTH RATE

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Bacteria are known to have beneficial (e.g., production of signaling/inducer molecules, nutrient release) and adverse (e.g., competition and pathogenic interactions) effects on algal growth rates and metabolite production. The goal of this study is determine the effect of single bacterial associations on the growth rate of *Phaeodactylum tricornotum*. An axenic strain of *P. tricornotum* and the same algal strain co-incubated with different single bacterial isolates were subsampled bi-daily for OD to determine the growth rates. Bacterial identification was accomplished by 16S rRNA gene sequencing. HPLC-TOF system was used to identify compounds and compare compounds associated with the axenic and mixed cultures. Enhanced growth occurred in some bacterial-algal cultures relative to axenic cultures in both exponential and linear phases ($p < 0.05$). Eight different species of bacteria from 6 different genera were identified through bacterial 16S sequencing. Eicosapentaenoic acid (EPA) was found in higher quantities in bacterial: *P. tricornotum* cultures compared to axenic cultures. The results from this study could enhance the efficiency of microalgae production for biofuels and other products. Ongoing work will determine the impact of specific bacterial associations on lipid content and fatty acid composition. HPLC-TOF will be used to identify regulated bioactive metabolites in these bacterial-algal cultures.

THE INFLUENCE OF TEMPERATURE ON THE GROWTH AND VERTICAL MIGRATION OF *MICROCYSTIS AERUGINOSA*

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Microcystis aeruginosa is a species of freshwater cyanobacteria which often dominates the eutrophic lakes and forms harmful algal blooms during summer months. The objective of this study is to investigate the effect of ambient temperature on the growth rate and vertical migration velocity of *M. aeruginosa*. Batch cultures of *M. aeruginosa* were cultivated at seven different temperatures to obtain the specific growth rate at each temperature. The results showed that the growth rate of *M. aeruginosa* increased with temperature up to the optimal temperature of 28.1°C and was inversely affected at higher temperatures. We proposed a cardinal temperature model for *M. aeruginosa* with the inflection point at the optimal temperature. The model describes 95% of the variability of experimental data from 5°C to 35°C. *M. aeruginosa* colonies migrate vertically by buoyancy regulations via intracellular gas vesicles and cell density changes. A digital inline holographic microscope was developed and employed to visualize and analyze the migration of *M. aeruginosa* colonies at two different temperatures. The results demonstrated that the migration velocity of *M. aeruginosa* colonies at 28°C was approximately five times as great as that at 17.5°C. A model was derived to calculate the density of a colony using the buoyant velocity and colony size. The findings of this study could facilitate the prediction and mitigation of harmful algal blooms in aquatic ecosystem.

WILLAPA BAY, WASHINGTON (USA): A MARINE GARDEN BEFORE ERADICATION
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Willapa Bay is one of the nation's largest commercial oyster producing estuaries, and juvenile oysters have been imported into the area for cultivation from the NW Atlantic, NW Pacific, and California since the late 1800's. There has been ample opportunity for hitchhiking seaweed and seagrass introductions. To detect these introductions, year-around collections were made in the Bay from 7/2006 to 6/2008, and 76 species were identified. About half of these species were globally widespread, and 12 were clear introductions. The introductions, illustrated in my poster, include species from both Asia and the Atlantic. Most appear to have been imported with oysters in the early 1900s before restrictions on oyster transplantations were imposed. The algal populations thrived, and oceanographic features of the area appeared to trap their natural escape from the Bay. A beautiful garden of *Dasya*, *Codium*, *Bryopsis*, *Ceramium* and other species covered the floating docks and oyster beds. However, near the end of my study, the State intensified their efforts to exterminate two other introduced species from the Bay, *Spartina alterniflora* and *Zostera japonica*. Quantities of the herbicides, glyphosphate and later imazapyr, were sprayed onto the Bay over a series of years. Although some control of these species was accomplished, the impact on the seaweeds was not determined. Did they survive? A comparison of the current flora with my earlier checklist will help to answer this question.

ISOLATION OF CYTOTOXIC COMPOUNDS FROM THE MASSIVE CULTURE OF A
MARINE DINOFLAGELLATE *PROROCENTRUM LIMA*

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Limaol (1), a new compound, dinophysistoxin 1 (DTX-1) derivatives and okadaic acid (OA) were isolated from the large-scale cultivation of the benthic marine dinoflagellate *Prorocentrum lima*. The structures of all compounds were determined by a combination of NMR spectroscopy and mass spectrometry. In particular, limaol was characteristic of the presence of tetrahydropyran, 1,3,5,7-tetra(methylene) heptane and octahydrospiro[pyran-2,2'-pyrano[3,2-b]pyran] subunits. Furthermore, the absolute configuration of 1 was completely elucidated on the basis of ROESY correlations, J-based configuration analysis and modified Mosher's ester method. The cytotoxicity of all compounds was evaluated and limaol showed moderate cytotoxicity when compared to OA against three cancer cells lines.

CYANOBACTERIA FLORA OF A GSMNP CAVE

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Cyanobacteria are among some of the most ancient forms of life on earth. Cyanobacteria commonly prefer alkaline waters, and are consequently common on wet limestone (CaCO₃) surfaces, such as those found in many seep walls and caves. Flora of the naturally lit front portions of caves have been studied only in very isolated areas by relatively few researchers. In North America, the best studied cave cyanobacterial flora is that of Mammoth Cave in Kentucky, USA. Other Appalachian caves, such as those in the Great Smoky Mountains National Park and surrounding area are greatly under represented. With the spread of the deadly white nose syndrome in bats, permits that allow entrance into caves of national parks have become increasingly difficult to acquire. We were able to obtain a permit that allowed us to sample one cave in the Great Smoky Mountains National Park in Tennessee. From this single small cave, we have recorded over 10 genera of cyanobacteria, some of which overlap with previous floristic studies of caves in Greece and Spain. Of particular interest are the rarer genera *Geitleria* and *Loriellopsis*, which are calcified, true-branching taxa reported only in caves.

A CONTRIBUTION TO THE KNOWLEDGE OF ALGAE AND CYANOBACTERIA IN FISHPONDS IN THE BLATNA REGION, CZECH REPUBLIC

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Carp ponds have been an integral part of the Czech landscape since the Middle Ages, when they were built to drain swamps in order to gain farmlands. These fishponds retained their oligo-mesotrophic character for centuries. However, with the onset of 20th century fishery management, demands for carp production with intense fertilization increased, and the ponds became eutrophied. To assess the algal community composition, and to investigate whether there is a relationship between species richness and trophic status, a floristic study was carried out in a pond-rich region, the Blatna Basin, Czech Republic. In total, 1021 taxa were identified, with Bacillariophyta being taxonomically the richest group (571 taxa). The continuously changing chemo-physical properties and competition at different trophic levels cause seasonal changes in algal community composition. Spring phytoplankton was oftentimes dominated by diatoms. During the summer cyanobacteria took over and caused blooms in many ponds. However, in some hypereutrophic ponds blooms composed of green coccoids and euglenoids emerged. As the water cooled during autumn, a slow transition back to diatom-dominated assemblages was

observed. Most of the fishponds show symptoms of advanced eutrophication due to fishery management practices. However, it may seem that high trophy does not necessarily lead to a loss of species richness but towards a uniform character of the algal community based on a fish stocking levels.

A FLORISTIC STUDY OF SEASONAL CHANGES IN WETWALL DIATOM (BACILLARIOPHYTA) COMMUNITIES OF VIRGINIA-KENDALL NATIONAL PARK, PENINSULA, OH.

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Diatoms (Bacillariophyta) are a highly-diversified group of microalgae that are found globally in almost any habitat that contains water, including aerial habitats such as: soils (terrestrial), terrestrial plants (epiphytic or epibryophytic), and wetwalls (pseudoaerial). Though there is an extensive literature covering the Bacillariophyta of aerial habitats, they have received less study than taxa of fully aquatic habitats. Of the aerial habitats, pseudoaerial habitats have received some of the least comprehensive study. There are several parks within the state of Ohio (e.g., Hocking Hills State Park & Gorge Metro Park) in which these wetwall habitats can be found. I have carried out a floristic study of the algal assemblages of three wetwalls in Virginia-Kendall National Park (located within Cuyahoga National Park). The objective of this study was to generate a finely detailed flora of the Bacillariophyta, as well as a coarser flora of other algal taxa, present on these wetwalls. Additionally, samples were collected over the course of three seasons (e.g., fall, winter, and spring), and a comparative analysis of changes in species composition at each site will be presented. The dominant diatom taxa of these sites include: *Diadesmis* spp.; *Eunotia* spp.; and *Microcostatus* spp. Other non-diatom algal taxa present include: *Klebsormidium* spp.; *Chlorella* spp.; and *Coccomyxa* spp.

AERIAL SAMPLING OF CYANOBACTERIA OVER LONGITUDINAL AND ALTITUDINAL GRADIENTS

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One of the most intriguing questions in microbial ecology is whether microbes are, in general, cosmopolitan or endemic. Cyanobacteria are photosynthetic, prokaryotic organisms that are the primary producers of oxygen on the planet. Ubiquitous in nearly every ecosystem, little is known about the long-range dispersal of these organisms. Our recent analysis of coastal, microbial communities has shown that several lineages of cyanobacteria in Florida are most similar to, and likely originated from, populations in sub-Saharan Africa. One potential mechanism for this long-range dispersal is aerosolization, perhaps due to major storms such as hurricanes. To determine the diversity and abundance of aerosolized cyanobacteria, a MASK (Microbial Aerial Sampling Kit) was constructed, tested, and deployed by aircraft over three distinct areas in Jacksonville, Florida. The MASK is a novel apparatus designed to collect multiple sterile samples by aircraft, motor vehicle, or water craft. Each cartridge consists of a sterilized polypropylene conical tube inoculated with sterile cotton. The deployment mechanism is a specially designed aluminum housing equipped with a handle for rapid deployment. Samples

were collected at sea level, 500 m, 1000 m, and 1500 m, and the contents of the MASK were cultured on Z-8 medium. Cyanobacterial and algal isolates were cultured and examined via microscopy. Cyanobacterial isolates were further characterized by genetic (e.g., 16S rDNA and ITS) analyses. Preliminary analyses indicated the presence of several lineages (i.e., the Chroococcales, Oscillatoriales) in the aerial samples.

POLYPHASIC CHARACTERIZATION OF A SPECIES OF *STAUROMATONEMA* (CYANOPROKARYOTA) FROM A WATERFALL IN "LOS TUXTLAS REGION", MEXICO.

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Stauromatonema Frey is a filamentous heterocytous genus in the Capsosiraceae, which can be characterized by its firm, gelatinous macroscopic colonies formed by densely packed parallel true branches arising from creeping basal filaments. At present, there are no available sequences from any of the three species in the genus. Using agar-solidified BG11 media fragments moistened with a patina of autoclaved site water, a strain from *Stauromatonema viride* Frey was isolated from a basalt wet associated with a waterfall from "Los Tuxtlas" region, Veracruz, Mexico. In this work we report the morphological changes associated with growth in culture with respect to the morphology of natural populations. In nature, the dense arrangement is diagnostic, but in culture the dense nature of the colony is lost and the strain resembles *Hapalosiphon*. Enlarged, granulated, akinete-like cells are also produced in culture. Phylogenetic analysis of our strain will be presented.

IDENTIFYING BIOGEOGRAPHICAL PATTERNS WITHIN *BRASILONEMA* (SCYTONEMATACEAE, CYANOPHYTA) USING 16S rRNA AND ITS SECONDARY STRUCTURES

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Microorganisms have long been considered ubiquitous, but recently there has been much debate regarding the biogeographical range of many microbes. *Brasilonema* is a genus of cyanobacteria belonging to the Scytonemataceae family that was recently split from the genus *Scytonema*. This genus has a wide distribution and can be found in many tropical and subtropical habitats from Hawaii to central and South America to the southern USA. Phylogenetic studies examining the highly conserved 16S rRNA gene show this genus forms a monophyletic clade and ITS secondary structures are used to delineate closely related species. When examining *Brasilonema* strains isolated from habitats in Florida, USA, the strains were found to be less closely related to each other than strains isolated from central Mexico and Costa Rica. Phylogenetic trees constructed using maximum parsimony and maximum likelihood showed one strain of *Brasilonema* falling out into its own clade, while the other strain clustered with those isolated from central Mexico and Costa Rica. In order to investigate this further, ITS secondary structures

were compared for all available clonal replicates of published *Brasilonema* strains both within and between species to gain insight into biographic patterns. The results of this study illustrate possible biogeographical differentiation among *Brasilonema* species due to previous, possibly random, dispersal events shedding light on the “everything is everywhere” debate in microbial ecology.

PHOTOSYNTHETIC GENES LHCF2 AND LHCF15 MRNA REGULATORY MECHANISMS IN RESPONSE TO HERBIVORY INDUCED ALDEHYDE IN THE DIATOM *PHAEODACTYLUM TRICORNUTUM*

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Photosynthetic organisms are challenged by diverse biotic stresses. In response to herbivory, various diatom species release lipid aldehydes which may impair reproduction in herbivores and alter photosynthesis-related gene expression in nearby diatoms. However, the mechanisms of photosynthesis gene regulation are poorly understood. In this study, the marine diatom *Phaeodactylum tricoratum* was treated with 10 μ M 2E, 4E-decadienal (DD). Lhcf2 mRNA was down-regulated to 33% and 54% of the solvent control within 1 hr and 6 hr, respectively. In contrast, Lhcf15 mRNA remained stable through 4 hr followed by 217% upregulation at 6 hr. To determine Lhcf2 mRNA half-life, Actinomycin D was used to block transcription. Lhcf2 mRNA half-life decreased from 4.8 ± 0.6 hr in control cells to 1.6 ± 0.88 hr in DD treated cells. To assess transcription and mRNA turnover changes with less perturbation, pulse labeling with 4-thiouracil was explored. Dose dependent sulfur labeling of RNA occurred, shown by biotinylation and chemiluminescence assays. 4-thiouracil (0.1-0.2 mM) was most effectively incorporated into RNA and cell viability was not detectably affected. These findings suggest that 4-thiouracil labeling can be utilized to elucidate transcription and mRNA half-life mechanisms in *P. tricoratum*. Future studies will seek to contribute to understanding how photosynthetic mRNA regulation may provide adaptive benefits under biotic stress conditions.

THE BIOGEOGRAPHY OF CYANOBACTERIAL COMMUNITIES IN THE SVALBARD ARCHIPELAGO

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Cyanobacteria are key in freshwater and terrestrial Arctic ecosystems, found in coastal and inland lakes, meltwater streams, cryoconites and soils. In these ecosystems, they drive many ecological functions, such as biomass accumulation and nitrogen and carbon fixation. To understand impacts of global change on Arctic ecosystems, baseline data on cyanobacterial diversity and distribution is crucial. Here we investigate the biogeographic patterns of cyanobacterial communities across Svalbard. A total of 72 microbial mats and biocrusts were collected from eight different locations in three distinct bioclimate subzones (Arctic Polar

Desert; Northern Arctic Tundra; and Middle Arctic Tundra) and analyzed by pyrosequencing of partial 16S rRNA. Community structure was fairly homogeneous across all locations, predominating phylotypes of filamentous, non-heterocytous Pseudanabaenales, but richness was significantly lower in the Arctic Polar Desert. When compared to data from similar Antarctic biotopes, there is a clear separation in community structure. Phylotype richness was significantly higher in the Arctic and multivariate analyses separate both Polar Regions. BLAST revealed a dominance of putative endemic and novel phylotypes in both poles (52-67%). Our results suggest constant dispersal of propagules across Svalbard, such that no clear biogeographic patterns are evident in the archipelago. However, a sharp barrier to dispersal seems to exist on a global scale, resulting in disparate cyanobacterial communities across the Polar Regions, despite similar environmental constraints.

OMEGA-7 PRODUCING ALKALI-TOLERANT DIATOM *FISTULIFERA* SP. 154-3 FROM LAKE OKEECHOBEE, FLORIDA

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Incorporating renewable fuels into practice, especially biofuel derived from microalgae feedstock, is a promising approach of reducing fossil fuel dependency. Microalgae are an exceptional feedstock since they can produce abundant biomass and oils in a short period of time. Achieving goals of producing algae fuels at competitive prices, however, involves further improvement of technology, one that involves a better control over microalgae cultivation. Manipulating cultivation conditions in order to promote growth and lipid storage while preventing contamination is desired. Contamination of algal cultures in the open systems is the major impediment in algal biotechnology, however this can be overcome by choosing an extremophile microalgae. This work aimed at isolation of alkaliphilic microalgae native to the South Florida with characteristics suitable for biodiesel production. For that purpose, water samples from Lake Okeechobee were inoculated into Zarrouk's medium (pH 9-12) and incubated for 35 days. This resulted in isolation of three algal strains that were screened for biomass yield and lipid accumulation. One of the isolates, *Fistulifera* sp. 154-3, was identified as a high-lipid accumulating, alkali-tolerant organism with biomass productivity of $0.285 \text{ g L}^{-1} \text{ day}^{-1}$ and lipid content of 20% dry biomass at pH of 10. Lipid analysis of *Fistulifera* sp. indicated the most abundant fatty acid to be palmitoleic acid, also known as omega-7, followed by palmitic acid and eicosapentanoic acid.

AN UNDESCRIBED SPECIES OF JAPANESE *PYROPIA* APPEARED ON THE COAST OF BRITISH COLUMBIA IN 2015

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In 2015, on the central coast of British Columbia, I documented the occurrence of a putative Japanese species of *Pyropia* that may have arrived with tsunami debris. The find occurred at a site that has been subjected to an annual intensive seaweed survey beginning in the summer of

2011 so there is little doubt that the species was new to the area in 2015. Even before sequencing the chloroplast *rbcL* gene, I suspected that this species had affinities with Japanese rather than North American species because it had a distinctive disposition of reproductive cells found on Japanese but not native North American species. In a molecular phylogeny, this species is basal in a clade of Japanese and other Far East species of *Pyropia* although this particular species has yet to be reported from Japan. In addition to the central coast of British Columbia, the species has been previously recorded from the South Island, New Zealand, and from Monterey Bay, California, based on molecular sequences. This find highlights the difficulty in documenting possible invasive species when the Japanese flora and fauna have not been sufficiently characterized to allow for comprehensive comparisons. The foliose phase of the species was not observed in 2016, but overall *Pyropia* diversity and abundance were down in 2016. However, the cryptic conchocelis phase was identified by sequencing pinkish barnacle tests collected near the area where the species was observed in 2015.

LATITUDINAL DIFFERENCES IN THE DISTRIBUTION PATTERNS OF EPIPHYTIC ALGAE AND THEIR ASSOCIATED MEIOFAUNA ON LIVE AND DEAD *SPARTINA ALTERNIFLORA* STEMS

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Spartina alterniflora marshes are critical habitats for economically and ecologically valuable species throughout the U.S. Atlantic coast. Within these marshes, a large percentage of the primary and secondary production is comprised of epiphytic algae and the meiofauna that inhabit the epiphytes. However, little is known about the latitudinal variation in the distribution and abundance of epiphytes and meiofauna on *S. alterniflora* stems. To assess these community features, we conducted monthly surveys of stem density, stem condition (live or dead), stem height, and the proportion of each stem covered by algae at two sites in Connecticut, USA, and three sites in Georgia, USA, throughout the *S. alterniflora* growing season. Samples of epiphytic algae were examined via light microscopy to identify and quantify meiofauna. It was observed that dead *S. alterniflora* stems and algae were both more prevalent in Georgia than in Connecticut. Meiofaunal diversity was also higher in Georgia than in Connecticut. In both states, dead *S. alterniflora* stems supported more epiphytic algae and meiofauna than live stems. Further study is needed to determine the underlying cause of the greater epiphytic abundance observed on dead *S. alterniflora* stems. One potential contributing factor is phenolic levels, which may deter epiphytic colonization of live plants. Pilot sampling in Connecticut marshes suggested a negative correlation between live stem phenolic concentrations and epiphytic abundance.

MITOCHONDRIAL GENOME OF *LYMPHA MUCOSA* GEN. ET SP. PROV. (BTRACHOSPERMALES, RHODOPHYTA)

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Although most Rhodophyta are marine, there is ~5% that inhabit freshwater. The majority of these freshwater reds are within the Batrachospermales. There have been a few studies of red algae, which have provided data on whole mitochondrial genomes. To date, no mitochondrial genome of a freshwater red alga has been published and only one in the Nemaliophycidae for *Palmaria palmata*. Therefore, the current study was initiated to provide a mitochondrial genome of a freshwater florideophyte *Lympha mucosa* gen. et sp. prov. as a second genome in the Nemaliophycidae and for comparison with marine rhodophytes. Sequencing was conducted using the Illumina Miseq and assembled with CLC workbench. The circular genome (~ 26,000 bp) was confirmed and annotated using previously published mitochondrial genomes in the Florideophyceae. Gene content (~ 50) and arrangement was compared to the mitochondrial genomes of Nemaliophycidae and Rhodymeniophycidae. Although annotated in this genome, the protein coding ymf39 and rpl20 sequences were highly divergent when compared to other red algae. These genes require further RNA study to verify that they produce functional products.

MACROALGAL PHYSIOLOGICAL AND ECOLOGICAL RESPONSE TO SUBMARINE GROUNDWATER DISCHARGE IN TROPICAL ISLAND ECOSYSTEMS

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Submarine groundwater discharge (SGD) results in release of substantial volumes of higher nutrient, lowered salinity, variable pH and variable temperature waters into coastal settings of oceanic islands via subterranean aquifers. Where riverine inputs are negligible, SGD may be the dominant source of nutrients to coastal ecosystems. Further, SGD flux volume and characteristics are highly variable among sites. While persistent macroalgal blooms have been linked to anthropogenic nutrient pollution of SGD, a clear gap in our understanding is the influence of SGD on native algae in benthic communities, the physiological trade-offs across algal species, and changes in community species composition. I hypothesize that SGD influences the physiology and ecology of marine plants. Second, I hypothesize that SGD conditions influence benthic species composition. Correlations between benthic cover and SGD characteristics can be complimented by measurements of marine plant physiology across a gradient of SGD influence. Measurements of photosynthesis, tissue $\delta^{15}\text{N}$ Nitrogen, tissue %Nitrogen, and internal solute potential are used to demonstrate the integrated marine plant physiological response to SGD conditions by native and invasive species. Demonstrating how these plants respond physiologically to different SGD characteristics in concordance with describing changes in benthic cover across SGD conditions elucidates this relationship between SGD characteristics, benthic species composition, marine plant physiology, and invasive macroalgal blooms.

MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF A NEW SPECIES OF *KYRTUTHRIX* FROM THE GULF OF MEXICO.

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Kyrtuthrix Ercegovic, 1929 is a heterocytous genus that has a crustous habit formed by the heteropolar disposition of folded filaments. Only three valid species have been described: *K. dalmatica* Ercegovic 1929, *K. maculans* (Gomont) Umezaki 1958 and *K. huatulcensis* León-Tejera, González-Resendiz & Johansen 2016, this strain is the only one with 16S rRNA, 16S-23S ITS molecular data published. *Kyrtuthrix* small crusts are common in the intertidal platform of Playa Muñecos, Veracruz, in the Gulf of Mexico, where three populations have been analyzed and two strains have been isolated in SN media as part of project PAPIIT IN225317. Our environmental material has morphological differences with the three previously described species concerning thalli size and general filament disposition within the crust, as well as cellular shape and dimensions. In culture this populations loose parallel disposition of filaments, show frequent heteropolar hormogonia and cell shape changes; however it conserves loop forming disposition of attenuated filaments. Molecular data was obtained from an environmental sample; selected molecular markers were 16S rRNA and 16S-23S ITS genes. Phylogenetic analysis shows that our population belongs to the Rivulariaceae clade and is closer to *K. huatulcensis* than to other members within this family. Morphology, 16S gene phylogeny and secondary structure of 16S-23S ITS support the description of a new species of *Kyrtuthrix*, the first one for the Gulf of Mexico.

KNOCKOUT OF THE MITOCHONDRIAL ACYL-COENZYME A DEHYDROGENASE GENE INCREASES THE LIPID CONTENT OF A MARINE DIATOM.

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Next generation biofuels can be generated from algal lipids. However, increasing the partitioning of carbon to lipids is necessary to make algal biofuels economically viable. Many species of diatoms store energy in the neutral lipid triacylglycerol during the day. The lipid is then catabolized by beta-oxidation cycles during the night to fuel metabolism. We aimed to characterize lipid catabolism in the model pennate marine diatom *Phaeodactylum tricoratum*. This species has bioinformatically predicted beta-oxidation pathways in the peroxisome and the mitochondria. We hypothesized that the mitochondrial pathway is the major route for fatty acid catabolism because multiple transcripts associated with this pathway are upregulated at night. The first step of fatty acid beta-oxidation is catalyzed by Acyl-CoA Dehydrogenase (mACD). We created mACD knockout mutants using a CRISPR-Cas9 system and characterized mutant strains during nutrient replete growth in day:night cycles. Mutant strains grew 82% slower than wild type (WT). Flow cytometry analysis suggested minor changes in cell size or pigment content of the mutants compared to WT. We estimated the neutral lipid content of cells using BODIPY fluorescence. BODIPY fluorescence in WT oscillated with day:night cycles, as expected. mACD mutants displayed no oscillation and 2.6 fold higher BODIPY fluorescence compared to WT at dawn. Our results suggest that the mitochondrial pathway for lipid breakdown is active in this diatom and reducing its activity may lead to increased lipid yields for conversion to biofuels.

BIOLOGICAL SOIL CRUST COMMUNITIES IN CONJUNCTION WITH SOIL STABILITY IN THE RIO PUERCO WATERSHED

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The Rio Puerco Watershed is a large drainage area in west central New Mexico facing great concerns with regard to soil loss and subsequent declining water quality. Various management attempts have been implemented with hopes to ease or reverse the effects of disturbance and minimize soil erosion. Although the watershed has been studied extensively, the contribution of soil microbiota to stability of its soils remains poorly known. Biological soil crusts (BSC) including lichens, bryophytes and algae are a common microbial soil surface feature in dryland regions such as central NM. BSC possess many features that increase soil stability and could influence factors linked to soil hydrological processes. The objective of this study is to characterize the BSC communities of the area as well as assess their contribution to relative soil stability. Preliminary results showed that BSC can cover up to 52% of the ground cover at 2 study areas surveyed within the watershed. The most abundant crust community types were incipient and light algal crusts. Dark pigmented algal crusts containing heterocytous cyanobacteria, lichens and mosses were least abundant. Distance from the river and soil texture seemed to influence abundance and presence of BSC community types. Comparison of soil aggregate stability between the top 1 cm and the associated subsurface soil indicated the importance of BSC to soil stabilization in the watershed. Our preliminary results promise interesting new perspective on land use and management of the Rio Puerco Watershed.

EXOGENOUS INDUCTION OF OXIDATIVE DNA DAMAGE IS ASSOCIATED WITH MUTAGENESIS IN *CHLAMYDOMONAS*

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We are beginning an investigation into the relationship between induction of oxidative DNA damage and mutation rates in *Chlamydomonas*. In a series of six consecutive biological experiments, we have found that induction of a relatively low level of oxidative DNA damage by treatment of cells in culture with visible light together with the photosensitizing dye acridine orange is associated in every case with a significant increase in the numbers of spectinomycin-resistant mutants, relative to the numbers of such mutants arising in the absence of this genotoxic treatment. We also find that this DNA damage is lost over time, consistent with the operation of DNA repair processes in these cells. Our results point to the possibility of determining the in vivo error-rate of DNA damage-removal processes in this organism.

BIODIVERSITY OF FRESHWATER MICROALGAE IN SOUTHERN APPALACHIAN COALFIELD REGION DETERMINED BY METAGENOMIC BARCODING

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The Southern Appalachian region of the Southeastern United States is one of the most biologically diverse temperate areas in North America, yet little is known about the diversity of microorganisms living in these ecosystems. We are interested in surveying single-celled planktonic algae in this region to create a baseline reference for future comparisons of areas affected by anthropological disturbances. To date, samples have been collected and analyzed from twenty-seven sites including standing (reservoirs, ponds, and ephemeral pools) and moving (streams) bodies of water. Microalgae were filtered from the samples and identified using the 23S and 18S rRNA barcode regions and sequenced using Illumina MiSeq technology. Sequences were compared to GenBank and a library of microalgal sequences was prepared from archived matches with $\geq 95\%$ identity. For the 18S barcode, an average of 1790 Observable Taxonomic Units (OTUs) were observed at each site with a 97% identification rate, meaning there was a sequence in GenBank with a matching identity; unfortunately many of these were not useful for identification. Despite this, 275 distinct genera within 139 families have been identified using the 18S barcode. When separated into phyla, Chlorophyta had the most genera (111) followed by Bacillariophyta (60), Dinophyceae (25), Chrysophyceae (16), Cryptophyta (8), and others. The largest populations, as extrapolated from the total number of sequences were from the Bacillariophyta and Chrysophyceae. The majority of the genera were represented within the sequence data at very low rates, which we interpret as spores and not blooms or active populations of cells.

VOLVOX BARBERI LIKELY USE WEAK FORCES TO AGGREGATE INTO OPTIMALLY PACKED TWO-DIMENSIONAL FLOCKS

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Volvox barberi are multicellular protists forming colonies of 10000-50000 cells. I established that typical colonies have diameters varying ten-fold from ~50 to ~500 microns, drawn from a log-normal distribution. I measured swimming speeds up to 600 microns/second, making this one of the fastest swimming *Volvox* species. I showed that *V. barberi* aggregates actively into “flocks” of 2 to more than 100 colonies, which move and rotate collectively at high speeds. The *Volvox* centers in flocks form a packed, irregular lattice. I hypothesized that the *Volvox* were dynamically finding the optimal packing for their size distribution. To test this, I built molecular dynamics simulations of spherical particles with a log-normal diameter distribution (matching the *Volvox*), and a weak long-range attractive force with strong local repulsion (to model mutual exclusion of colonies). Such “soft-spheres” are known to form random close-packed configurations that pack nearly optimally. I found that the lattice angle distribution in these close-packed configurations was identical to that of *Volvox* flocks. This suggests that the *Volvox* achieve random optimal packing by exerting weak attractive forces on one another. My ongoing experiments test whether the forces drawing the *V. barberi* together arise from water currents produced by the rotation of colonies driven by the beating flagella of each colonies’ cells.

EFFECTS OF COPPER AND LEAD ON *SPIRULINA MAXIMA* IN CONTAMINATED WATER AND THE ABILITY OF THE CYANOBACTERIA TO SEQUESTER METALS
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Toxic metal waste generated due to anthropogenic activities by contaminating water bodies are one of the major threats to the environment. Cyanobacteria such as *Spirulina maxima* can survive in stressed condition, contain high anti-oxidant, adsorption, and absorption properties that make it a promising tool for bioremediation. The objective of this study was to investigate the effects of copper (Cu) and lead (Pb) with the initial concentrations of 0.5 and 2.0 ppm on the growth and pigment concentrations of *Spirulina maxima*. The ability of the microorganism in adsorbing metals was also determined. The growth curve was studied in 0.5 and 2.0 ppm Cu and Pb contaminated aquatic solution. Confocal Laser Scanning Microscopy (CLSM- λ scan) was used to determine the *in vivo* effects of these metals on *S. maxima*. Fourier Transform Infrared Spectroscopy (FTIR) was used to determine the possible functional groups of *Spirulina* that participated in the metal adsorption. The cells were more tolerant to 0.5 ppm Cu compared to 2.0 ppm Pb as they could survive for 13 and 9 days, respectively. CLSM- λ scan indicated that the absorption intensity at 685 nm dropped from 45% to 28% in 30 minutes of 0.5 ppm Cu and 2.0 ppm Pb treated cells, respectively. The absorption intensity at 640 nm dropped from 46% to 30% in 30 minutes of 0.5 ppm Cu and 2.0 ppm Pb treated cells, respectively. The absorption intensity suggested the better tolerance of Cu by the cyanobacteria. Cu and Pb treated biomass were dependent on OH-, COO-, amide/amide, and carboxyl functional groups for biosorption. The results obtained from the study suggested that *Spirulina maxima* has the better tolerance ability of copper compared to lead and to bioaccumulate the metals extra- and intracellularly.

THE BCCM/ULC COLLECTION FOR EX-SITU CONSERVATION AND EXPLORATION OF POLAR CYANOBACTERIAL DIVERSITY

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The BCCM/ULC public collection funded by the Belgian Science Policy Office since 2011 aims to gather a representative portion of Polar cyanobacterial diversity with different ecological origins (limnetic microbial mats, soil crusts, cryoconites, endoliths, etc.). It is available to researchers for study of taxonomy, evolution, adaptations to harsh environmental conditions, and genomic make-up. Presently, it includes 226 cyanobacterial strains, with more than half of Polar origin (<http://bccm.belspo.be/catalogues/ulc-catalogue-search>). Morphological identification shows that the strains belong to the orders Synechococcales, Oscillatoriales, Pleurocapsales, Chroococciopsidales and Nostocales. This large diversity is also supported by phylogenetic analyses based on 16S rRNA. This broad distribution makes the BCCM/ULC collection particularly interesting for phylogenomic studies. In addition, cyanobacteria produce a range of secondary metabolites (e.g. alkaloides, cyclic and linear peptides, polyketides) with different

bioactive potential. Bioassays have shown antifungal activities of cell extracts of strains *Plectolyngbya hodgsonii* ULC009 and *Phormidium priestleyi* ULC026. Due to the geographic isolation and the strong environmental stressors of the habitat, the exploration of these metabolites in Antarctic cyanobacterial strains seems promising for biotechnology or biomedical applications.

VOLUNTEER ALGAE MONITORING PROGRAM (VAMP) IN THE INDIAN RIVER LAGOON ESTUARY (FLORIDA)

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Eutrophication has increased cyanobacterial harmful algal blooms (CHABs) worldwide. This is prevalent in Florida, since the state is a mix of rural and urban areas affected by nutrients from runoff, sewage and agriculture, in addition to having a huge phosphate deposit. In summer 2016, FL Treasure Coast communities in Martin, St. Lucie and Indian River counties were impacted by CHABs in the Indian River Lagoon estuary, which led to residents demanding cessation of fresh water from Lake Okeechobee. Public health authorities in Martin Co. issued recommendations for people to protect themselves, their families and pets from exposure to the HABs. This impacted businesses, residents and visitors as the news spread worldwide on media outlets. These episodes demonstrate the importance of having informed citizens with an understanding of the problems and threats. Studies have shown the value of using citizen scientists to aid in HAB monitoring programs. Thus, UF/IFAS research and extension faculty devised the Volunteer Algae Monitoring Program (VAMP) as a test pilot program to address the need to obtain long-term algae and water quality data and to engage local citizens in these efforts. UF/IFAS FL Master Naturalist volunteers were selected to adopt a sampling point in the estuary and received training and supplies for monthly water quality testing and algae collection. The Laughinghouse Lab at UF/IFAS Ft. Lauderdale REC surveys these samples and reports are submitted to UF/IFAS St. Lucie Co. Extension, where local decision-makers assess the algae-related issues impacting the estuary.

EXPLORING THE POTENTIAL OF AN ALGAL-BASED CONCRETE

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Algal ecotechnologies are being developed for water quality management and other purposes. In some cases, algal biomass is an intended output of these technologies; in other cases it is a by-product. In this study, algal biomass used to scrub nutrients from Chesapeake Bay waters (using Algal Turf Scrubbers), and thereby improve water quality conditions of the Bay, was dried and

tested as an additive for making concrete because of its high inorganic ash content. Different proportions of dried algae were added to a commercially available concrete mix to create a range of algal-based concretes. Mixes with 5% algae or less were found to be similar to the control (100% standard concrete mix with no added algae) in terms of strength and stability. The potential values of algal-based concrete for sequestering nutrients and for creating a business opportunity are discussed.