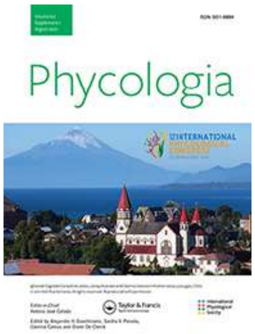

Phycologia

ISSN: (Print) (Online) Journal homepage: https://www.tandfonline.com/loi/uphy20

12th International Phycological Congress

To cite this article: (2021) 12th International Phycological Congress, Phycologia, 60:sup1, 1-153, DOI: 10.1080/00318884.2021.1922050

To link to this article: https://doi.org/10.1080/00318884.2021.1922050

Volume 60
Supplement 1
August 2021

ISSN: 0031-8884

Phycologia

Iglesia del Sagrado Corazón de Jesús, Llanquihue Lake and Osorno Volcano in Puerto Varas, Los Lagos, Chile.

Editor-in-Chief
António José Calado

Taylor & Francis
Taylor & Francis Group

International
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Edited by Alejandro H. Buschmann, Sandra V. Pereda,
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Abstracts of papers to be presented at the

12th International Phycological Congress
Puerto Montt, Chile
22–26 March 2021

Edited by
Alejandro H. Buschmann, Sandra V. Pereda, Carolina Camus, Olivier De Clerck

Copies of the abstracts will be distributed among registered delegates
at the 12th International Phycological Congress.

12TH INTERNATIONAL
PHYCOLOGICAL
CONGRESS
22-26 March 2021, Chile

Phycologia
Journal of the International Phycological Society
Volume 60 Supplement
March 2021

Area: PLENARY LECTURE

PHYTOPLANKTON AND THE APOCALYPSE – WHAT TO EXPECT IN A CHANGING WORLD

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Life was much easier when there were only four horsemen of the apocalypse. Today's oceans face a multitude of environmental drivers that affect their ecosystems down to the very foundations, where microbial primary producers govern biogeochemical cycles and food-webs. If we are to understand and predict how the manifold aspects of the climate crisis will impact marine microbial primary producers, questions need to be asked and answered across organismal (individuals to communities) and temporal (short-term to long-term) scales. Experimental evolution can provide crucial conceptual insights into the ways in which short- and long-term responses are linked and how evolution acts in complex environments, but cannot – on its own - yield answers about the ecologically relevant characteristics of individual phenotypes. In order to address the latter and uncover replicable phenotypic patterns, we must also take the organisms' particular biological background into account. This talk explores recent advances in combining the powers of evolutionary and marine biology.

Keywords: Phytoplankton, climate change, evolution

Area: PLENARY LECTURE

SEX CHROMOSOMES AND SEX DETERMINATION IN THE BROWN ALGAE

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Over the last few years, the brown algae have emerged as a highly valuable group to study the evolution of sex chromosomes and reproductive systems because they exhibit a remarkable diversity of sexual traits and because there have been multiple transitions between sexual systems over a relatively short evolutionary time period. The maintenance of a high level of diversity of sexual features in a single, evolutionarily young group is outstanding among the eukaryotes, and points to a complex evolutionary history of the underlying regulatory systems. I will describe how we are using the brown algae to gain novel insights into the mechanisms and evolutionary trajectories of sex determination systems and to reveal the functional and evolutionary interactions between the sex chromosomes and key reproductive and life cycle traits.

Keywords: sex determination, genetics, brown seaweeds

Area: PLENARY LECTURE

WHAT LONG-TERM DATA TELL US ABOUT A SHORT-LIVED FOUNDATION SPECIES

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Foundation species are disproportionately important to the continued maintenance of a community and disturbances that alter their demographic rates have the most consequential impacts on the structure and function of the ecosystems that they define. Unlike other widely recognized foundation species (e.g., trees, sponges, hermatypic corals), the giant kelp *Macrocystis pyrifera* lives only a few years. As a result, decadal-scale observations and experiments involving *M. pyrifera* span multiple generations that experience different environmental conditions. These characteristics make giant kelp an ideal study species because they enable its foundational role to be directly tested rather than asserted. In this talk I report on the results of long-term observations and experiments from giant kelp forests in southern California, USA that capture the demographic, morphological, and functional responses of *M. pyrifera* to variation in the severity and frequency of disturbance and to an extreme marine heatwave. Results highlight giant kelp's high resilience to environmental perturbations, and its importance in structuring the abundance and diversity of understory algae and the overall productivity of the kelp forest community.

Keywords: *Macrocystis pyrifera*, foundation species, long-term

Area: PLENARY LECTURE

STRUCTURE, BIOGENESIS, AND ENGINEERING OF THE EUKARYOTIC CO2-CONCENTRATING ORGANELLE, THE PYRENOID

Moritz Meyer[1], Shan He[1], Elizabeth Freeman Rosenzweig[2], Alan Itakura[2], Xiaobo Li[3], Nicky Atkinson[4], Hui-Ting Chou[3], Tabea Mettler-Altmann[7], Weronika Patena[1], Tobias Wunder[7,11], Doreen Matthies[3], Ursula Goodenough[6], Mark Stitt[7], Benjamin Engel[8], Oliver Mueller-Cajar[11], Zhiheng Yu[3], Alison Smith[9], Howard Griffiths[10], Alistair McCormick[4], Luke Mackinder[5], Martin Jonikas[1]

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Approximately one-third of global carbon-fixation occurs in an overlooked algal organelle called the pyrenoid. The pyrenoid contains the CO$_2$-fixing enzyme Rubisco, and enhances carbon-fixation by supplying Rubisco with a high concentration of CO_2. The molecular structure and biogenesis of this ecologically fundamental organelle have remained enigmatic. By using high-throughput localization of proteins and identification of protein-protein interactions in the model alga *Chlamydomonas reinhardtii*, we increased the number of known pyrenoid components from 6 to over 80, and discovered the existence of three new protein layers in the pyrenoid: a plate-like layer, a mesh layer, and a punctate layer. We discovered that an abundant pyrenoid protein, Essential Pyrenoid Component 1 (EPYC1), works as a molecular glue that binds Rubisco holoenzymes together to form the matrix at the core of the pyrenoid. We then found that a simple mechanism involving a Rubisco-binding motif explains both targeting of proteins to the pyrenoid and the overall architecture of the three pyrenoid sub-compartments. Finally, contrary to longstanding belief that the pyrenoid matrix is a solid structure, we discovered that the matrix behaves as a liquid droplet, which mixes internally, divides by fission, and dissolves and condenses during the cell cycle. Our data provide insights into pyrenoid protein composition, structural organization and biogenesis. Working with our collaborators in the Combining Algal and Plant Photosynthesis project, we aim to transfer algal pyrenoid components into higher plants to enhance carbon fixation and yields in crops.

Financing: U.S. National Science Foundation U.S. National Institutes of Health U.S. Department of Energy HHMI and Simons Foundation

Keywords: CO_2 assimilation, *Chlamydomonas*, cell biology

Area: PLENARY LECTURE

PHYCOLOGY IN SOUTH AMERICA: FROM MONTE VERDE TO CURRENT TRENDS, 14,000 YEARS OF HISTORY

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Monte Verde is an archeological site in southern Chile, where remains of seaweeds have been found in a geological stratum dated at around 14,000 years before the present. Studies indicate that algae were probably used as food and medicine by these early human populations. Today algae remain a diverse and important resource, or sometimes a nuisance, for people living in South America (SA) attracting the attention of scientists. Furthermore, SA has a variety of environments ranging from tropical to temperate (12oN to 55oS), including around 30,000 km of coastline and three oceans, The Caribbean, the Pacific, and the Atlantic, plus high mountains, deserts, and the Amazon forest, among other continental environments that harbor a diversity of algae groups and species, many of which are still unknown. Studies of algae in SA can be divided into three phases: (1) initial studies in the 18th and 19th centuries were carried out mostly by European and North American travelers, such as Martius, Glaziou, and D'Orbigny, that collected samples and took them abroad for taxonomical identification; (2) in the 20th century resident scientists worked mainly describing floras (taxonomy-based research) training new phycologists; (3) beginning in the 1970s, there was a diversification of research fields and an increase in the number of phycologists, which led to the establishment of national phycological associations, in such way that the foundations for Phycology are considered well established in SA, which allowed for more in-depth and integrated research. Future trends in phycological studies in South America will be discussed.

Keywords: Foundations, phycologists, research trends

SYM01: Introducing single-cell omics technologies in phycology

Keynote lecture

ELECTRICAL IMPEDANCE AS AN INDICATOR OF MICROALGAL CELL HEALTH

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Separating specific cell phenotypes from a heterotypic mixture is a critical step in many research projects. Traditional methods usually require a large sample volume and a complex preparation process that may alter cell property during the sorting process. Here we present the use of electrical impedance as an indicator of cell health and for identifying specific microalgal phenotypes. We developed a microfluidic platform for measuring electrical impedance at different frequencies using the bacterium-sized green alga *Picochlorum* SE3. The cells were cultured under different salinity conditions and sampled at four different time points. Our results demonstrate the utility of electrical impedance as an indicator of cell phenotype by providing results that are consistent with known changes in cell size and physiology. Outliers in the cell data distribution are particularly useful because they represent phenotypes that have the ability to maintain size and/or membrane ionic permeability under prolonged salt stress. This suggests that our device can be used to identify and sort desired (e.g., experimentally evolved, mutant) cell phenotypes based on their electrical impedance properties.

Keywords: Microfluidic, electrical impedence, single cell

Keynote lecture

ZOOMING IN ON HOST-VIRUS DYNAMICS OF A BLOOMING ALGAE ONE CELL AT A TIME

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Blooms of the microalga *Emiliania huxleyi* have been associated with global carbon cycle and biological climate forcing from local to geological time scales. *E. huxleyi* blooms are terminated by a specific giant virus imposing a top-down control by infecting and lysing the host cell. Recently, these algae-virus interactions have been proposed to represent a new entity, the 'virocell', where an infected cell represents a metabolic state that is different from either the non-infected cell, or the virus. Virocells pose a potential impact on the structure and evolution of microbial populations, and possibly influence global biogeochemical processes. However, we know little about their prevalence, metabolic function, or cell fate. Here, striving to elucidate the virocell entity, we use single-cell approaches to probe algae-virus interactions with unprecedented resolution. We show heterogeneity in the progression of viral infection, probe early host response for potential resistance markers, and quantify virocells in natural populations.

Keywords: Virus, *Emiliania*, blooms

Oral presentation

AUXIN FUNCTION IN THE BROWN ALGA *DICTYOTA DICHOTOMA*: A CASE FOR A DEEP ORIGIN OF AUXIN TRANSPORT?

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The extent to which algal phytohormones are similar to those of land plants is unclear. Auxin controls body plan patterning in land plants and has been proposed to play a similar role in the development of brown algae (Phaeophyta) despite their distant evolutionary relationship with land plants. In this study, we used *Dictyota dichotoma* as a model system to show that auxin plays a role during the apical-basal patterning of the embryo of brown algae. Indole-3-acetic acid was detectable in *D. dichotoma* germlings and mature tissue. Like in mosses, the application of exogenous auxins causes multiple ectopic rhizoids to form. The effect was strongest at lower pH and when variable extrinsic informational cues were applied. 2-[4-(diethylamino)-2-hydroxybenzoyl] benzoic acid, an inhibitor of the ABC-B/multidrug resistance/P-glycoprotein subfamily of transporters in land plants, affected rhizoid formation by increasing rhizoid branching and inducing ectopic rhizoids.

In order to assess whether this auxin function evolved from scratch at the advent of multicellularity in both brown and green algae, an *in silico* survey of the known auxin biosynthesis, response and transport genes from land plants was conducted. This analysis suggests that a diverse range of biosynthesis genes together with transport genes such as PIN-LIKES from land plants have homologues outside the green lineage. The presence of putative auxin transporters in these clades, together with recent reports from diverse unicellular clades, suggests that auxin function predates the divergence between the green and the brown lineage and the evolution of multicellularity.

Financing: FWO (1150111N), FP7 (227799-ASSEMBLE) to KAB; VINNOVA, Swedish Research Council to KL; EMBRC Belgium, FWO (GOH3817N), BOFGOA2017000603 to ODC

Keywords: Brown algae, auxin, development

Oral presentation

SEMI-QUANTITATIVE TARGETED GC-MS PROFILING SUPPORTS A LATE SIDE-CHAIN REDUCTASE CYCLOARTENOL-TO-CHOLESTEROL BIOSYNTHESIS PATHWAY IN SOME BROWN ALGAE

Jean Girard[1], Goulven Lanneau[1,2], Ludovic Delage[1], Cédric Leroux[2], Arnaud Belcour[3], Jeanne Got[3], Jonas Collén[1], Catherine Boyen[1], Anne Siegel[3], Simon Dittami[1], Catherine Leblanc[1], Gabriel Markov[1]

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Sterols are biologically important molecules as membrane fluidity regulators and precursors of signalling molecules, either endogenous or involved in biotic interactions. There is currently no model of their biosynthesis pathways in brown algae. Here, we take benefit of the availability of genome data and new GC-MS sterol profiling using our database of internal standards to build such a model. We expand the set of observed sterols in ten species of red, brown and green macroalgae and integrate this with genomic data, giving metabolic support for some reaction being conserved despite the loss of canonical eukaryotic enzymes, like the sterol side-chain reductase. Our findings are consistent with metabolic pathway drift through enzymatic replacement, and show that cholesterol synthesis from cycloartenol may be a widespread, though variable pathway among chlorophyllian eukaryotes. Among the factors contributing to this variability, one could be the recruitment of cholesterol biosynthetic intermediates to make signaling molecules, such as the mozukulins that were found in some brown algae belonging to Ectocarpales, for which we also provide a first biosynthetic model. Our results demonstrate that integrative approaches can already be used to infer experimentally testable models that will be useful to further investigate the biological roles of those new algal pathways.

Financing: French Government: IDEALG (ANR-10-BTBR -04); Région Bretagne: « SAD 2016 - METALG (9673)

Keywords: Brown algae, sterols, metabolic pathway evolution

E-Poster

GAMETOGENESIS IN THE GREEN SEAWEED *ULVA MUTABILIS* COINCIDES WITH MASSIVE TRANSCRIPTIONAL RESTRUCTURING

Xiaojie Liu[1], Jonas Blomme[1,2,3], Kenny Bogaert[1], Olivier De Clerck[1]

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Unlike land plants, the genetic basis involved in the onset of reproduction, gametes formation, fusion and meiosis remain elusive in most of algae. Here, we characterized the gametogenesis in the green seaweed *Ulva* at the molecular level. We performed a series of RNA-sequencing experiments and compared transcript profiles on different timepoints. Transcriptome analysis showed that nearly half of the predicted genes in the genome are differentially expressed during the gametogenesis process. The transcriptome dynamics related to the different stages of gametogenesis were deciphered in detail. In addition, we identified several transcription factors that possibly play a key role in the early gametogenesis of Ulva given the function of their homologs in higher plants and microalgae. The detailed expression pattern of a particular RWP-RK domain containing a transcription factor further suggests a key role during *Ulva* gametogenesis. This study provides the first transcriptional framework to study the molecular mechanisms of gametes formation in *Ulva* as a model.
Financing: China Scholarship Council and Ghent University BOF Special Research Fund

Keywords: *Ulva* gametogenesis, transcriptome, RWP-RK

SYM02: Macroalgal bloom: A global concern

Keynote lecture

GREEN MACROALGAL BLOOMS: A GLOBAL PROBLEM WITH GLOBAL IMPACTS

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Blooms of green macroalgae (seaweeds) occur in coastal systems worldwide, and they frequently cause significant and severe environmental and economic impacts to local as well as global communities. In the northeastern United States, an increase in green macroalgal bloom abundance and duration has been documented over the past several decades, and blooms have negatively impacted fisheries, commerce, and tourism. In this presentation, I give an overview of the current status of knowledge of green blooms, focusing on this region. I then compare and contrast these bloom dynamics with blooms of green algae from different ecosystems worldwide, all framed within the broader context of global climate change. In my lab's research, we have found significant impacts of increased water temperature, CO2, and nutrients on the survival, growth rates, and palatability of bloom forming green algae in the genus *Ulva* (sea lettuce). Our results indicate that higher growth rates in some green macroalgal species, coupled with decreased consumption from herbivores, could enhance macroalgal bloom formation and abundance in coastal ecosystems.
Financing: US National Science Foundation, US EPA, and RI Department of Environmental Management

Keywords: *Ulva*, algal bloom, green tides

Keynote lecture

IMPACTS OF *SARGASSUM* BROWN TIDES ON SEAGRASS MEADOWS IN THE MEXICAN CARIBBEAN

Brigitta Ine van Tussenbroek

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Macroalgal blooms are becoming more frequent as anthropization of the planet increases. The Mexican Caribbean coast experienced the first massive influx of pelagic *Sargassum* species (*S. fluitans and S. natans*) from mid-2014 to the end of 2015 and massive influxes have been recurrent since. These amassed algae on the coasts resulted in the accumulation of decaying organic material on the beaches, turning the transparent coastal waters into a dark brown color. We call this phenomenon Sargasso Brown Tide (SBT). The effects of SBT on four seagrass meadows near the coast included reduced light, oxygen (hypoxia or anoxia) and pH; in addition, the temperature and concentration of ammonia increased. Seagrass meadows near the coast dominated by *Thalassia testudinum* were replaced by a community dominated by calcareous rhizophytic algae and drifting algae and/or epiphytes, resulting in a loss of 61.6 to 9.5% belowground biomass. Recovery of affected seagrass meadows is likely to take decades. The influxes were repeated once again in 2018 and 2019, and it is estimated that in 2018 *Sargassum* contributed 40.3 Tons of N, and 3.44 Tons of P for each km of coast of the Mexican Caribbean; this was approximately 20 times greater than the usual contributions to the sea through the discharge of groundwater. If massive influxes are recurrent and adequate management actions are not taken, the coastal ecosystems will change permanently, resulting in the loss of ecosystem services provided by offshore seagrass meadows, such as facilitating biodiversity, increasing water transparency and stabilizing the beach.

Keywords: Bloom, *Sargassum*, Caribbean Sea

Oral presentation

BIOMASS COMPOSITION OF THE GOLDEN TIDES PELAGIC SEAWEEDS *SARGASSUM FLUITANS* AND *S. NATANS* TO INFORM VALORISATION PATHWAYS

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Massive strandings of the pelagic brown algae *Sargassum* have occurred in the Caribbean, and to a lesser extent in western Africa, almost every year since 2011. These events have major environmental, health, and economic impacts in the affected countries. Once on the shore, *Sargassum* is mechanically harvested and disposed of in landfills. Existing commercial applications of other brown algae indicate that the pelagic *Sargassum* could constitute a valuable feedstock for potential valorization. However, limited data on the composition of this Sargassum biomass is available to inform on possible application through pyrolysis or enzymatic fractionation of this feedstock. To fill this gap, we have conducted a detailed comparative biochemical and elemental analysis of the three pelagic Sargassum morphotypes identified so far as forming Atlantic blooms: *Sargassum natans* I and VIII, and S. *fluitans* III. Our results showed that morphotypes accumulated different quantities of metals and metalloids, contained variable amounts of phenolics and non-cellulosic polysaccharides, and released limited quantities of sugars after individual enzyme saccharification treatments. No differences in the content and composition of the cell wall polysaccharide alginate were identified among the three *Sargassum* morphotypes. Additional analyses are underway to extend the scope of this compositional analysis, and to assess the influence of storage conditions on this feedstock. These data will inform routes for future valorization of pelagic *Sargassum* biomass.

Financing: Research England's Quality Research Global Challenges Research Fund funding awarded to the University of York. Economic and Social Research Council

Keywords: Algal bloom, biomass valorization, biochemical composition

Oral presentation

CRYPTIC INTRODUCTION AND INVASION OF *RUGULOPTERYX OKAMURAE* (DICTYOTALES, OCHROPHYTA) AT THE STRAIT OF GIBRALTAR: REAL THREAT TO THE MEDITERRANEAN ECOSYSTEMS

María Altamirano[1], Julio De la Rosa[2], Hiroshi Kawai[3], Takeaki Hanyuda[3], Raquel Carmona[4], Marianela Zanolla[5], Antonio Román Muñoz[6]

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A new exotic seaweed with invasive behaviour was detected in the Strait of Gibraltar in 2015. Tentatively identified as *Rugulopteryx okamurae* (Dictyotales, Ochrophyta), its correct identification became difficult due to its morphological similarity with other native Dictyotales. Since then, the species has been expanding its distribution Eastward in the Mediterranean Sea. The aim of the present work is to provide morphological and genetic identification, information on ecological performance and economic impacts, together with the updated distribution to be used to perform species distribution models as a tool to predict its potential range. Results of genetic analyses confirm that sequenced samples of this new invader in the Alboran Sea correspond to *R. okamurae*. Furthermore, the taxonomical identity is supported by morphology. Uncertainty remains regarding the life history of the species in the invaded area, as only vegetative propagules and asexual monospores have been observed. A strong ecological impact is observed on macroalgal assemblages and *Posidonia oceanica* meadow communities, due to a wide homogenization by the invader. Economic impacts have been estimated to be 0.8x106 € in nine months in the fishery industry due to reduced captures, and 0,.4x106 € in the same period due to removal of drifted material on the beaches. Our findings show that the Western Mediterranean is a favorable area for this invasive species. The models appear to be well calibrated and the risk of invasion is high along the Andalusian coast, especially in the coast of Almeria in areas of high ecological value.

Financing: Fundación Biodiversidad (MITECO) (Spain) Universidad de Málaga (Spain)Instituto de Estudios Ceutíes (Spain)

Keywords: *Rugulopteryx*, invasive species, distribution model

Oral presentation

SUBSTRATA USAGE BY THE INVASIVE SEAWEED *CAULERPA RACEMOSA* (CAULERPALES, CHLOROPHYTA) IN GALAPAGOS NATIONAL PARK: IMPLICATIONS FOR ITS MANAGEMENT

Amparo Cid Iturbe[1], Inti Keith[2], Raquel Carmona[3], María Altamirano[1]

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The Galapagos archipelago rises thousand kilometers from the continent, allowing its ecosystems to evolve in a unique way, being its main tourism attraction and economical engine. Nowadays, marine ecosystems of Galapagos are threatened by several invasive species, among them the green seaweed *Caulerpa racemosa*, with a markedly invasive character and found on several islands in the archipelago. Due to this, management of this species is of much concern for Galapagos National Park. The aim of the present work was to compare the usage of hard and soft substrata by *C. racemosa* on a temporal base during winter 2019 at Tortuga-Bay (Santa Cruz Island), in order to provide valuable scientific information to improve management approaches of the species. Samples of *C. racemosa* were collected every fortnight from a population in the upper sublittoral on soft and rocky substrate. For each sample, biomass of fronds and stolons, number of fronds and growth apexes, total stolon length, frond average length and frequency of frond size classes were estimated. Results showed that the studied variables did not present significant differences along the sampling period, but they did with respect to the substratum. Total biomass remained constant during the study (44.5 ± 17.7 g/m2); However, the rocky substratum favoured the development of stolons and therefore, the development of fronds. Special attention should be paid to populations of *C. racemosa* on rocky substratum, as they present greater potential for dispersion than the soft substratum, by producing a greater number of stolons.

Financing: Department of Botany and Plant Physiology, Faculty of Sciences, University of Málaga

Keywords: *Caulerpa racemosa*, marine invasive species, Galápagos National Park

Oral presentation

COMPOSITION AND ABUNDANCE OF PELAGIC *SARGASSUM* LANDING ONTO SOUTH FLORIDA SHORELINES

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Historically observed with low abundance across North Atlantic shorelines, pelagic *Sargassum* increased dramatically in 2011 with landings encompassing the Caribbean, North America, South America and West Africa due to the formation of a new source, The Great Atlantic *Sargassum* Belt. Patterns in wind and currents have facilitated landings which are variable in its composition of species and morphotypes. During surveys conducted from September 2018 to July 2020 at Dania Beach, Florida, USA, four 1.0 m2 quadrats along a 1.0 km transect were collected at low tide with a minimum distance of 250 m separating each. Collections were separated at the species/morphotype level, dried for 48 hours, and weighed. An average biomass of 310g/m2 was observed with the highest biomass (1775 g/m2) reported in April 2019. Due to large variations within biomass collections, there were no significant differences annually (p = 0.526). When separated at the morphotype level, significant differences between the composition of pelagic *Sargassum* (p < 0.001) were observed with *S. natans I* most abundant and S. *natans VIII* sparse compared to other Caribbean islands. High abundance of *S. natans I* and *S. fluitans III* with low observations of *S. natans VIII*, which is typically associated with The Great Atlantic *Sargassum* Belt, support a working hypothesis that Florida shorelines may be affected by multiple sources of pelagic *Sargassum*. Monitoring shorelines for species composition of pelagic *Sargassum* can contribute to further understanding its oceanic movement patterns, while monitoring its abundance will facilitate the development of managerial strategies of shorelines.

Keywords: *Sargassum*, biomass, morphotypes

Oral presentation

TRACE METAL CONCENTRATIONS OF PELAGIC *SARGASSUM* IN SOUTH FLORIDA

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South Florida landings of pelagic *Sargassum* have increased since 2011. Large patches inundate shorelines posing environmental risks for wildlife, including endangered sea turtles, the economy, and human health. *Sargassum* is known for its affinity to absorb heavy metals and subsequent leaching into soils and groundwaters. To assess trace metal accumulation, three turtle nesting beaches, impacted by *Sargassum*, were surveyed in south Florida from 2019 to 2020. Trace metals were quantified in tissues of *S. natans I, S. natans VIII*, and *S. fluitans III* using ICP-MS. Sixteen metals, including toxic elements such as Arsenic, Cadmium and Mercury were detected. Variation among morphotypes were observed, no significant differences were found except for Cobalt (p = 0.005) and Vanadium (p = 0.024). It was notable that 66.6% of Vanadium samples were below the Method of Detection (MDL). Samples for Beryllium and Chromium were 100% below the MDL, Mercury 84.6% < MDL, Lead 86.6% < MDL, and Silver was not detected in 60% of samples. Arsenic was the highest concentrated element, found in 100% of samples, ranging from 58 - 119 ppm (n=15/average 79 ppm). Arsenic levels exceed the maximum threshold limits set by the FDA and toxicity levels described in medical literature. High Arsenic and Vanadium levels have been associated with embryonic risk for sea turtles and other reptiles. An average of 200 sea turtle nests are laid annually at just one of these locations, a potential 2000 eggs at risk. Further investigation is needed to evaluate the risks to wildlife and humans.

Financing: National Save The Sea Turtle Foundation

Keywords: *Sargassum*, sea turtle, Florida

Oral presentation

DRIFT MACROALGAL BLOOMS IN A HIGH HYDRODYNAMIC ESTUARINE SYSTEM IN SOUTHERN BRAZIL

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Drift macroalgal blooms have been increasing in frequency and magnitude in the Patos Lagoon estuary (PLE, southern Brazil), with potential impacts on the functioning of such highly hydrodynamic subtropical ecosystem. Through monitoring and field experiments, we investigated the drivers of the onset and magnitude of blooms, and their impacts on nutrient cycling, sediment biogeochemistry and seagrasses meadows in estuarine shallow areas. The macroalgal blooms in the PLE were comparable to those found in temperate eutrophic lagoons, being triggered by interactive effects of hydrological (i.e., water residence times) and water physico-chemical parameters (i.e., water nutrient concentration, salinity). Under favourable conditions for growth, wind-driven waves and currents controlled algal advection, thereby setting the magnitude and persistence of the blooms. Large algal accumulations represented a substantial nutrient stock within the system but no feedbacks between biomass accumulation and sediment nutrient regeneration were detected after blooms die-offs. Indeed, field experiments showed that algal mats advection can alleviate deleterious biogeochemical conditions in the sediment-water interface. Nonetheless, transitory algal depositions promoted significant reductions in seagrasses biomass and associated macrofauna, highlighting an ongoing phase-shift in the local submerged aquatic vegetation. We conclude that, although harmful drift macroalgal blooms are a global phenomenon, their impacts and the mechanisms through which macroalgae impair local biogeochemical cycles and seagrasses communities may vary according to the environmental context. Further studies are necessary to determine the effects of blooms on the long-term balance of nutrients as well as the underlying mechanisms of drift macroalgae-seagrass-macrofauna interactions in high hydrodynamic systems.

Financing: This work was funded by the Brazilian Long Term Ecological Research through CNPq/Ministry of Science and Technology, CAPES and FAPERGS.

Keywords: Phase-shifts, estuarine ecosystem functioning, blooms

E-Poster

SEASONAL CHANGES IN ARSENIC, HEAVY METALS AND TRACE ELEMENT CONCENTRATION IN PELAGIC SPECIES OF *SARGASSUM* FROM THE MEXICAN CARIBBEAN

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The frequency and intensity of seaweed massive influx and arrival phenomenon has been increasing globally. Along the Mexican Caribbean coast three species and morphotypes of the brown algal of genus *Sargassum* have been identified as dominant during these events. Massive landings of *Sargassum* have had many negative effects on the public and touristic sectors. There is a need to generate basic information of the species present to be incorporated into future sustainable strategies for the use of *Sargassum* biomass. In this study, concentrations of arsenic (As), cadmium (Cd) and lead (Pb), copper (Cu), iron (Fe) and zinc (Zn) were assessed for pelagic *Sargassum* species collected along the Mexican Caribbean coast over an annual cycle. Quantitative analysis of these elements was performed using Atomic Absorption Spectrophotometry. The presence of As was detected in 100% of the samples, all species and morphotypes (*S. fluitans III, S. natans I* and *S. natans VIII*). The maximum concentrations obtained were: As 255.20 mg kg-1, Cd 3.11 mg kg-1, Pb 20.70 mg kg-1, Cu 6.44 mg kg-1, Fe 78.27 mg kg-1 and 62.84 mg kg-1 for Zn. Statistically significant differences ($p < 0.05$) were found between species for As, Pb, Cu and Fe, whereas for Cd and Zn no significant differences ($p > 0.05$) were found. The morphotype currently named as *S. natans VIII* showed the highest concentration of As (102.74 mg kg-1). Statistically significant differences ($p < 0.05$) were found between seasons (warm and dry, rainy and winter storm) for all elements. The rainy season showed the highest concentration of As (97.68 mg kg-1).

Financing: PN215-01-575: Valoración de la Biomasa de arribazón del género *Sargassum* para su uso y aprovechamiento.

Keywords: Heavy metal adsorption, *Sargassum*, blooms

E-Poster

TEMPORAL VARIABILITY OF MORPHOLOGY AND REPRODUCTIVE YIELD OF THE INVASIVE SEAWEED *RUGULOPTERYX OKAMURAE* (DICTYOTALES, OCHROPHYTA) AT THE STRAIT OF GIBRALTAR

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When native and exotic species are very similar in morphology, and only the expert eyes can distinguish them by precise anatomical characters, this represents a handicap in the management of those species which become invasive. This is the case of *Rugulopteryx okamurae* (Dictyotales, Ochrophyta), a Pacific seaweed, closely related to *Dictyota*, at the Strait of Gibraltar, where the massive proliferation of *R. okamurae* results in important ecological and economic impacts. One of the aims of the present work was to test the null hypothesis of a temporally constant morphology of *R. okamurae* in the introduced area. Furthermore, and in order to improve management strategies for the species, temporal variation of reproduction has been also studied. Experimental design consisted in monthly sampling of thirty thalli of *R. okamurae* at an upper subtidal population at

Punta Carnero (Cádiz, Spain) between December 2019 and October 2020, followed by analysis of vegetative and reproductive characters related to habit and anatomy of the species. Results showed that morphology of *R. okamurae* at the introduced region significantly differed with the time of the year, apparently exhibiting distinct morphotypes. Moreover, a window of increased reproductive yield has been identified during summer. These findings contribute to scientific support for the management of the species, helping in the correct identification of the species, avoiding confusion with native *Dictyota* species, as well as pointing to the high reproduction windows as the period when reinforce control actions for the species should be performed.

Financing: Department of Botany and plant physiology, University of Málaga, Science Faculty, Campus de Teatinos s/n, E-29080 Málaga, Spain

Keywords: *Rugulopteryx*, invasive species, bloom

E-Poster

STRANDED *SARGASSUM* IN THE MEXICAN CARIBBEAN: EPIBIONT HYDROIDS

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Since 2011 unusual pelagic *Sargassum* biomass influxes have been stranded on the Eastern Caribbean Sea shores and the Gulf of Mexico. Hydrozoan polyps are known as epibionts of *Sargassum*. Some hydrozoan species are capable invaders, and the toxins contained in the hydrozoan nematocyst may produce stings and dermal lesions. Thus, to characterize the epibiont hydroid fauna and their prevalence on beachcast *Sargassum* in the Mexican Caribbean Coast, thalli of fresh pelagic *Sargassum* were collected at Puerto Morelos, Mexico. The occurrence and percentage cover of hydroids on *Sargassum* was studied from April 2018 to March 2019. Three pelagic *Sargassum* species and morphotypes were analyzed: *Sargassum fluitans III, S. natans I*, and *S. natans VIII*, as well as a benthic species, *S. polyceratium var. ovatum*. Fourteen taxa of hydroids were observed; four species were recorded on *S. fluitans III*, five on *S. natans I*, five on *S. natans VIII*, and two exclusively on *S.polyceratium var. ovatum*. The dominant species were *Clytia noliformis* in S. fluitans III and *S. natans I* and *Aglaophenia latecarinata* on *S. natans VIII*. Colony parts of some species had an intact coenosarc, indicating that hydroids growing on pelagic *Sargassum* may potentially attach to local substrata. Also, nematocysts were observed, indicating that the stinging capacity was maintained.

Financing: CONACyT projects PN2015-01-575 and A1-S-26700 and Meduzosoa México (https://meduzosoamexico.com.mx)

Keywords: Caribbean Sea, Medusozoa, *Sargassum*

E-Poster

COMPARATIVE SPATIOTEMPORAL ANALYSIS OF ACCUMULATED PELAGIC *SARGASSUM* LANDINGS USING COMMUNITY SCIENCE DATA

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The regional impact of pelagic *Sargassum* landings that have occurred periodically since 2011 requires large-scale visualization and monitoring efforts to forecast their arrival. While efforts to monitor *Sargassum* were emphasized on satellite imagery, these efforts were limited in nearshore areas where the resolution is less refined. Community science initiatives can not only compensate the shortcomings of satellite imagery, but can also enhance the resolution of the imagery by ground-truthing the models at various sites. This study aims to detect spatiotemporal variation in *Sargassum* accumulation levels and species composition using currently available data from the "Sargassum Watch" Community Science Initiative. Data collection started in 2019 via collaborations with volunteer groups using the Epicollect5 app. Spatiotemporal variability was compared between Broward County of south Florida and south Grand Cayman. Accumulation photos were classified on a scale from 0-5, and species photos were identified to morphotype level. Inter-annual comparisons showed 2019 having higher accumulation levels in earlier months (April-May) than similar months in 2020 ($p < 0.001$). Significant differences were found between geographic locations during the 2020 season ($p < 0.001$), with Grand Cayman showing higher accumulation levels than Broward in June, though accumulations did not differ in later months. *Sargassum fluitans III* was the most commonly found macroalgae among the influxes, followed by *S. natans I* and *S. natans VIII*. This study showcases the potential of community science initiatives as a robust method of data collection to monitor *Sargassum* in the Caribbean.

Financing: Department of Biology, Institute of Environment, Florida International University, Miami, Florida, USA

Keywords: *Sargassum*, bloom, citizen science

E-Poster

SEASONAL VARIATION OF PHENOLIC COMPOUNDS AND ANTIOXIDANT ACTIVITY IN SPECIES OF SHORE CAST PELAGIC *SARGASSUM*

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The amount of phenolic compounds present in marine organisms varies between species and even organism level. In addition, this variation has been recorded due to environmental effects (salinity, temperature, pH, desiccation, nitrogen availability, solar radiation, and artificial UV radiation) that vary seasonally. The extraction of phenolic compounds present in the algae collected in Puerto Morelos Quintana Roo, Mexico from May 2018 to December 2019 was carried out. The antioxidant activity was analyzed by three different methods (DPPH, ABTS, FRAP). In our study, we found that there is a strong relationship between seasonality and the production of phenolic compounds in all species present (*Sargassum natans, Sargassum fluitans, Sargassum sp*.). The production of phenolic compounds increases in the months with the highest water temperature (June-August) reaching a maximum in the month of August in the 3 species. In addition, there is a tendency of increase of these compounds with the increase of solar radiation. Significant differences were found with $p \leq 0.05$ between the months with the lowest and highest temperatures. The maximum elimination values using the DPPH* method was found in the summer months, reaching 62% in the month of August, while using the ABTS and FRAP methods this relationship was not observed, but a good antioxidant capacity was maintained during the analysis time, reaching values up to 88.88%.

Financing: CONACYT for the Ph.D. scholarship N° 776098 and to the PN-CONACYT PN2015-01-575 project

Keywords: *Sargassum*, phenolic compounds, antioxidant activity

E-Poster

METAL CONCENTRATIONS (FE, CU, MN, ZN) IN MACROALGAL SPECIES FROM A COASTAL LAGOON IN THE GULF OF CALIFORNIA

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Metal concentrations in coastal regions are a subject of study since they are important ecosystems where many anthropogenic activities tend to develop, most of them influencing environmental concentrations of metals that increase in quantity. Macroalgae are suitable indicators of metal concentrations in the water column, therefore, they have been used in biomonitoring studies. Tissue samples of three macroalgal species (*Spyridia filamentosa, Padina mexicana*, and *Ulva ohnoi*) were collected from three sites at La Paz Bay, during three contrasting seasons in 2013, 2014 and 2015. Sampling was carried out during the dry, rainy, and cold seasons. Tissue concentrations of iron (Fe), manganese (Mn), copper (Cu) and zinc (Zn) were determined by atomic absorption spectrophotometry. MANOVA analyses were performed. During this study period P. mexicana showed the highest Fe, Mn and Cu concentrations, Zn concentrations were lower in *Ulva ohnoi* compared to *P. mexicana* and *S. filamentosa*. At San Juan de la Costa, Fe and Mn showed the highest metal concentrations while Zn and Cu were higher at Casa del Marino. Metal concentrations varied depending on the species, site, season and year. Both *P. mexicana* and *S. filamentosa* proved to be good indicators of metal concentrations, highlighting that depending on the site metal concentrations varied, such as San Juan de la Costa a site with influence of mining activities.

Financing: CONACYT-CB154415, CIBNOR grant PC 0.5, and SEP-CONACyT grant A1-S-26700. Project SIP20201260 by Instituto Politécnico Nacional, EDI and COFAA scholarships.

Keywords: Metals, macroalgae, biomonitoring

E-Poster

A NEW KID ON THE BLOCK: THE EXOTIC SPECIES *DICTYOTA CYANOLOMA* (DICTYOTALES) IS SPREADING INTO NATURAL HABITATS OF MEDITERRANEAN SEA

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There are six species of the genus *Dictyota* in the Mediterranean Sea. One of them is *D. cyanoloma*, originally from Australia. Its presence was reported in 2010, although the first record of the species in Spain dates back to the early 90's, identified as *D. ciliolata*. Since then, records of *D. cyanoloma* have mostly been associated with artificial port infrastructures. In this work, we present an updated distribution of this species in the Alboran Sea (Western Mediterranean), together with a morpho-anatomical, ecological and photosynthetic performance analyses

of an established population in natural habitats in Granada (Southern Spain). The vegetative morpho-anatomical characters of the thallus concur with those of the description of the species, highlighting its strikingly iridescent blue margins. The species was found along Andalusian coasts from Cádiz to Almería, and in Ceuta and Chafarinas Islands (Northern Africa). The population in Granada exhibited a coverage between 50-80%, with a patchy distribution, together with native macroalgal species and the invasive *Rugulopteryx okamurae*. Thalli showed vegetative structures (propagules), and abundant reproductive structures, asexual (monospores) and sexual (tetraspores and antheridia). It appeared to have "shade-plant" photosynthetic characteristics, although no photoinhibition was observed within the irradiance range assayed. Results of this work focus attention on an exotic species that seems to have been introduced recently in natural environments after a period confined to port environments. From a preventive perspective for its control, both environments should be monitored, due to the increasing number of recent records and its presence in marine protected areas.

Financing: Fundación Biodiversidad, Instituto Estudios Ceutíes, Universidad de Granada

Keywords: Mediterranean Sea, *Dictyota cyanoloma*, invasive species

E-Poster

PELAGIC *SARGASSUM* TISSUE NUTRIENT CONTENT ANALYSIS AND ITS CONTRIBUTION TO SOUTH FLORIDA SHORELINES

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Within the last decade an increase of pelagic *Sargassum* blooms has resulted in nutrient enrichment of coastal ecosystems. Quantifying the nutrient contribution of periodic influxes of pelagic Sargassum on shorelines is important to understand the allochthonous sources of pollution and its potential impact in coastal systems. From September 2018 to July 2019 samples of pelagic *Sargassum* were collected at study sites Bill Baggs, Crandon Park, and Dania Beach in South Florida, USA. Three replicates of healthy *Sargassum* per species/morphotype (*S. natans I, S. natans VIII* and *S. fluitans III*) were collected from the water and cleaned of epiphytes, dried for 48hr at 60°C, and ground. A CHN analyzer was used to estimate Carbon (C) and Nitrogen (N), and a dry-oxidation acid hydrolysis extraction and colorimetric analysis for Phosphorus (P). N and P tissue content were low and limiting compared with average values for macrophytes, while C values were high. No significant differences between the three species/morphotypes CNP concentrations and their C:N, C:P and N:P ratios were found. P and N between Bill Bags and Crandon Parks, and between Crandon Park and Dania Beach were similar, but different between Bill Bags and Dania Beach. C was different across all sites. While tissue nutrient concentration was low for this study, the large biomass quantities landing seasonally causes nutrient enrichment. A proper and consistent management strategy to collect the excess of Sargassum from beaches will reduce significantly the impact of this bloom.

Financing: National Save the Sea Turtle Foundation

Keywords: *Sargassum*, nutrients, South Florida

E-Poster

EFFECTS OF TEMPERATURE AND IRRADIANCE ON GROWTH, VEGETATIVE PROPAGATION AND PHOTOSYNTHETIC ACTIVITY OF THE INVASIVE SEAWEED *RUGULOPTERYX OKAMURAE* (DICTYOTALES, OCHROPHYTA)

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The invasive brown algae *Rugulopteryx okamurae* (Dictyotales, Ochrophyta) recently forms important blooms in southern Spain, affecting biodiversity, fishing industry and tourism. For this reason, it is essential to identify the factors that determine the high invasiveness. In this context, the objective of this study focuses on determining the effect of temperature and irradiance on growth, vegetative propagation and photosynthetic activity of *R. okamurae*. Apical and inter-dichotomous fragments of thallus were cultivated under different temperatures (14 and 22 °C) and irradiance (35 and 70 µmol photons m-2 s-1) under controlled laboratory conditions. The effects of these treatments were studied in the relative growth rate, propagules proliferation and the photosynthetic activity expressed as fluorescence of chlorophyll a. Results show that the growth capacity of the thallus depends on the presence or not of the apical cells in the thallus, and that the presence of these, determines the potential of the thallus for vegetative propagation. Moreover, it has been observed that conditions of low temperature and irradiance favour the propagation capacity of the species, as well as its photosynthetic activity. These results are of great interest to understand the invasive behaviour of the species, since they allow us to identify, on the one hand, the breakdown of thallus as a propagation mechanism of the species that favours the recruitment of new clone individuals, and, on the other hand, to determine that this capacity is active in the annual thermal range of the invaded region.

Financing: Instituto de Estudios Ceutíes, Fundación Biodiversidad (MITECO), International Phycological Society

Keywords: Growth rate, *Rugulopteryx*, blooms

E-Poster

TEMPORAL VARIABILITY OF THE PHOTOSYNTHETIC ACTIVITY OF THE INVASIVE SEAWEED *RUGULOPTERYX OKAMURAE* (DICTYOTACEAE, OCHROPHYTA) IN THE STRAIT OF GIBRALTAR

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Rugulopteryx okamurae (Dictyotaceae, Ochrophyta) is a seaweed native from the Pacific Ocean, that since recently exhibits strong invasive behaviour in the Strait of Gibraltar. In the invaded area, this species is present throughout the year, colonizing hard substrata with a *wide* bathymetric range (less than 1 m to 50 m). This suggests a high phenotypic plasticity of the species related to photosynthetic activity. However, many biological aspects of the species are still unknown, such as the temporal variability in relation to the main environmental factors. Therefore, the objective of the present study is to analyze the photosynthetic performance of a population of *R. okamurae* in the introduced area during several months and its possible relationship with local temperature and solar radiation. Photosynthesis–irradiance curves of algal samples collected monthly from November 2019 to March 2020 were analyzed to estimate the photosynthetic parameters (FNmáx, α, Ic, Ik). Furthermore, photosynthetic pigment content (chlorophylls and carotenoids) was determined. Results showed that *R. okamurae* presented an increase of photosynthetic activity with higher temperatures, but it was not related to solar radiation during the sampling period. On the other hand, no clear pattern of change in the concentration of photosynthetic pigments was found. In addition, *R. okamurae* exhibited a photosynthetic activity higher than native species from the invaded area. These results may explain the high presence of the species during the months studied and its photosynthetic plasticity as a common character of the algal invasion process.

Keywords: Photosynthesis, *Rugulopteryx*, invasive species

SYM03: Seaweed aquaculture: from cultivation to marine agronomy

Keynote lecture

FROM "TACIT KNOWLEDGE" TO "FORMAL KNOWLEDGE" OF WAKAME (*UNDARIA PINNATIFIDA*) CULTIVATION IN THE SANRIKU COAST OF HONSHU, JAPAN

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The Sanriku coast is the main area for cultivation of wakame (*Undaria pinnatifida*) in Japan. Since the 1950s, the cultivation techniques and processing methods have been established by assimilation of experiments by local fishermen. However, recently the effects of climate change have damaged production, particularly with regard to poor growth of sporelings and withering of juvenile sporophytes, so that it is difficult to maintain production by conventional techniques alone. In addition, the number of fishermen in the industry has halved in comparison with 15 years ago, so future productivity will need to be more intensive than at present. Therefore, we are encouraging collaboration between fishermen and researchers in order to develop the wakame industry, shifting the focus from "tacit knowledge" to "formal knowledge". In this talk, I shall introduce the following aspects of our recent research on wakame. 1) Sporeling production: The optimum growth conditions for gametophytes and juvenile sporophytes were revealed by Response Surface Methodology to develop the production base. 2) Anti-withering: To reduce the risk of withering during the early stages of cultivation, we investigated the effects of water depth adjustment on juvenile sporophytes. 3) Cultivation density: Verification of fishermen's knowledge to maximize productivity. 4) pH: Monitoring the relationship between pH of wakame and seawater temperature to maintain the color of wakame products.

Keywords: Cultivation, wakame, *Undaria pinnatifida*

Keynote lecture

EXTRACTS OF SEAWEEDS (BIOSTIMULANTS/PLANT DEFENCE AGENTS) AND THEIR SIGNIFICANCE IN PHYCONOMY

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The global biostimulant market in 2016 was calculated at EUR 1.45 billion (USD 1.54 billion @0.94, 2016 rate) and was expected to increase collectively by 10.5% (CAGR) to EUR 2.66 billion (USD 3.2 billion @0.82, 2020 rate) by 2022. These are big, big numbers, very big, big numbers. The data presented here look at major groups of biostimulants (i.e. seaweed extracts, humic substances, vitamins and amino acids, microbial amendments, trace minerals and "others"), as applied to selected, major crop categories (i.e. row crops, fruit and vegetables, turf and ornamentals and "others") and the hectarage covered, in the major geographies of the world (i.e. Europe, Asia Pacific, North America, South America and the "rest of the world"). Future markets for all biostimulants look promising. In particular, humic substances and extracts of various seaweeds are expected to make up over

60% of the market combined. Most growth of these agricultural technologies is expected in the European/Asia Pacific markets. These numbers are forecast by various agents, i.e. global values of this category of agricultural and horticultural inputs in the range of USD 4.6-9.22 billion with a CAGR between 8.3 – 14.2% by 2027. In contrast the novel, phyconomic applications of extracts of various seaweeds to the cultivation of commercial macroalgae will be briefly presented as an emerging tool for the micropropagation and production of volume and quality of selected seaweeds.

Keywords: Phyconomy, biostimulants, cultivation

Oral presentation

NATIVE HAWAIIAN MACROALGAE CULTIVATION IN SCALABLE OFFSHORE ARRAY WITH A FOCUS ON NUTRIENTS AVAILABILITY FOR BIOMASS PRODUCTION

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A large portion of the U.S. Exclusive Economic Zone is inhospitable to commercial macroalgae cultivation due to the lack of nutrients in surface waters and the high cost of mooring arrays. Our Blue Fields project addresses these issues with a wave-driven, low-cost mooring and nutrient delivery design that pumps nutrient rich deep sea water (DSW) over the macroalgae array, thus, enabling macroalgae cultivation in an oligotrophic environment. This pilot array aims to validate the hydrodynamic designs and nutrient flux models of our partners, Makai Ocean Engineering, for both Blue Fields and future offshore systems. Several native Hawaiian macroalgal species have undergone growth trials with varying levels of DSW as nutrient supply ([0% - 10%] or 73-128μg TDN/L) and results will be discussed. Additional growth trial data will be presented on the following species: *Sargassum echinocarpum, Gracilaria parvispora, Ulva lactuca* and *Halymenia hawaiiana.*

Financing: Department of Energy ARPA-e MARINER, Award #: DE-AR0000924.

Keywords: Deep sea water, Hawaiian macroalgae, mooring array

Oral presentation

BIOMASS ESTIMATION OF THE CULTIVATED RED ALGA *PYROPIA* USING UNMANNED AERIAL PLATFORM BASED MULTISPECTRAL IMAGING

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The high-throughput estimation of biomass is important for cultivated macroalgae in their management and researches on breeding and phenomics. The cultivated *Pyropia*, important economic macroalgae in East and Southeast Asia, was investigated using multispectral imaging based on an unmanned aerial vehicle (UAV) system in the north of Haizhou Bay, midwestern coast of the Yellow Sea. The spectrum characteristics and derived indices of normalized difference vegetation index (NDVI), ratio vegetation index (RVI), difference vegetation index (DVI) and normalized difference of red edge (NDRE) were used for evaluating the data acquisition methods and establishing the regression models. It showed that the seawater had a significant effect on the reflectance spectra of submerged *P. yezoensis* in seawater, but there was no significant difference of the four indices (NDVI, RVI, DVI and NDRE) between the time that *P. yezoensiswas* completely emerged (exposing to the air) and 1h later. The quadratic model of DVI (Biomass=-5.550DVI2+105.410DVI+7.530) showed more accuracy than the other index or indices combination, with the highest values of R2 (0.925) root mean square error (RMSE, 8.06) and relative estimated accuracy (Ac, 74.93%), respectively. The regression model was further validated by consistently predicting the biomass with a high R2 value of 0.918, RMSE of 8.80, and Ac of 82.25%. This study suggests that it is effective to estimate biomass of *P. yezoensis* using UAV based spectral imaging with high accuracy and consistency. It also implied that multispectral aerial imaging is potential to assist digital management and phenomics research on cultivated macroalgae in a high-throughput way.

Financing: Marine S&T Fund of Shandong Province for Pilot National Laboratory for Marine Science and Technology (No. 2018SDKJ0302-4)

Keywords: *Pyropia*, biomass estimation, multispectral imaging

Oral presentation

EFFECT OF TEMPERATURE AND DIFFERENT STORING METHODS ON SPORULATION AND SPORE DEVELOPMENT OF GIANT KELP (*MACROCYSTIS PYRIFERA*)

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Many studies have investigated the life history of giant kelp *M. pyrifera*. Through contrasting these bodies of work it is apparent that the conditions needed for successful growth are variable from one region to another, making it difficult to establish robust and reliable culturing practices. Little information is available regarding the potential effects of sporulation temperature and storing methods for sporophylls on developmental parameters and this is an area of research that requires further work given its potential ecological importance. The aim of this study is to answer whether temperature or dehydration affect spore density, and do temperature interfere germination process of kelp? Sporophylls of kelp was collected and divided in two sub samples, one was cleaned, dried and stored at 4°C (as dehydration) and another was cleaned and introduced to Provasoli-enriched seawater (as fresh). Sporulation was done in elevated temperature from 9 to 24°C. The spores were incubated in such temperature at 20 µmol m-2 s-1, 16L:8D photoperiod for 5 days. The results indicate that temperature can stimulate the number of spore release but dehydration. The number of spores increased with rising temperature, and germination rate ranging from 4.6% to 78% significantly decreased from temperature above 220C.

Financing: We thank the Ministry of Business, Innovation and Employment, New Zealand for funding this study through 2019 Endeavour Fund

Keywords: *Macrocystis pyrifera*, sporulation, temperature

Oral presentation

GROWTH AND BIOFOULING IN KELP AQUACULTURE (*SACCHARINA LATISSIMA*): THE EFFECT OF LOCATION AND WAVE EXPOSURE

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Seaweed aquaculture is receiving increasing attention for food and non-food applications in Europe, where it is still an emerging industry. The cultivation of seaweeds in the sea is attractive as it does not compete with agricultural crops for land and freshwater, whilst generating high yearly biomass yield. The selection of suitable cultivation sites in coastal waters is essential for the sustainable establishment and further development of seaweed aquaculture in Europe. Here, we investigate the effects of wave exposure and geographic location on growth and biofouling of kelp (*Saccharina latissima*), using a transplantation experiment along the Swedish west coast. Biofouling of kelp decreased with increased wave exposure, from 10 and 6% coverage at sheltered and moderately exposed locations, respectively, to 3% at exposed locations. Growth, measured as blade surface area, generally increased with decreased wave exposure, with approximately 40% less growth at exposed locations compared to sheltered or moderately exposed location. We identified that there is large spatial variation in growth and fouling of the seaweed biomass at the selected farm sites, with significant differences from the km-scale to the m-scale. In addition, exposure level affected the tissue composition, with a high carbon, but low nitrogen and water content at exposed locations compared to moderate and sheltered sites. Isotope signatures (i.e. δ13C and δ15N) also differed between exposure levels. Together, these results indicate that wave exposure is an important factor to consider in site selection for both yield as well as quality of the seaweed biomass for future kelp farms.

Financing: The Swedish Foundation for Strategic Environmental Research MISTRA (no. 2013/75) and The Swedish Research Council Formas (no. 213- 2013-92)

Keywords: Seaweed aquaculture, biofouling, wave exposure

Oral presentation

INNOVATIVE APPROACHES TO SEAWEED CULTIVATION: OPTIMISING SEEDING TECHNIQUE FOR *SACCHARINA LATISSIMA*

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The cultivation of macroalgae is an emerging field in the UK and Europe. Traditional 'twining' methods, in which seedlings are grown-on in a hatchery for several weeks prior to deployment at sea, incur high laboratory costs. The development of a 'biobinder' glue allows direct seeding onto cultivation lines, followed quickly by deployment, which can potentially reduce production costs by bypassing the grow-out stage. However, this technique requires validation. Here, we trialled two different direct seeding methods with a *Saccharina latissima* gametophyte suspension. A one-stage technique involved mixing gametophytes and binder solution together prior to application onto cultivation lines, while a two-stage technique involved application of gametophytes to lines prior to coating with binder solution. Gametophytes were applied at a standardised density of 2.45 mL m-1 to cultivation lines, which were deployed at sea as 6m long 'droppers' at a mixed seaweed and mussel farm in Porthallow Bay, Cornwall, UK, for eight months. Six lines of each treatment were harvested at three time points and all kelp biomass from 0-1m and 3-4m dropper depth was removed. Total biomass yield (wet weight) and detailed biometric information for 10 adult sporophytes per meter were recorded for *S. latissima*, and also *Saccorhiza polyschides*, which opportunistically settled on lines from adjacent wild populations. Preliminary results indicate that seeding method has a considerable effect on total biomass yield, morphology, and adult density of both the macroalgal species. These initial findings have the potential to progress the nascent British macroalgal cultivation industry towards commercial scale production.

Financing: Financed by the European Maritime Fisheries Fund

Keywords: Kelp, cultivation, binder

Oral presentation

A TECHNIQUE TO SEED FRAGMENTS OF *GELIDIUM LINGULATUM* (RHODOPHYTA, GELIDIALES) IN WAVE-EXPOSED, LOW INTERTIDAL ROCKY SHORES

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A seeding technique for repopulation purposes was developed for the agarophyte *Gelidium lingulatum*. The effect of different thallus parts, type of substratum (calcareous, not calcareous), calcium addition, irradiance and temperature on the production of secondary attachment structures were evaluated in separate experiments in laboratory conditions. The basal axes kept in close contact with the substratum produced significantly more attachment structures than vegetative blades or reproductive blades, whereas the other factors had a smaller or negligible effect. A device to seed fragments in the habitat of *G. lingulatum*, the lower zones of wave-exposed, rocky shores, was tested in three localities in the Biobío Region, southern Chile. Thalli fragments with basal axes were wrapped around nylon rivets containing a plastic mesh washer and introduced in holes previously drilled into the rocks (sandstone or shale) with a battery drill. The type of substrata (bare rock, barnacle patches and coralline crusts) was included as a factor. Results indicated that, in the absence of human intervention, more than 90% of the devices were still in place four months after the seeding, allowing fragment attachment and production of new basal axes and blades, and the formation of small patches of *G. lingulatum*. The type of substratum had no consistent effect, but growth was affected by the local conditions of the experimental sites. This simple, low cost technique proved effective in establishing new small patches, and could be used for reestablishment *of* *G. lingulatum* and other species with similar secondary attachment characteristics.

Financing: FONDEF Regional D13R20031

Keywords: Restoration, vegetative reproduction, agarophyte

Oral presentation

THE LARGE-SCALE CULTIVATION POTENTIAL OF *ULVA FENESTRATA*: A CASE STUDY FROM A SCANDINAVIAN OFF-SHORE SEAFARM

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Sustainable seaweed aquaculture is receiving increasing attention of food and non-food sectors in Europe, where it is still an emerging industry. The cultivation of green seaweeds of the genus *Ulva* is mostly performed in on- or near-shore pond- or tank cultivation systems whereas its cultivation in the sea becomes more attractive as it does not require large on-shore facilities. The core aim of the here described study was to assess the large scale off-shore cultivation potential of northern hemisphere *U. fenestrata* in a Swedish seafarm located in the Kosterfjord, Skagerrak. Here, we investigated the effects of temperature, growth-medium addition and seedling density during the early hatchery stages of *U. fenestrata* and their subsequent effects on the growth performance and biochemical composition (fatty acid, protein, carbohydrates, phenolic, pigments) on the off-shore cultivated biomass. Furthermore, we investigated the effect of shifted (April, May, June) harvesting periods on the growth performance, biochemical composition, fertility, and amount of fouling on the cultivated biomass. Our study confirms the large scale off-shore cultivation potential of northern hemisphere *U. fenestrata* and underpins suitable pre-treatments during the hatchery phase of seedlings to facilitate a successful and cost-efficient large-scale rope-cultivation. Furthermore, our study shows that the harvest period significantly defines the biochemical properties of the biomass. Together, our results indicate that the optimal off-shore cultivation conditions for Swedish *U. fenestrata* are dependent on the desired biomass traits (biomass yield or biochemical composition).

Financing: Funding for this study was received by the Swedish Foundation for Strategic Research (SSF), project number RBP14-0045,

Keywords: Aquaculture, *Ulva*, protein

Oral presentation

PORPHYRA DIOICA CULTIVATION IN SOUTH WALES – FROM AUTECOLOGICAL UNDERSTANDING TO SUCCESSFUL LIFE CYCLE CONTROL

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Demand in seaweed biomass is increasing in Europe. Currently, only a few native species can be cultivated, resulting in growing harvesting pressure on wild stocks and the need for cultivation protocols for local species of interest. Red algae of the genus *Porphyra/Pyropia* are becoming very popular due to their nutritional value but cultivation of European *Porphyra* species still faces several bottlenecks as a result of limited control of the complex heteromorphic life cycle (alternating between a macroscopic gametophytic/microscopic sporophyte). In this study, we developed a cultivation

protocol for *Porphyra dioica*, a common representative on North-Eastern Atlantic rocky shores. A seasonal study investigated autecological patterns in two P. dioica populations in South Wales between April 2016 and June 2018 recording gametophyte percentage cover, density, size of individuals and recruitment in ten 1m2 quadrats. Laboratory experiments followed based on findings from the seasonal observations and focused on the effect of temperature, photoperiod and light intensity on the development and maturation of the sporophyte and young gametophytes. The gametophyte was present on the studied rocky shores throughout the year with highest percentage cover (41±5%) and largest individuals (25.3±1.5cm) in spring, while recruitment mainly occurred during winter. Under laboratory conditions, sporophytes grew best at 18°C and under long day conditions. A decrease in temperature from 18°C to 9°C initiated a mass conchospore release (498±146 spores mL-1), tackling a major bottleneck in European *Porphyra* cultivation. These results increase our ecological understanding of a European *Porphyra* species while having important implications for commercial production.

Keywords: Conchosporangia, temperature, *Porphyra*

Oral presentation

LARGE SCALE MARICULTURE OF *SACCHARINA LATISSIMA* IN THE GULF OF ALASKA

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We are currently working on a DOE/ARPA-E MARINER funded project to determine an optimal way to grow *Saccharina latissima* in large, offshore arrays for the eventual purpose of biofuel production with the goal of keeping the cost below $80 USD per dry metric ton of kelp. This project is specifically looking at how *Saccharina latissima* can be grown in the Gulf of Alaska to reach that goal. There are three major aspects of the research: 1) optimizing nursery production and seeding lines for outplanting, 2) designing an economical, modular outplanting structure and 3) developing methods to efficiently harvest the product. For hatchery improvement we are researching "direct seeding" on longlines. With direct seeding, we initially mass culture male and female kelp gametophytes in the lab. At specific points in the life cycle, we apply the mixed cultures of gametophyte or juvenile sporophytes directly on the longline using innovative methods to help the plants adhere. Direct seeding will be especially useful for growing selected kelp strains that will be uniquely suited for the Gulf of Alaska. For outplanting, we deployed our first outplant array near Kodiak, Alaska in November 2019. Lines were seeded with *S. latissima* and growth occurred over the winter and early spring. More than 3353 m of seeded longline were outplanted. Harvest occurred in June, 2020 with a yield of 8.0 kg/m for a total of 26,751 kg harvested. Finally, new processes for harvest and transporting the harvested kelp have been assessed.

Financing: US DOE ARPA-E MARINER Program, award DE-AR0000911

Keywords: Kelp aquaculture, *Saccharina*, production

Oral presentation

FROM THE INTRODUCTION TO COMMERCIAL FARMS: THE CHALLENGES OF *KAPPAPHYCUS ALVAREZII* CULTIVATION IN SANTA CATARINA, BRAZIL

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The red seaweed *Kappaphycus alvarezii* was introduced in 2008 in Santa Catarina state's subtropical waters, located in the South of Brazil. The seedlings came from Sao Paulo University, and they were kept in quarantine for one year until the experimental licensing was granted to Federal University of Santa Catarina (UFSC). Since then, UFSC and Santa Catarina Agricultural Research and Rural Extension Company (EPAGRI) developed works related to economic viability and environmental safety. One of the main issues is the low temperature during wintertime, which can kill the seedlings in marine farms. Tank cultivation has been developed using shrimp rearing effluents as fertilizers to keep them until the environmental conditions become favorable again. Another problem is the seaweed drying since Santa Catarina shows a high rainfall index. The drying process's influence has been studied since the beginning of the experimental introduction, focusing on low-cost prototypes of dryers. By the beginning of 2020, after ten years of negotiation, the Brazilian Government finally authorized the commercial cultivation on the Santa Catarina coast. In particular, this state has a good profile for mariculture projects since it is the largest producer of bivalve mollusks in Brazil, and seaweed cultivation can be an alternative source of income to local producers. The next step is to start the pilot farms and understand the best manner to establish a sustainable production chain integrated with mollusks.

Financing: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) - Productivity Fellowship (Process number 308631/2017-0)

Keywords: Aquaculture, production chain, eucheumatoids

Oral presentation

DISTRIBUTION OF THE TROPICAL SEAWEED CROPS *EUCHEUMA SPP.* AND *KAPPAPHYCUS SPP.* INSIDE AND OUTSIDE OF THEIR NATIVE RANGE

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Seaweed aquaculture is a fast-growing industry worldwide and has the potential to change the seascape of coastal regions, including the movement of species outside their native range. Two of the crops with the highest global production are the tropical red algal eucheumatoids, *Kappaphycus* spp. and *Eucheuma denticulatum*. Cultivation of these species has become an important source of income for coastal communities especially in many areas in South East Asia and the Western Indian Ocean. Low initial investment and a simple vegetative propagation through cutting fostered a rapid expansion of eucheumatoid cultivation and its introduction in diverse tropical and subtropical countries around the world. Despite the economic importance of eucheumatoid cultivation, its relevance for many coastal communities and its global expansion knowledge on genetic variation between and within cultivars of *Eucheuma* and *Kappaphycus* and their wild counterparts is yet limited. Through an international consortium we designed a global sampling campaign of cultivated and non-cultivated eucheumatoids from seaweed farms and natural habitats with focus on South East Asia (the Philippines, Malaysia and Indonesia) and the Western Indian Ocean (Tanzania and Madagascar), as well as specimens from non-native areas including islands in the Pacific (Hawaii, Kiribati, Fiji and Solomon Islands). In this talk, we will give an update of this ongoing project and outline initial results from a new initiative to determine diversity within cultivated eucheumatoid specimens from Tanzania. Our project aims at providing novel knowledge on the genetic resources of eucheumatoids in support of a sustainable seaweed industry.

Keywords: Eucheumatoids, cryptic invasion, aquaculture

E-Poster

EFFECT OF NUTRIENT AND SEAWATER TEMPERATURE ON THE GROWTH AND BIOCHEMICAL PROFILE OF SELECTED TROPICAL SEAWEED, *CAULERPA LENTILLIFERA*

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Caulerpa lentillifera, an edible green seaweed that is naturally distributed in the tropical regions was first commercially cultivated in the Philippines in the late 1980s. *Caulerpa lentillifera* is rich in protein, carbohydrates, essential minerals (Na, K, Ca, and Mg), dietary fibers, vitamins (A and C), omega-3 fatty acids, and polyunsaturated fatty acids. Bioactive compounds, such as phenolic compounds, polysaccharides, and siphonaxanthinhave been identified in *Caulerpa lentillifera* where these compounds are reported to have high antioxidants, anticancer, anti-diabetic, and immunomodulation properties. *Caulerpa lentillifera* has the potential to be used for commercial development in Malaysia, but there is no *Caulerpa lentillifera* cultivation in Malaysia. To succeed in the commercial cultivation of *Caulerpa lentillifera*, culture conditions and a cost-efficient medium have to be developed. In this study, the effect of nutrients, viz. different combinations and concentrations of (NO3-) and phosphate (PO43-), as well as seawater temperature (20, 24, 28° C) on the growth and biochemical profile of the Malaysian *Caulerpa lentillifera*, was investigated. Preliminary studies showed that the highest production rate was 5.21±0.16 g d-1 in a 20L nutrient-enriched (320 µmol NO3-& 10.6 µmol PO43-) indoor seaweed culture system, at 28° C). The highest protein (37.73 ± 1.77 % DW) and carbohydrate (67.71 ±0.57 % DW) contents were observed on Day 29 and Day 20 respectively. On Day 20, the highest chlorophyll-a (3.53 ± 0.14 mg/g) and carotenoids (1984.42 ± 123.67 µg/g) contents were obtained respectively. This study is part of an ongoing project to optimize the culture of *Caulerpa lentillifera* in the nutrient-rich effluent generated from an ocean thermal energy conversion (OTEC) system.

Financing: Sciences and Technology Research Partnership for Sustainable Development (SATREPS)- Ministry of Higher Education, Malaysia Programme (Grant No: IF045-2019)

Keywords: Seaweed Cultivation, biochemical Composition, temperature and nutrients

E-Poster

POTENCIAL GROWTH OF *MACROCYSTIS PYRIFERA* SPOROPHYTES UNDER FARMING CONDITIONS: EFFECT OF THE GENETIC BACKGROUND

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Kelp farming is essential to cope with the actual demand of raw material, conservation of natural stocks and genetic diversity. The giant kelp *Macrocystis pyrifera*, can potentially become a farmed crop; however, whether the performance of wild species from a specific genotype is limited to their local environment needs validation under farming conditions. In this proposal we experimentally test whether sporophytes presenting different genetic origins may show differences in productive traits when cultivated under the same farming conditions. To produce sporophytes from two distinctive populations, reproductive material was collected in Valparaíso (central population) and Los Lagos (southern population) regions of Chile to obtain zoospores, gametophytes, and finally sporophyte to be grown under controlled culture conditions. When juvenile sporophytes reached a length of 10-15 cm were transplanted to the field by attaching each individually marked sporophyte (n= 40 per origin) to a suspended 100 m longline at Metri bay, during Autumn-Winter season 2020 (limiting light condition). The outgrow experiment run for 84 days, maximum length and environmental parameters were measured biweekly. Growth curves were constructed with the algal total length and statistical compared (Minitab 18.0); sporophyte loss (%) from the longline was also registered. Our results showed that when comparing the growth curves for both populations, Valparaíso showed a slight but significantly higher growth response than the population of Los Lagos (F= 361.13; $p<0.01$); however, there is a higher loss of sporophytes from the longline. We concluded that breeding strategies should be improved to increase kelp production under farming conditions.

Financing: ANID-FONDECYT N° 1180647 and Basal CeBiB (FB-0001)

Keywords: Kelp farming, genetic background, Southern Chile

E-Poster

THE 'SEA TRUFFLE', *VERTEBRATA LANOSA* (RHODOPHYTA), A NEW SEAWEED RESOURCE FOR COMMERCIAL EXPLOITATION ON SHORES OF NOVA SCOTIA

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As part of a study to develop the species for commercial exploitation, we evaluated the population ecology of the red seaweed, *Vertebrata lanosa* aka the 'sea truffle', on shores of Digby Neck and adjacent islands in the outer Bay of Fundy of Nova Scotia. *V. lanosa* is an obligate epiphyte on the dominant intertidal fucoid *Ascophyllum nodosum*. We sampled 12 sites using three, 30–m transects, aligned parallel to the shore and separated by two meters. We used a 25 x 25 cm quadrat with sampling every meter (conditions 1 and 2), or every two meters (condition 3) along the 30–m transect. Transects were randomly assigned one of three conditions for data collection: (1) cover of *Vertebrata* and *Ascophyllum*, and depth of *Ascophyllum* (control transect); (2) as in condition 1, but *Vertebrata* was then hand-harvested in a 1–m band parallel to the transect line to mimic commercial picking; and (3) as in condition 1, but the entire quadrat was then destructively harvested using garden shears to establish relative biomass of *Ascophyllum* and *Vertebrata*. Transects with sampling types 1 and 2 were resampled monthly or bimonthly (six sites each) for up to four evaluations. Harvesting removed about 10% of the standing crop of *Vertebrata*, and no declines in cover were found on subsequent harvests. We suggest that *V. lanosa* is a harvestable resource suitable for small-scale exploitation in Nova Scotia.

Financing: Nova Scotia Productivity and Innovation; Natural Sciences and Engineering Research Council of Canada

Keywords: Natural resources, seaweed harvesting, *Vertebrata lanosa*

E-Poster

BIOLOGICAL AND GENETIC BASES OF *PALMARIA PALMATA* DOMESTICATION

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Palmaria palmata is a harvested edible red alga commonly found on the coasts of the North Atlantic Ocean. Most of the

commercial production comes from the harvest of wild populations which are subject to seasonal variations in their biomass, and threatened by climate change and overexploitation in some areas. The growing demand for dulse for food, feed and cosmetic markets, as well as the increasing human pressure on wild populations, underscores the need to domesticate this species in order to develop its commercial cultivation. Domestication is a long and complex co-evolutionary process that requires a good knowledge of the biology, reproduction and genetics of the target species. In this context, we are interested in studying the different stages necessary for the development of the cultivation of *P. palmata* in Brittany. This will involve (i) evaluating the genetic resources of wild populations in Brittany, which is the main production site of dulse in Europe, using DNA microsatellite markers, (ii) building unialgal collections of strains from wild populations for aquaculture and experimental purposes in order to improve varieties and (iii) control the reproductive cycle of this species in order to improve the efficiency of crosses as well as sowing of crops.

Financing: This work was supported by a doctoral fellowship from Région Bretagne and Sorbonne Université to Aurélien Baud.

Keywords: Life cycle, breeding, population genetics

E-Poster

FARMING OF *KAPPAPHYCUS ALVAREZII* IN SRI LANKA: CURRENT STATUS AND OPPORTUNITY DEVELOP CARRAGEENAN INDUSTRY

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The current annual world production of *Kappaphycus alvarezii* is about 200,000 Mt and its value-added product carrageenan is approximately 60,000 MT/yr. *K. alvarezii* has been farmed successfully since 2012 in Sri Lanka. Over 250 fisher folks from 3 districts viz. Mannar, Kilinochchi and Jaffna are involved in farming to sustain their livelihood and additional income. Floating bamboo rafts and mono-lines, the two popular cultivation methods were adapted, resulting in an ADGR % of *K. alvarezii* in 45 days with 150 grams of seed propagule, across different locations with respect to seasons ranged between 3.50 ± 0.50 times. The average monthly production of dry seaweed of a cultivator was 450-550 kg corresponding to a monthly income of US$ 150 - 225. The quality of dry seaweed moisture (35 ± 3.0%), clean anhydrous weed (CAW 38 ± 5.0%), soluble salt (28 ± 3.0%) and impurities (<1.0%) were comparable to the quality of commercial material. The yield of SRC ranged between 30 ± 3.0% whereas refined carrageenan was 25 ± 2.5%. *K. alvarezii* farming has been introduced to over 25 countries over the last 35 years. However, only five countries produce commercial volumes (>1,000mt/year) for the carrageenan industry today. Sri Lanka has recently been added to the list of countries doing farming of *K. alvarezii* and it is estimated that it has a potential to produce dry-weed over 25,000 Mt/yr. Current status of farming of *K. alvarezii*, scope for expansion and opportunity to develop carrageenan industries in Sri Lanka are discussed in the present study.

Keywords: *Kappaphycus*, cultivation, Sri Lanka

E-Poster

SEAWEED SOLUTIONS FOR SUSTAINABLE AQUACULTURE CRC-P: AN OVERVIEW

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The global demand for seaweed is increasing and more and more investors are looking at seaweed aquaculture as a sustainable and high-value new industry. In south-eastern Tasmania, three Australian native kelps, *M. pyrifera, L. corrugata and E. radiata*, have been selected to be cultivated in an Integrated Multitrophic Aquaculture (IMTA) system in proximity to salmon and mussels farming sites. The project "*Seaweed Solutions for Sustainable Aquaculture CRC-P*" is the result of a collaboration between industry (Tassal Group Ltd and Spring Bay Seafoods) and research partners (Institute for Marine and Antarctic Studies and Deakin University), that aims to define a viable and sustainable seaweed aquaculture and from this develop an IMTA partnership model that brings together salmon, shellfish, and seaweed production to optimize regional economic, environmental, and societal benefits. The project is divided into three Working Packages (WP) that focus on 1) unlocking the seaweed potential, 2) developing farming technology and 3) assessing the sustainability of the IMTA model proposed. These WPs are interconnected and will provide viable seaweed culture options for Southern Australian and Tasmania, identifying the best species and growing techniques, understanding the nutrient uptake potential of the selected species, establishing products and management structures for a successful and scalable seaweed aquaculture and IMTA. This will lead to identifying or developing further commercial applications and markets of valuable seaweeds in multiple sectors (e.g. food, feed, agriculture, and nutraceutical) that will guide the development of a profitable Australian seaweed industry, expected to reach a value of $1.5 billion by 2040.

Financing: Australian Government-Business CRC-P, Tassal Ltd, Spring Bay Seafoods Pty Ltd, Institute of Marine and Antarctic Studies/University of Tasmania, Deakin University

Keywords: IMTA, kelp, seaweed industry

E-Poster

DEVELOPMENT OF A PAN-EUROPEAN, GENETICALLY CHARACTERISED *SACCHARINA LATISSIMA* SEEDBANK

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The brown macroalga *Saccharina latissima* has been identified as a key biological resource, in part due its increasing use in European aquaculture. To improve *S. latissima's* viability as a crop, an increasingly popular approach called genomics-assisted breeding can be used, which relies on identifying the loci and alleles underpinning the expression of traits of interest (e.g. chemical profile, disease resistance, biomass yield). To put this into practice, a biobank comprising the broadest genetic diversity of the target species must be created. In collaboration with partners of the H2020 GENIALG consortium (https:/https://genialgproject.eu/), fertile *S. latissima* sporophytes were sampled from 23 populations found across the species' European biogeographic range. From these individuals, 423 gametophytes were isolated and cryopreserved according to methods established by Visch et al. (2019). In addition, each strain is to be genetically characterised using the ddRADseq sequencing approach (double digest restriction-site associated DNA). Following ongoing post-cryopreservation viability testing, these strains will be deposited in the Culture Collection of Algae and Protozoa (CCAP, UK). Once publicly available, these cultures will represent an extensive, genetically characterised biological resource encompassing the European range of *S. latissima*. Such a collection can be then utilised for investigating a wide variety of ecologically and commercially relevant questions that would benefit from genome-wide associations between phenotype and genotype. As a proof of concept, these strains will be utilised to investigate the heritability of disease resistance in *S. latissima* against an intracellular oomycete.

Financing: Funded by European Union Horizon 2020 programme (project ID 727892, GenialG - GENetic diversity exploitation for Innovative Macro-ALGal biorefinery, http://genialgproject.eu/)

Keywords: Biobank, *Saccharina latissima*, GENIALG\

SYM04: Connectivity, speciation and biogeography of algae in the Southern Hemisphere

Keynote lecture

BEYOND BIOGEOGRAPHIC PATTERNS: PROCESSES SHAPING MACROALGAL EVOLUTIONARY TRAJECTORIES IN THE SOUTHERN COLD-TEMPERATE WATERS

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Recent progress in macroalgae phylogeography and genetic species delimitation have allowed reevaluating patterns of species distribution, diversity and degree of endemism in the cold-temperate waters of the Southern Hemisphere. Consistently, these studies have shown that our taxonomic understanding is not congruent with the genetic patterns and that far more diversity (and higher endemism) exists than previously recognized. The general processes that contribute to speciation and genetic breaks, and how these relate to biogeographic boundaries and vicariance have also been of particular interest in the region. Molecular data have generally corroborated the classically defined biogeographic boundaries but also pointed out to a particular history of connectivity and divergence in these organisms. For example, Antarctic macroalgae are isolated from the rest of the Southern Ocean flora, with splits related to the strengthening of the Antarctic Circumpolar Current (ACC) during the Miocene, postdating the fragmentation of the continental landmasses. Antarctic macroalgae have clearly withstood Quaternary glacial cycles in situ with range contractions and bottlenecks drastically impacting their populations. All studied species are characterized by very low genetic diversity, absence of genetic structure (at regional or even continental scale) and significant signatures of recent population expansion linked to long-distance dispersal. North of the ACC, rare but recurrent long-distance dispersal events, sometime followed by divergence/radiation, have also highly affected the diversity of macroalgae communities. Finally, importance of microallopatric or parapatric divergence processes, related to eustatic and isostatic sea level changes, presence of gyres or resurgences, has been proposed at more local/regional scale.

Financing: FONDECYT REGULAR No. 1130797 and 1170541; Centro FONDAP IDEAL No. 15150003, Agence Nationale de la Recherche Grant ANR-10-BTBR-04

Keywords: Comparative phylogeography, past oceanographic and climatic dynamics, long-distance dispersal follow

Keynote lecture

DRIFTING ON SHIFTING SEAS: WHAT DNA CAN TELL US ABOUT SEAWEED DISPERSAL AND EVOLUTION

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The Southern Hemisphere is largely oceanic, with many landmasses separated by hundreds or thousands of kilometres of water. Around the Southern Hemisphere, however, there are striking similarities in coastal communities – the same or closely related species are often found growing on far-distant shores. Scientists have long speculated that buoyant seaweeds might drift long distances at sea, potentially carrying diverse passengers such as non-buoyant seaweeds and invertebrates. Only relatively recently, however, with the development of genetic and genomic technologies, have we been able to demonstrate just how powerful a dispersal mechanism algal rafting can be. Indeed, genomic approaches can allow us to pinpoint precisely where a dispersing macroalgal raft originated from, and have revealed that drifting seaweeds can sometimes travel tens of thousands of kilometres. Somewhat surprisingly, however, dispersal does not always lead to population connectivity; instead, modelling indicates that in some cases major disturbances are needed before dispersing lineages can establish at new locations. Genetic approaches are also revealing greater diversity in seaweeds than we had previously been able to detect, with new cryptic or morphologically similar species being discovered/described through DNA analyses. Drawing on examples from the high latitudes of the Southern Hemisphere, this talk will highlight how genetic and genomic tools can provide powerful insights into the evolutionary and biogeographic processes shaping the diversity and distribution of seaweeds.

Keywords: Dispersal, southern hemisphere, genetic diversity

Oral presentation

SPATIAL PATTERNS OF THE GIANT KELP, *MACROCYSTIS PYRIFERA*

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In this talk, I will explore the global spatial patterns of the giant kelp (*Macrocystis pyrifera*). The total extent of giant kelp forests in a conservative estimate is 17,088 km2, but their actual length is fractally scalable according to the level of resolution in which the coastline is analyzed. This extent will be compared with other marine ecosystems and geographical features. Additionally, their level of protection and coverage of Marine Protected Areas per province, ecoregion, and countries will be discussed. Finally, I will comment on the potential of kelp mapping in the context of the Nationally Determined Contributions (NDCs) or climate actions per-country for the Paris Agreement (United Nations Framework Convention on Climate Change).

Keywords: *Macrocystis pyrifera*, spatial patters, NDCs

Oral presentation

CONNECTIVITY OF THE ANTARCTIC RED SEAWEED *PLOCAMIUM* SP. AND THE DISTRIBUTION OF ITS DEFENSIVE METABOLITE DIVERSITY

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Inter- and intraspecific interactions between organisms can be a form of communication, environmental sensing, or defence, and are often mediated by chemicals like secondary metabolites. Sessile marine organisms, such as macroalgae, commonly produce chemical defenses against grazers, pathogens, and biofoulers. *Plocamium* sp. is a finely branched red understory alga that is common in Antarctic macroalgal forests. It supports a high abundance of amphipods of which most are not able to feed on it as *Plocamium* sp. is heavily chemically defended. Different individuals produce differing mixtures of halogenated secondary metabolites which are referred to as chemogroups. Around Palmer Station, Antarctica, from 2016 to 2018, a total of 16 different chemogroups were identified which fit well into two haplotypes identified by the cox1 gene. These data also suggest that chemogroups are to some extent site and depth specific. In order to determine the mechanisms driving the geographic patterns of chemogroups in *Plocamium* sp., a variety of approaches were taken. Transplant experiments revealed that the environment does not play a strong role in chemogroup production. Using microsatellites, preliminary analyses of multilocus genotypes have revealed that underlying patterns of genetic differentiation likely play a strong role in chemodiversity distribution, expanding on the patterns based on single gene sequencing. Thus, findings indicate that patterns of gene flow play a larger role in the geographic distribution of chemogroups. These results help our understanding not only of patterns of macroalgal population connectivity, but also the patterns that drive intraspecific diversity in general.

Financing: National Science Foundation (PLR-1341333); Antarctic Science Bursary; Phycological Society of America - GIAR; Sigma Xi - GIAR; Department of Biology

Keywords: *Plocamium*, chemodiversity, polar

Oral presentation

CROSSING THE SOUTH PACIFIC OCEAN: STUDY OF *AGAROPHYTON CHILENSE* RANGE EXPANSION BASED ON DDRAD DATA SET

Oscar R. Huanel[1,2], Sarai Morales-González[3], Suany Quesada-Calderón Quesada-Calderón[3], Cristian Rios[3], Pablo Saenz-Aguledo[3], Wendy A. Nelson[4,5], Natalia Arakaki[6], Stéphane Mauger[2], Sylvain Faugeron[1,2], Marie-Laure Guillemin[2,3]

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Long-distance dispersal is a key process shaping evolutionary biology and ecology of the Southern Hemisphere biota. *Agarophyton chilense* present a disjunct distribution across the South Pacific Ocean, with populations located in New Zealand, Chatham Island, Chile and Peru. Various phylogeographical studies have documented marine species range extension, including algae, from New Zealand to Chatham Island and South America, however still lack information about the precise origin and timing of the colonization events and the oceanic processes associated with the propagules transport. In this study, we used 2,232 SNPs to describe *A. chilense* patterns of genetic diversity and structure in the Pacific and to study the colonization routes and timing of range expansion of the species. The contrasting patterns of genetic diversity and structure observed between the two main Islands in New Zealand (with low diversity and genetic homogeneity in the South Island) attest to the important effects of Quaternary glacial cycles on *A. chilense*. Structure analyses pointed out to two independent events of expansion in the Pacific: one from the east coast of the North Island to Chatham Island and the other from the northern part of the Cook Strait to South America. Demographic inferences indicated a much older colonization of the Chatham Island than South America; with both events likely corresponding to founder effects without migration following the colonization. The estimation of colonization times emphasized the importance of changes in marine currents strength and position, especially the East Auckland Current, linked to glacial-interglacial cycles in *A. chilense* expansion.

Financing: FONDECYT Regular Grant#1170541 (ANID, Chile) and BECA DOCTORADO NACIONAL Grant# 21171226 (ANID, Chile)

Keywords: Long-distance dispersal, Rhodophyta, South Pacific Ocean

Oral presentation

PHYLOGEOGRAPHIC STRUCTURE IN CRYPTIC RED ALGA, *BOSTRYCHIA INTRICATA* (RHODOMELACEAE) OF THE SOUTHEASTERN COAST OF AUSTRALIA

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The southeast Australian coast demonstrates a major biogeographic transition that correlates with a historical land-bridge, the Bassian Isthmus, between mainland Australia and Tasmania. This historical geographic barrier results in deep genetic differentiation between some marine taxa across southern Australia. Here, we investigated the genetic diversity and phylogeography among 26 populations of red alga *Bostrychia intricata* along the southeast Australia coast. Mitochondrial DNA sequences revealed the occurrence of five cryptic *B. intricata* species (lineags N5, N7, N8, N9 and N10), two of which (N9 and N10) are newly discovered and endemic to Tasmania. While cryptic species N5 and N7 were confined to mainland Australia. Species N8 was more genetically diverse and extensively distributed, occurring both on mainland Australia and Tasmania, than other cryptic species. We also detected a clear east-west phylogeographic break between cryptic species N7 and N5 and between haplotype of species N8 on either side of Wilson Promontory (the southernmost tip of mainland Australia). In addition, AMOVA analysis of species N8 populations showed moderate to high levels of genetic differentiation with populations grouped into three clusters: north of Long Bay, west of Wilson Prom and east of Wilson Prom. Our data suggests that phylogeographic break and genetic differentiation in cryptic *B. intricata* likely corelates to the historical Bassian land-bridge and different oceanographic circulations.

Keywords: Rhodophyta, phylogeography, population structure

Oral presentation

LOCAL ADAPTATION PATTERNS IN THE GIANT KELP *MACROCYSTIS PYRIFERA* ALONG THE PERU-CHILE COAST

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The giant kelp *Macrocystis pyrifera* is a cosmopolitan species of cold-temperate coasts, yet encompassing a considerable

temperature gradient across its distribution range, from 3 to 22°C. Its large distribution may strongly rely on a great dispersal capacity to (re)colonize distant habitats and maintain the species cohesion through gene flow. Yet, dispersal is expected to counter-balance diversifying selection on thermal tolerance. This study aimed at testing for the existence of local adaptation among regions separated by up to 6700km and strong thermal divergence. Common garden experiments mimicking reciprocal transplants were performed on gametophytes and F1 sporophytes, each habitat being assimilated by a given temperature corresponding to the regional average of the sampled populations. Several proxies of fitness were measured in the haploid stage of the kelp, and sympatric versus allopatric conditions were compared. Additionally, regional divergence in thermal tolerance was assessed by quantifying outbreeding depression. Significant differences among regions were observed in the responses to thermal variability, and local adaptation was detected at the juvenile sporophyte stage but not the gametophytes. Fertility was more influenced by the geographic origin than by temperature per se, with possible effects of marginal conditions at the extremes of the distribution range. The effect of deme quality was also strongly determinant, suggesting that local stochasticity (i.e. genetic drift) may actually restrict the process of local adaptation. Outbreeding depression patterns were related to thermal divergence among habitats.

Keywords: Thermal adaptation, outbreeding, common garden

Oral presentation

THERMAL FRONT IN THE GERLACHE STRAIT REVEALS TWO DISTINCT PHYTOPLANKTON PATTERNS IN NEARSHORE AREAS (64° - 65° S, ANTARCTICA)

Martina Mascioni[1,2], Gastón Almandoz[1,2], Allison Cusick[3], Jack B. Pan[3], Martha Ferrario[1,2], Maria Vernet[3]

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The Gerlache Strait is a highly productive coastal area, a breeding and feeding location for penguin, seal, and whale populations, located on the western coast of the Antarctic Peninsula (WAP). Several previous studies recorded a thermal front in the Gerlache Strait around 64.5° S during summer, separating warmer waters to the north and colder waters to the south, but little is known on its effect on phytoplankton distribution. The setting of a citizen science project – FjordPhyto – in collaboration with the International Association of Antarctica Tour Operators vessels (IAATO) allowed us to analyze phytoplankton biomass and composition by light and electron microscopy in six nearshore areas connected to the Gerlache Strait (between 64° and 65°S) from November to February 2016–2018. The thermal front in the Gerlache Strait divides these areas in two zones: 1) northern areas, Cierva Cove and Wilhelmina Bay; and 2) southern areas, Cuverville and Danco Islands, Neko Harbor, and Paradise Bay. In both years we were able to identify two different patterns of biomass and phytoplankton composition. Biomass in the northern areas was considerably lower than in the southern ones, mainly during December and January. In the warmer northern areas, the abundance was dominated by cryptophytes and small flagellates. In the colder southern areas, the abundance was dominated mainly by small flagellates and diatoms, with important contributions of prasinophytes during January. This study reveals two different phytoplankton composition patterns north and south of the thermal front in the Gerlache Strait during two consecutive austral summers.

Keywords: Thermal front, western Antarctic Peninsula, citizen science

Oral presentation

BIOGEOGRAPHIC STRUCTURE AND CONNECTIVITY OF TWO KELP ECOSYSTEM ENGINEERS

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Macroalgal assemblages in sub-Antarctic regions are characterised by high levels of endemism compared to cold-temperate latitudes, while the strong impact of ice cover during the last glacial period supposedly extirpated most of the marine flora. In the Southern Ocean, potential refugia and source populations for postglacial recolonizations as well as dispersal pathways are still poorly understood. The aim of this work is to assess the genetic diversity and regional-scale connectivity of *Macrocystis pyrifera* and *Lessonia* sp. (Laminariales, Phaeophyceae) and understand their biogeographic history in the Falkland Islands and Magellan region. We used mitochondrial and microsatellite markers in a comparative analysis of genetic diversity, population structure and phylogeography. Ocean transport models were used to infer the potential for present-day regional connectivity. Results show strong genetic differentiation between the Falkland Islands and the South American continent suggesting limited connectivity. Distinct genetic groups were found to be endemic to the Falkland Islands possibly explained by long-term isolation in independent refugia during glacial periods. Also, distinct structuring patterns could be associated with the dispersal potential of the species. For *Macrocystis pyrifera*, a species common to both

the Falkland Islands and South Africa, long-distance connectivity was revealed in accordance with high dispersal potential through floating rafts, suggesting an important role of ocean currents for maintaining connectivity. In contrast, *Lessonia* sp. had no shared genetic groups between regions and includes endemic and geographically segregated genetic clusters along the coastline of the Falkland Islands, suggesting present contact of lineages that diverged in distinct regions and/or environments.

Financing: Portuguese Foundation for Science and Technology (FCT): UIDB/04326/2020, SFRH/BSAB/150485/2019, PTDC/MAR-EST/6053/2014, PTDC/BIA-CBI/6515/2020, SFRH/BD/140197/2018. Project FONDECYT 1160930 and a Pew Marine Fellowship.

Keywords: Kelps, biogeography, microsatellites

Oral presentation

FLOATING SEAWEEDS IN FILDES BAY, ANTARCTIC PENINSULA: TRAVELING UNDER EXTREME ENVIRONMENTS

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After detachment, many seaweeds can drift or float at the surface, thus facilitating their dispersal and connectivity. Floating and drifting seaweeds have been found through all major oceans, however information from Antarctica is scarce. Most of the records correspond to drifting thalli from several species (38) and few have been found floating (4). The aim of this study was to evaluate the presence of floating seaweed in Fildes Bay, Antarctic Peninsula during January 2018, February 2019/2020. Surveys and collections were carried out aboard of a zodiac, during daytime navigation. Number of floating items (pieces or whole individuals) and biomass (wet weight) were recorded. During the three years surveys 11,273 items from 24 species were found. The brown seaweed *Adenocystis utricularis* was the most abundant, with 10,866 items (96,4%) followed by *Cystosphaera jacquinotti* an endemic brown seaweed with 126 items (1,1%). A total of 152,4 kgs were recorded, with *C. jacquinotti* as the most abundant with 92,0% (140,3 kgs) followed by *A. utricularis* with 5.6% (8,9 kgs). Large and whole individuals were recorded at the surface (e.g., up to 6,3 m long in *C. jacquinotti*), most of them reproductive. A few of the floating species have been reported as recent introductions (e.g., the green seaweed *U. intestinalis*). Some floating thalli were also carrying associated organisms. Dispersal through floating thalli might be an alternative mechanism to spread in Antarctica, especially in a global change scenario where water temperatures and wind speeds will be affected, and more substrate will be also available.

Financing: Funding: FONDAP-IDEAL 15150003

Keywords: Floating seaweed, Antarctica, dispersal

E-Poster

MOLECULAR TOOLS REVEAL AMPHIPOLAR DISTRIBUTION FOR VARIOUS ANTARCTIC MARINE GREEN ALGAE

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Marine Antarctic green macroalgae actually comprises seventeen species with only three of them described as endemic. Because of the historical isolation of the Antarctic continent, this rate could be considered as low and is indeed only half the one reported for red and brown seaweeds in the region. Recent studies including molecular tools have allowed to improve the knowledge on diversity and level of endemism characterizing the Antarctic flora. In this study, we investigated marine green macroalgae diversity for specimens sampled along the Western Antarctic Peninsula (62°S up to 66°S), using two genetic markers (i.e plastid genes *tuf*A and *rbc*L). Our sequences were compared to public data depository, thanks to NCBI Nucleotide Blast Tool, and only the highest score was recorded for a match. In total, 122 specimens of Chlorophyta were sampled, and 85 *tuf*A and 16 *rbc*L sequences were obtained. Specimens belonged to 11 distinct genetic species supported by both genetic markers, and three new species were reported for the area: *Rosenvingiella radicans, Urospora wormskioldii* and *Ulvella islandica*. Molecular identification revealed strong match (interval confidence > 95%) between our Antarctic sequences and Genbank Northern hemisphere sequences for *Acrosiphonia arcta, R. radicans, U.islandica, Urospora penicilliformis* and *Urospora wormskioldii*. Our results are congruent with previous studies showing amphipolar distribution for various Antarctic *Trebouxiophyceae* and *Ulvophyceae. Amphipolar* distribution seems more common in green than red or brown Antarctic seaweeds and we hypothesize that recurrent long dispersal events could explain the low level of endemism observed for this phylum along the Antarctic coasts.

Financing: This work received financial supported from two projects led by Dra. Marie-Laure Guillemin: FONDAP-IDEAL 1515003 e INACH RG_15_16

Keywords: Antarctic green algae, barcoding, tufA and rbcL, amphipolar distribution, endemism.

E-Poster

MORPHOLOGICAL, GENETIC, AND ECOLOGICAL DIFFERENCES AMONG THE LOW-LATITUDE KELPS *EISENIA COKERI* AND *E. GRACILIS*

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The *Macrocystis* and *Lessonia* kelp have been extensively studied due to their commercial importance. While the third genus of kelps that is distributed in Peru, Eisenia, remains relatively poorly known, there is a growing interest in exploring its potential economic value. In a first step towards this aim, we used surveys along the Peruvian coast to characterize the distributional ranges of *E. cokeri* (6-14°S, 960 km of coast) and *E. gracilis* (15-17°S, 490 km), including previously unrecorded populations. DNA sequencing with mitochondrial, chloroplastic, and nuclear markers confirmed the distinctiveness of the two species. We then selected 3 populations of *E. cokeri* and 2 populations of *E. gracilis* to conduct a comparative ecology study of kelp populations and the epibiont macrobenthic communities associated with their holdfasts. At each location, we collected 30 individuals from the shallow subtidal, and then recorded several morphometric attributes and mass for each specimen. Compared to *E. gracilis*, *E. cokeri* specimens were significantly larger and more robust, with larger holdfast and longer and wider stipes. The macrobenthic community also tended to be more diverse and structured in *E. cokeri* holdfasts, compared to in *E. gracilis*. In addition, greater average richness and abundance was observed in the south compared to our northern sites. In the current context of assessing the commercial potential of *E. cokeri*, our results contribute to the development of conservation and sustainable management measures for *Eisenia* species.

Financing: Peru: Convenio de Cofinanciamiento N° 017-2016-FONDECyT, CONCYTEC; Inventario y Monitoreo de la Diversidad Biológica-IMARPE; UCSC Chile: DIN 22/2016; CIBAS-UCSC.

Keywords: Peru, holdfast, kelp

E-Poster

EVALUATING POSSIBLE INTROGRESSION BETWEEN TWO *AGAROPHYTON* NON-SISTER SPECIES LIVING IN SYMPATRY IN NEW ZEALAND

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Evidence of hybridization and introgression has been frequently observed in the field and in the lab in brown algae, even between species from distinct genera. Much less is known in red algae, but barriers to gene flow seem to be less porous with a gradual reduction of probability of crossing with increased genetic divergence and most report of hybridization made between sister species. This is for example the case in the family *Gracilariaceae* between *Gracilaria gracilis* and *G. dura*. Recently, the presence in sympatry of *Agarothyton chilense* and *A. transtasmanicum* (Gracilariaceae) was reported in New Zealand. *A. transtasmanicum* is a sibling lineage of *A. tenuistipitatum* and genetically divergent from *A. chilense*. While the distribution of *A. chilense* is extensive in New Zealand, *A. transtasmanicum* was observed in only five sites with the two species present jointly in four of these. *Agarophyton* species have the ability to shift between sexual reproduction via spore settlement on hard substrata and vegetative reproduction via growth of thallus fragments separated from their holdfast in sand and mud. In this study we used ddRAD and a 536 SNPs data set to study possible hybridization and/or introgression between the two species, in particular in the localities of Ohope and Hinahina where they reproduce sexually. Our results indicate only a low level of admixture between the two species (< 9% of the genome introgressed in 26 individuals over the 458 individuals studied), possibly reminiscent of historical rare crosses. The introgression was bidirectional between *A. chilense* and *A. transtasmanicum*.

Financing: FONDECYT 1170541

Keywords: *Agarophyton*, New Zealand, introgression

E-Poster

THE 33°S GENETIC BREAK IN CHILE: GENETIC CLINES AND INTROGRESSION PATTERNS IN A RED ALGA AND A SEA SQUIRT

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Hybridization zones are generally characterized by narrow geographic areas, with gene flow connecting differentiated lineages. Clinal variation of allelic frequencies, maintained by a balance between dispersal and selection against hybrids, is commonly observed. On the southeast Pacific coast, previous studies in *Mazzaella laminarioides* and *Pyure chilensis*

have shown the existence of a genetic break at 33-34°S with possible hybridization and introgression between the divergent lineages present in parapatry. *Mazzaella*, present a typical haplodiplontic red algal life cycle with the fecundation occurring on the female thalli and a low dispersal capacity. Contrastingly, *Pyure* is a tunicate with external reproduction, short larval dispersal, and sessile adult phase. The objective of this work was to characterize in detail the contact/hybrid zones of these two marine organisms at 33-34° S using two types of genetic markers (i.e., COI sequences and microsatellites genotypes) and a genetic cline approach. The cline approach allows to characterize the changes in population admixture along geographic transects and to contrast the shape of the discontinuities between mitochondrial maternally inherited markers and nuclear microsatellites. Spatial distribution of ancestry coefficients showed strong support of a cline in both organisms and identified narrow zones of genetic discontinuities in the Central coast of Chile for both organisms but with a sharper transition (<10km in *Mazzaella*, =30km in *Pyure*) characterized by less admixture in the case of *Mazzaella*. Differences in genetic patterns could be indicative of differences in the strength of barriers to reproduction and the magnitude of gene flow in these organisms.

Financing: Fondecyt regular N°1170541 and N°1130797

Keywords: Genetic clines, microsatelites, COI

E-Poster

LARGE-SCALE POPULATION GENOMICS OF *MACROCYSTIS PYRIFERA* ALONG THE SOUTHEASTERN PACIFIC COAST

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The giant kelp *Macrocystis pyrifera* is a cosmopolitan species that has the capacity to colonize large areas along the coast characterized by biogeographic discontinuities and large-scale environmental gradients. Here we provide an assessment of the spatial variation of the genetic diversity in natural populations of *M. pyrifera* present along the coast of Peru and Chile (12°S – 55° S) using RADseq markers. This was achieved by genotyping 834 individuals from 34 locations, using a total of 2000 filtered loci. We identified the presence of four genetic clusters separating the Peruvian (12°S-18°S), Chilean northern (18°S-32°S), Chilean central (32°S-42°S) and Chilean southern (42°S-55°S) regions, as well as significant substructure within regions (mean FST = 0.42). Isolation by distance patterns were observed within central and northern Chile clusters, but not in the Peruvian and Southern Chile clusters where other factors than dispersal capacity may operate. We explored the potential effect of temperature regimes in shaping effective population sizes and local adaptation patterns.

Financing: Programa de Magíster en Ecología Marina UCSC Facultad de Ciencias UCSCCONICYT/FONDECYT Regular (N° 1160930)

Keywords: Kelp, genomic structure population, Peruvian-Chilean coast

E-Poster

MORPHOLOGICAL AND MOLECULAR FEATURES OF THE GENUS *GRATELOUPIA* (RHODOPHYTA: HALYMENIALES): KEY TRAITS TO DETECT INVASIVE SEAWEED SPECIES IN URUGUAY (33º-35ºS)

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The frequency of biological invasions has been on the rise in recent years, with the increase of transport by humans moving many species out of their native ranges all across the globe. Uruguayan waters harbor dozens of non-native species and have been considered a critical biogeographical and ecological crossroad because of the complex interaction of currents and water masses. This region is thus a particularly well-suited system for the study of processes underlying biodiversity patterns. The red algae *Grateloupia turuturu* Yamada, native to Japan and Korea, has been reported as an introduced species in Europe, Oceania, North America and South America. Since 2015, *G. turuturu* has been recorded along the Atlantic coast of Uruguay, where there have been growing records of its presence. According to previous studies there are two putatively native species of *Grateloupia* on the coast, *G. cuneifolia* and *G. filicina*, reported since 1926. However, these three species possess variable morphological features implying possible misidentification. Morphological characterization is an efficient tool, but the addition of molecular markers adds confidence to the characterization of cryptic and morphologically variable species. Here we analyze samples collected over the past five years and retrieved from the MVM herbarium. Based on morphology, the three species of *Grateloupia* were detected along the Uruguayan coast. The molecular features are being attained via DNA barcoding using rbcL and cox genes, which are expected to further contribute to the understanding of the origin and diversity of *Grateloupia* in the temperate Southwestern Atlantic.

Financing: Fondo Vaz Ferreira, Ministerio de Educación y Ciencia, Uruguay

Keywords: Bioinvasion, Southwestern Atlantic, species identification

SYM05: Marine Forest ecology: sentinels and restoration

Keynote lecture

‘RESTORATION’ OR NATURAL RECOVERY OF MARINE ECOSYSTEMS: LESSONS FROM A DEVASTATING EARTHQUAKE IN SOUTHERN NEW ZEALAND

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Cataclysmic events are instructive about the ecological architecture needed to support nearshore ecosystems dominated by algal assemblages and attempts to restore them after disturbances. The 2016 Kaikoura earthquake in southern New Zealand lifted the coastal platform by up to 6m and caused devastation of algal beds and their associated communities along 130 km of coastline. Major algal species, such as the southern bull kelp *Durvillaea* spp., became locally extinct and because of their life histories and poor population connectivity have not recovered over 4 years. Attempts at using lab-reared individuals to establish small localised populations of bull kelp and other species, which could potentially act as propagule sources, have failed because of continuing problems of high temperatures, reef erosion, sedimentation, and altered reef topography. Our attempts at algal restoration contrasts with the good success we’ve had in restoring abalone populations in the same areas. Ours and other studies highlight that vital keys for restoration are minimising stressors and ensuring there is appropriate habitat relevant to early life stages. Even so, the best we can do is ‘jump start’ the natural processes that will lead to full recovery after disturbances.

Financing: MBIE, Ministry of Primary Industries, Sustainable Seas National Science Challenge

Keywords: Kelp, restoration, earthquake

Keynote lecture

GLOBAL EXTENT, PRODUCTION AND TRENDS OF MARINE ALGAL FORESTS

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lgal forests represent the most extensive coastal habitat in the ocean, believed to play an important role in supporting biodiversity and carbon fluxes in the ocean. Yet, reliable estimates of the area and global production of algal forests are not available, and estimates available in the literature have been carried over along a chain of citations from estimates, representing best guesses rather than empirical assessments, for nearly half a century. Here we build on new developments on global data on environmental drivers and observations of macroalgal presence and production around the world to provide a first estimate of their global extent, production and trends in marine algal forests globally.

Keywords: Marine algal forests, carbon fluxes

Oral presentation

A PICTURE OF KELP ECOSYSTEM RESILIENCE IN IRELAND

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Subtidal kelp forests in the north east Atlantic are dominated by the perennial species *Laminaria hyperborea*, which can produce over 11 kg raw biomass m–2 and provides carbon for food webs from the intertidal to the deep sea. This cold-water kelp is an ecosystem engineer that is slowly retreating from its southern distribution limit as the North Atlantic Ocean warms. Over the past three years, extensive collections of both bedrock and kelp tissue from kelp forests located across the coastline of Ireland have been sampled to investigate resilience in this foundation species from (1) an evolutionary perspective, as genetic structure in *L. hyperborea* will inform each population’s ability to withstand disturbance events and (2) an ecological perspective, as presence of microscopic kelp stages (outside their normal reproductive window) in the benthic biofilm (a theoretical ‘spore bank’) would inform the capacity of kelp forests to recover from periodic storm events throughout the year. We discuss how intensive sampling of this kind can reveal more intricate patterns of diversity in foundation species that display isolation by distance and have repositories of high genetic diversity in areas known to be refugia during the last glacial maximum. We also discuss the potential banking of microscopic stages as a mechanism to promote genetic diversity over longer timescales. This is the first step toward understanding population dynamics of *L. hyperborea* at a genetic level, including those of the microscopic haploid stage which is rarely studied.

Financing: Environmental Protection Agency 2018-W-MS-35 (“KelpRes: the diversity and resilience of kelp ecosystems in Ireland”)

Keywords: Population genetics, spore banks, *Laminaria hyperborea*

Oral presentation

FUCUS SERRATUS (FUCACEAE) IN NOVA SCOTIA FORMS A NEW PATTERN OF INTERTIDAL ZONATION IN THE WESTERN ATLANTIC

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Fucus serratus is a non-native species in Nova Scotia that, since its introduction in the 19th century, has become widely distributed, and is known primarily as a subtidal species. New observations starting in August 2020 showed a pattern of *F. serratus* in which the species had become a dominant canopy-forming species in the low intertidal zone. Here it was replacing the previously characterised zone-forming species, Chondrus crispus, and was becoming a dominant in parts of the lower shore that would have been occupied by Ascophyllum nodosum. Qualitative evidence in the form of photographs and the occurrence of F. serratus in wrack demonstrated abundant populations along sites examined over 30 km and 40 km stretches of outer coast in Yarmouth and Lunenburg Counties, respectively. Quantitative estimates of cover based on transects at Chebogue Point and Kingsburg indicate dramatic changes in intertidal zonation along the Atlantic coast of Nova Scotia in which 10–15 m of intertidal zone comprising 15% to 40% of the horizontal extent of the shore had 75% to 100% cover of *F. serratus*. Further surveys are needed to confirm the overall distribution and impact of this invasive fucoid on intertidal communities. Experimental evaluation of colonisation is currently being carried out to further characterise the dynamics of this process, and the potential threat to the commercial harvest of *Ascophyllum.*

Keywords: *Fucus serratus*, fucaceae, intertidal zonation

Oral presentation

INCREASED HEAT RESILIENCE OF INTRASPECIFIC HYBRIDS COMPARED TO INBRED LINEAGES OF THE KELP *LAMINARIA DIGITATA*: PHYSIOLOGY AND TRANSCRIPTOMICS

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Kelps, the marine forest foundation species, are threatened by ocean warming at their warm distributional edges. To mechanistically investigate inheritance of thermal traits, we assessed thermal tolerance of inbred (selfings) and outbred (crosses) sporophytes of the N-Atlantic kelp *Laminaria digitata* among isolates from the genetically distinct populations of Helgoland (North Sea) and Spitsbergen (Arctic). First, we investigated the upper thermal tolerance of microscopic sporophytes in a 14-day experiment applying 20–23°C. The upper survival temperature was lower for the Spitsbergen selfing (21°C) than for the Helgoland selfing and the reciprocal crosses (22°C). We then subjected 4–7 cm long sporophytes to a control temperature (10°C), moderate (19°C) and sublethal heat stress (20.5°C) to assess metabolic regulation via whole-transcriptome analysis in addition to physiological parameters. Growth and optimum quantum yield decreased similarly in both crosses and the Helgoland selfing at 19 and 20.5°C, while inbred Spitsbergen sporophytes died within seven days at both 19 and 20.5°C. At 10°C, the Spitsbergen selfing showed the highest differential gene expression. Considering only the three surviving lineages at 20.5°C, differential gene expression was 61–78% lower in the crosses compared to the Helgoland selfing, including reduced expression of transcripts related to cellular stress responses. This implies that both intraspecific crosses maintained a growth response similar to the Helgoland selfing with reduced metabolic regulation during sublethal heat stress, indicating subtle heterosis (hybrid vigour) as a beneficial effect of outbreeding. Results are discussed in the frame of mariculture and marine forest restoration.

Financing: Funded by German Research Foundation (DFG; grant no. VA 105/25-1) in the 2015-2016 BiodivERsA COFUND call (program MARFOR)

Keywords: Heat stress, transcriptomics, outbreeding

Oral presentation

INTEGRATING LOCAL ECOLOGICAL KNOWLEDGE IN THE STUDY OF LONG-TERM CHANGES ON MARINE KELP FOREST ECOSYSTEMS

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Kelp forests are one of the most important marine habitats in temperate areas, supporting populations of species with high socio-economic value. However, in the last decades have been reported dramatic retreats of kelp species worldwide, with consequences for the ecosystem services that these habitats specifically provide for Small-Scale Fishing Communities (SSFC). In addition, there is a clear lack of wider knowledge on the consequences of Kelp forest reduction and the ecosystem services for SSFC. In this regard, as a first step, in this study we have integrated the SSFC knowledge to assess the loss of kelp forests and its implications in NW Iberia, using the historical perspective of fishers whose fisheries are associated with this habitat. For this porpoise, data on fishers' ecological knowledge was documented through interviews.

A semi-structured questionnaire with open-closed questions about their small-scale fishing activity and target species was made. Then, they were asked to color in a nautical chart the areas in which they were aware of the presence of kelp forests 20 years ago and now. Features mapped were systematized in a GIS with polygon shape files, and compared with maps developed with the help of key informants (i.e. divers, scientists). Preliminary results have allowed us to obtain a map with the distribution of kelp forests dominated by *Laminaria ochroleuca* in the last 20 years, and key fisheries associated. This information will be very useful to develop tools for the conservation of this key species and evaluate its socio-ecological and economic implications for SSFC.

Keywords: Kelp forest, Small-Scale Fishing Communities (SSFC), mapping

Oral presentation

FUCALEAN ALGAL FORESTS IN THE MEDITERRANEAN SEA: CURRENT STATUS AND CHALLENGES FOR RESTORATION

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Fucalean brown algae of the genera *Carpodesmia, Cystoseira* and *Treptacantha* are a typical feature of shallow subtidal Mediterranean habitats, where these habitat-forming seaweeds produce canopies playing a key role in the functioning of coastal ecosystems. In recent decades these communities have undergone a major decline in cover and biomass; this has generated increasing interest towards their conservation and restoration. Recent modelling studies based on distribution data for 20 species showed that fucalean canopies are currently present along the Mediterranean coastline for 6,342.41 km out of a total coastal length of 46,000 km. Topographic coastal slope and nature of substrate were shown to be the main factors controlling their distribution. Factors considered proxies of human impact, such as the distance from ports and urban areas, were also identified as important, confirming the negative effects of pollution and urbanization on these communities. Recent restoration initiatives have utilized recruitment enhancement methods by ex situ and in situ techniques based on production of juvenile specimens in the laboratory and in the field, respectively. Successful reforestation at local scale was obtained for *Carpodesmia amentacea* in northern Italy, *Treptacantha barbata* in the Balearic Islands and *Treptacantha elegans* in Catalonia. These trials indicated also that heavy grazing and destructive storms represent major challenges for these projects. We conclude that large scale restoration is possible, but requires baseline information with an in-depth knowledge of the species ecology and of the areas to be restored, together with the development of cultivation protocols to make consistently efficient restoration interventions.

Financing: Executive Agency for Small and Medium Enterprise (EASME) and European Maritime and Fisheries fund (EMFF) - AFRIMED Project

Keywords: Fucales, Mediterranean Sea, environmental restoration

Oral presentation

MITIGATION SOLUTIONS IN THE RESTORATION OF A CANOPY-FORMING BROWN ALGA TO FACE REPRODUCTIVE STOCHASTICITY AND GRAZING IMPACTS

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The decline of *Cystoseira sensu lato*, due to the interplay of human and climatic impacts, emphasizes the need to implement effective solutions to restore these habitats and to re-establish the services they provide. Two ex situ restoration efforts of *Treptacantha barbata* were performed in a marine protected area in the Adriatic Sea in 2019. The first one in winter, after a marine heatwave that anticipated the species fertility, the second one in spring, when the species usually reproduces. This is the first case in which the effects of a reproductive shift in response to a sea thermal anomaly are assessed for seaweed in a restoration context. The study aimed to evaluate the disruptive effects of a thermal anomaly on the reproductive biology and culture performance of *T. barbata*, and the impact of grazing on juveniles. The first cultivation was ten times more efficient in terms of zygote release with germlings four times longer, despite both cultures being performed under the same conditions. To mitigate the low efficiency of the second culture and to avoid prolonged highly-demanding maintenance in the mesocosms, the cultivation period was extended outdoors using a suspended structure that also avoided the impact of mesograzers on small juveniles. The modular frames conceived for *T. barbata* proved to be effective for the outplanting of subtidal species, because of their easy operability and low cost. Controlling for herbivorous fish had significant positive effects on both juvenile survival and growth.

Financing: This study was supported by the LIFE financial instrument of the European Community, project ROC-POP-LIFE (LIFE16 NAT/IT/000816).

Keywords: *Ex situ* restoration, heatwave, grazing

Oral presentation

LAMINARIA OCHROLEUCA PARADOXICAL FAILURE TO CONSOLIDATE KELP FOREST INSIDE A MARINE NATIONAL PARK

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Kelp forests, one of the world's most productive ecosystems, have been in decline in many regions in recent years. Climate change, through gradual sea warming or marine heatwaves, is one of the main culprits of the deforestation. Nevertheless, kelp forest decline may also depend on another non-climatic stressor such as grazing. In NW Spain, the conservation status of these habitats is poorly known but a range of stakeholders has reported the decline of *Laminaria ochroleuca* inside the Islas Atlánticas Marine National Park (Cíes archipelago) in the last years. However, the extent of this decline has not yet been investigated. Using a combination of quadrat-scale (biomass, abundance) and transect-scale (cover) surveys over one year, we found striking differences between the populations of *L. ochroleuca* located inside and outside the Marine National Park (MNP). As expected for a perennial seaweed, outside populations were typical kelp forests, stable year round, and mostly composed of adults. In comparison, *L. ochroleuca* seemed unable to attain the mature kelp forest stage inside the MNP. Mid-sized young plants were detected only in autumn but many had disappeared by winter, and the ones that remained were just a stipe with no blade and no growth meristem. As a result, spring and, in particular, summer populations were entirely composed of new recruits. Therefore, grazing seems to be inhibiting the recovery of mature kelp forests within the MNP; the causes that may have led to this new regime are discussed.

Financing: Biodiversity Foundation and the Ministry of Ecological Transition and Demographic Challenge and Xunta de Galicia and the European Social Found.

Keywords: Kelp, herbivory, NW Spain

Oral presentation

TOWARDS THE RESTORATION OF CANOPY-FORMING BROWN ALGAE IN THE MEDITERRANEAN SEA: BIG CHALLENGES AND SOME WINS

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In the Mediterranean Sea, marine forests constituted by brown algae of the genus *Cystoseira sensu lato* (s.l.) play a valuable role as foundation species. Due to the evidences of regression/loss of these habitats caused by different factors, active restoration techniques are encouraged by European legislation. In the framework of the EU project ROCPOP-Life, the *ex situ* outplanting restoration technique was applied in the Mediterranean to repopulate two different *Cystoseira s. l.* species: *Cystoseira amentacea* var. stricta and *Treptacantha barbata*. This technique consists in three main steps: i) collection of fertile apices, ii) culturing juveniles under laboratory conditions and, iii) outplanting, i.e., the deployment of the cultured juveniles in the field. Since the two target species thrive in different habitat, midlittoral for *C. amentacea* and subtidal for *T. barbata*, these species are differently subjected to environmental factors. Therefore, the implementation of the *ex situ* restoration action was designed according to the requirements of each species, particularly for the outplanting step. In the case of the midlittoral species the direct attachment of the substrates was used to deploy the juveniles in the field, where heat, desiccation and wave exposure are the main factors to face. For the subtidal species, a complex multiple attachment device and strategy was used against grazing, the most challenging disturb. However, unpredictable challenges as thermal anomaly and huge storms were also tackled during the performance of these restoration actions. Nevertheless, both actions obtained relevant results encouraging further studies of this novel approach to guarantee and preserve marine biodiversity.

Financing: This study was supported by the LIFE financial instrument of the European Community, project ROC-POP-LIFE (LIFE16 NAT/IT/000816)

Keywords: Restoration, *ex situ* outplanting, *Cystoseira sensu lato*

Oral presentation

USING GENOMICS TO DESIGN AND EVALUATE RESTORATION AND FUTURE-PROOFING OF UNDERWATER FORESTS

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Restoration is an emerging intervention to reverse the degradation and loss of marine forests and the ecosystem services they underpin. Genetic characteristics of restored populations have the potential to greatly influence both short and long-term success, however this is rarely empirically examined within restoration projects. We used genomics to design a restoration program for lost forests of *Phyllospora comosa*, a dominant macroalga that went locally extinct from reefs off Sydney, Australia. Population genetic diversity and structure of extant populations informed choice of donor sites. We tested whether donor provenance influenced adult transplant survival, condition and the genetic characteristics of recruits at restoration sites. Donor provenance influenced survival and condition of transplanted adults and recruitment levels varied significantly among restoration sites. Yet, recruitment was rapid and genetic diversity and structure of the F1 generation resembled extant populations, suggesting the ability to "design" populations. We then used seascape genomics to characterise gene-environmental associations along *Phyllospora's* entire latitudinal (12o latitude), and thermal (~14oC) range to screen for potential thermally-adapted genotypes that may be used in future-proofing efforts. Despite low diversity, range-edge populations are likely to harbour beneficial adaptations to marginal conditions and the overall adaptability of this species may be compromised by their loss. As restoration and the need to 'future-proof' marine ecosystems increase globally, it will be critical to understand and harness the role of donor provenance, genetic diversity and structure to optimise restoration success.

Keywords: Restoration, genomics, climate change

Oral presentation

IMPROVING ECOSYSTEM REPRESENTATIONS WITH ECOTONES – CASE STUDY OF SUBTIDAL BENTHIC COMMUNITIES IN SOUTHERN NEW ZEALAND

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The characterisation of ecological communities has long been influenced by typological approaches, resulting in the consideration of communities as separate, albeit linked, entities. In other words, the transitions (i.e. ecotones) between communities are rarely characterised. In this study, an alternative approach, based on fuzzy clustering, is used to integrate ecotones in ecological representations. It marks a shift from considering ecological communities as coherent blocks to the recognition of continuity and variability both within, and between ecosystem components. To test this method, we used data from 684 photoquadrats along six transects in the benthic subtidal environment of Southern New Zealand fjords. Our results confirm the narrow depth stratification of benthic communities, and identify diverse community types in the region, confirming the importance of these fjords for the conservation of marine biodiversity. The position of ecotones coincided with main environmental transitions. Ecotones characteristics, however, were community dependent, and probably the result of a mixture of biotic interactions and individual species responses to stress gradient. Alpha diversity was mostly constant within community types, but varied across ecotones, with occasional peaks around communities dominated by canopy forming species (e.g. *Ecklonia radiata* and *Carpophylum flexuosum)*. The integration of ecotones in community characterisation facilitates investigations on the patchiness of ecosystems, and improves our understanding of community assembly rules and biodiversity patterns. The set of analyses used in this study have been compiled in a R package and are freely available. We therefore encourage the integration of ecotones in future research on the spatial structure of ecosystems.

Keywords: Ecotone, fjords, fuzzy-cluster

Oral presentation

THE FATE OF TREPTACANTHA BARBATA (FUCALES) IN THE NORTH-WESTERN MEDITERRANEAN SEA

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In the Mediterranean Sea, seaweed marine forests are shaping the rocky reefs and are considered as one of the most important benthic assemblages for the coastal ecosystem functioning. Among the Fucales, *Treptacantha barbata* (syn. *Cystoseira barbata*) is a long-lived species usually growing in very shallow, sheltered and well-lit reef habitats and inside coastal lagoons. This habitat forming species has a high primary production and sheds in winter floating secondary branches with aerocysts. Within the genus *Cystoseira sensu lato*, it is one of the rare species able to spread over long distances. We assessed the past and current distribution of the species along the French Mediterranean coast, including Corsica and lagoons. Thanks to historical data dating back to the 19th century, we reconstructed and analyzed the long-term evolution of its distribution in relation to a variety of disturbances. The current distribution was established based on an extensive survey by snorkeling (~ 2 600 km of coast). From a GIS analysis, *Treptacantha barbata* can currently be considered regionally extinct in French Catalonia and Western Provence and functionally extinct in the French Riviera. In Languedoc, the species is extinct in the open sea and still present in some coastal lagoons despite severe competition with introduced seaweeds, especially the invasive *Sargassum muticum*. In contrast, populations of *T. barbata* have remained stable in Eastern Provence and Corsica. The main possible causes of decline are overgrazing by herbivores, habitat destruction and the competition with invasive species. Potential sites for restoration have been identified.
Financing: MARFOR

Keywords: Fucales, Mediterranean Sea, conservation

Oral presentation

LESS THAN THE SUM OF ITS PARTS: BLADE CLUSTERING REDUCES DRAG IN THE BULL KELP *NEREOCYSTIS LUETKEANA*

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Flow-induced drag is an important determinant of kelp morphology. Kelps have various strategies to minimize drag and avoid dislodgment, many of which have been well documented and studied. In this study, we consider how the multi-bladed morphology of the bull kelp, *Nereocystis luetkeana*, might reduce drag through the interactions between its many blades. To understand this, we measured drag on individual blades and developed a model to estimate how much drag a bull kelp might experience if interactions between its many blades afforded it no drag-reducing benefit. We compared these estimations to measurements of drag on intact kelps, and continued measuring drag as we removed blades one by one in order to understand how drag depends on blade number. We found that intact bull kelp experience less than half of the drag that their blades would experience in isolation, and that this benefit is actually more pronounced at higher blade numbers. This may be why this species tends to have more blades when found in habitats with more intense flow. Overall, this species' multi-bladed morphology is likely part of what allows it to grow in hydrodynamically stressful environments.

Financing: Natural Sciences and Engineering Research Council of Canada, The University of British Columbia, Bamfield Marine Sciences Centre

Keywords: Drag, biomechanics, kelp

Oral presentation

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

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Large canopy-forming seaweeds are essential to support biodiversity through habitat provision and amelioration in coastal ecosystems worldwide. These habitats are being threatened by environmental and anthropogenic disturbances with severe consequences for community functioning and the benefits provided by coastal ecosystems to mankind. Therefore, understanding the ability of coastal communities to resist and recover from severe disturbances, such as the local extinction of canopy-forming species, is of widespread relevance for fundamental and applied ecology. We manipulated the presence of *Durvillaea incurvata* in field experimental plots (n=20), to assess canopy loss effects on community composition and function. We focused on their ability to remain unchanged under external stress (resistance) as well on their ability to return to its former reference state (recovery). Canopies were completely removed once in half of the plots, while the others were kept undisturbed. Plots were monitored each three months after the pulse disturbance and species cover and density were quantified to indirectly estimate community biomass as a measure of community function. After the pulse disturbance, a notable increase (relative to controls) in barnacles, red calcified seaweeds *Lithothamnion* sp. and *Corallina officinallis* was observed. Albeit a high recruitment of *D. incurvata* could have enhanced the compositional resistance of the disturbed communities, the decrease in community biomass due kelp loss was not fully recovered a year after the disturbance. Hence, we conclude that functioning and composition resistance were low, and that the "alternative" community was unable to compensate and recover the biomass of bull kelps in the short term.

Financing: Proyecto Fondecyt 1190529

Keywords: Stability, marine forest, bull kelp

Oral presentation

CLIMATE-DRIVEN EVOLUTION OF MARINE FORESTS ACROSS OCEANS

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Climate-driven contact zones, caused by convergent range shifts of compatible but differentiated genetic lineages, are opportunities for evolutionary breakthroughs by rapid genome recombination creating novel selective variants. Such climate drivers of rapid evolution may also take place during colonization/migration into novel habitats/niches, leading to rapid genetic biodiversity change. These processes shape the major question of this talk: What are the consequences of rapid climate-driven genomic changes, by lineage recombination and other rapid selective or stochastic climate effects, for the distribution of genetic biodiversity along changing marine coastlines? This talk will describe case-studies of climate-driven evolutionary patterns and processes of genome divergence and recombination taking place in marine forests of brown algae as lineages radiate by dispersal and vicariance, with realized niche divergence and re-contact in parapatry. These questions are here addressed with fine population-scale genetic markers combined with geographic scale distribution data and local fine-scale habitat mapping among distinct and recombined lineages. Changes in genomic differentiation and diversity develop phenotypically undetected until tipping points are overturned. Since marine forests are key foundation species, shaping complete ecosystems where they occur, such genomic biodiversity tipping points may directly affect their ecological roles and evolutionary potential under a shifting climate.

Keywords: Marine forests, contact zones, evolution

E-Poster

FFECT OF IRRADIANCE ON THE EMBRYOGENESIS OF THE THREATENED MACROALGA *TREPTACANTHA ABIES-MARINA* FROM THE CANARY ISLANDS

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The populations of brown canopy-forming algae of the genus *Treptacantha* are showing a drastic decline in the Canary Islands, which is directly affecting the ecosystem services they provide. The threatened species *Treptacantha abies-marina* has reduced more than 90% the extent of its populations during the last 30 years. The environmental factors responsible for population regression are still unknown. Among them, irradiance can be a potential factor causing losses, since the populations on the northern coasts of the islands affected by the natural protective screen of the sea of clouds are the best conserved. As populations decrease in density, the early developmental stages of the life cycle (zygotes) that colonize sustrate next to parent plants lose the protection (filter) of the canopy. To test this hypothesis, a laboratory experiment was designed selecting three irradiance scenarios: (1) zygotes remain under the protection of adults in dense populations (150 µmol photons m-2 s-1); (2) zygotes exposed to population fragmentation (300 µmol photons m-2 s-1); (3) zygotes exposed to sunlight (450 µmol photons m-2 s-1) simulating a highly fragmented population. After 21 days of experiment, statistical analyzes indicate that irradiance is not a limiting factor in embryogenesis or subsequent establishment of zygotes. Knowing the drivers that cause the loss of populations will help in the selection of adequate conditions and methods to address their restoration.

Financing: Research reported was funded by Fundación Biodiversidad (Ministerio para la Transición Ecológica y el Reto Demográfico, Gobierno de España)

Keywords: *Treptacantha abies-marina*, zygotes, irradiance

E-Poster

AUTOMATED DETECTION OF LARGE BROWN MACROALGAE USING MACHINE LEARNING ALGORITHMS – A CASE STUDY FROM WELLINGTON, NEW ZEALAND

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Large, canopy-forming brown macroalgae (Laminariales and Fucales), are globally recognised as critical components of coastal ecosystems. International studies have reported on the loss of subtidal macroalgal forests in temperate and subtropical marine ecosystems, particularly on urbanised coasts. In New Zealand, rocky reefs are dominated by diverse algal communities which form large beds with species composition differing with geographic distribution, but the lack of baseline data mean it is not possible to assess changes. We investigated the potential of Machine Learning (ML) in the analysis of underwater videos, and developed an algorithm to identify four macroalgal groups: *Ecklonia radiata, Lessonia variegata, Carpophyllum* spp. and all macroalgae. The machine learning models were successful at identifying and distinguishing all four macroalgal groups across the entire survey, with overall models attaining high performance accuracies of between 80.6 to 87.1 % for individual species and genera, and 97.2% for the 'all-macroalgal' group. Two distribution maps (presence/absence) for each of the four species/groups were produced: the overall prediction map (which indicated the highest certainty for determining the distributions), and the overall uncertainty map (to examine where rare occurrences of each taxon occurred). This study shows that ML can provide a significantly faster and cost-effective approach to post-processing video imagery and will improve as more data are collected. ML models performed well at detecting and distinguishing between closely related species (*Lessonia variegata* and *Ecklonia radiata*), highlighting the accurate fine-tuned performance of these models.

Keywords: Kelp, machine learning, monitoring

E-Poster

EPIBIONT HYDROIDS OF *SARGASSUM* SEEDLINGS IN LA PAZ BAY, BAJA CALIFORNIA SUR, MEXICO

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Macroalgae are among the most recurrent natural substrate for hydroids because they offer a rigid space, constant growth, and stable abiotic conditions. Hydroids are cnidarians of the Hydrozoa class belonging to the superorders "Anthoathecata" and Leptothecata; they are characterized by alternating generations and a planula's development larva, which can originate a sessile polyp benthic organism. To the west of La Paz Bay, Baja California Sur, Mexico, the genus *Sargassum's* macroalgae predominate in number and cover large areas. The studies on distribution, seasonality, or Sargassum's phenology do not consider the associated fauna in their different development stages. Hydroids are pioneers in the settlement and colonization of new substrates; thus, it was decided to work with *Sargassum* seedlings since they are the first phase of *Sargassum* development, allowing the colonization pattern seedlings. Therefore, this study aims to characterize the epibiont hydroids of benthic seedlings of the genus *Sargassum*. The samplings were made monthly from November 2019 to March 2020 on two beaches in La Paz Bay. The samples were fixed in 70% ethanol, the height of each thallus axis was measured, and the hydroids were identified morphologically. Also, the percentage of hydroid coverage in Sargassum seedlings was calculated. As a result, we recorded 18 colonies of hydroids associated with 24 *Sargassum* seedlings. All hydroids belong to Leptothecata; two species correspond to the Obeliida infraorder, and two more to the Plumupheniida infraorder. Hydroids on leaves were more frequently observed than with axes and aerocysts.
Financing: CONACYT-428225, Macroalgas introducidas. Medusozoa México. Proyecto 20411_Cursos Medusozoa CIBNOR

Keywords: Marine epibiosis, Phaeophyceae, sessile life

E-Poster

KELP FOREST PRIMARY PRODUCTION AT A ROCKY SHORE SITE IN TIMES OF GLOBAL WARMING - *LAMINARIA HYPERBOREA* ALONG HELGOLAND

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Investigating the primary production of kelp forests is crucial for a validated ecological model of these important habitats in face of ocean warming. The island of Helgoland (North Sea, Germany) is a hotspot of biodiversity and primary production. Here, *Laminaria hyperborea* is the biomass-dominant kelp species with the widest depth distribution (approx. -1 to -15m). In autumn 2020, *L. hyperborea* was sampled along a depth gradient; discs cut from the meristem were exposed to different temperatures (14 and 18°C) over one-week. We measured maximum quantum yield (Fv/Fm), growth, photosynthesis-irradiance curves (PI-curves), oxygen production and carbon fixation (14C-method). Finally, the photosynthetic quotient (PQ) was calculated. Over one week, discs did not grow and showed no change in Fv/Fm. After the acclimation period, the saturating irradiance showed no significant difference between depths; however, 6m algae were saturated at lower irradiance. Furthermore, the maximum photosynthetic rate showed significantly higher values at 18°C than at 14°C. After one week, oxygen production was significantly lower in *L. hyperborea* from 4m and 14°C, while carbon uptake rate did not significantly differ between depths and temperatures. In general, the PQ was higher at 18°C among both depths due to a high oxygen production. These preliminary data suggest a higher production under increased temperatures. Conclusively, the PQ is influenced by different abiotic factors and should be calculated for every setup separately to receive a specific PQ. Our measurements will be repeated in every season and this knowledge will be integrated in a dynamic kelp primary production model.
Financing: DFG-funded project GR5088/2-1

Keywords: Primary production, photosynthetic quotient, carbon fixation

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E-Poster

ECOLOGICAL QUALITY STATUS OF THE MARMARA SEA (TURKEY) BY THE FELDMANN INDEX, WITH A NEW FORMULA PROPOSAL

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Marine macroalgae are a good bioindicators to assess for the ecological quality status of the marine coastal waters. In the present study, the Feldmann Index R/P (Rhodophyta/Phaeophyceae) was tested to assess of the ecological quality status of the Marmara Sea (Turkey) by using marine algal flora. Macroalgal sampling was made from 25 stations between 2015 and 2017. In total, 320 macroalgal taxa (98 Phaeophyceae, 158 Rhodophyta, 64 Chlorophyta) were found. The study revealed high ecological quality for 2 sites, good quality for 4 sites, moderate quality for 5 sites, poor quality for 7 sites, and bad quality for 7 sites. Also, a new formula, P/R+C (Phaeophyceae/Rhodophyta+Chlorophyta), are proposal to assess of the ecological quality status of the marine coastal waters by using marine algae. The study revealed good ecological status class for 4 sites, moderate for 4 sites, poor for 5 sites, and bad for 12 sites. The relationship between the pressure index MA-LUSI (Land Uses Simplified Index for shallow water macroalgal communities) and new formula was tested, and a negative linear relationship was found.

Financing: This study has been supported by Tübitak (Project Number 114Y238).

Keywords: Ecological status, Feldmann Index, Turkey

E-Poster

DECLINE OF SUBLITTORAL CANOPY SPECIES IN THE SUBTROPICAL ATLANTIC OCEAN: THE CASE OF *TREPTACANTHA ABIES-MARINA* IN THE CANARY ISLANDS (SPAIN)

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Fucoids and kelps are engineering species that play an important role in the coastal marine ecosystems. But in the last decades, these species have suffered a drastic regression, especially in temperate regions. This study presents the recent spatial distribution of *Treptacantha abies-marina*, the most important canopy-forming macroalgae of the occidental islands of the Canary Archipelago, in the northeast of the Atlantic Ocean. Besides, the methodology used to get reliable maps of distribution and the environmental variables that may be drivers of decline are detailed. The comparative analysis of the spatial distribution of this species with historical maps of 1987 allows establishing the present conservation status of this species that is found here its southern range limit. The results show that nowadays the extension of the populations of *Treptacantha abies-marina* represents only 3% of the area occupied 30 years ago. As a consequence, it has been considered to increase the level of protection as a vulnerable species in the Spanish Catalogue of Threatened Species.

Financing: European Regional Development Fund and the Government of the Canary Islands

Keywords: *Treptacantha abies-marina*, decline, spatial distribution

E-Poster

SMALL-SCALE HABITAT COMPLEXITY EFFECTS OF MARINE MACROALGAL HABITAT ON ASSOCIATED EPIFAUNAL ASSEMBLAGES

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Marine macrophytes, such as seagrasses and macroalgae, are essential habitat-forming organisms in temperate and subtropical marine ecosystems. The diversity of macroalgal species and morphological forms can directly impact the biodiversity of associated fauna, including small invertebrate epifauna. This especially applies to tropical areas where there is a vast diversity of macroalgae and invertebrate epifauna. However, these same tropical shallow coastal systems are also limited in study. Furthermore, there are many approaches to quantify habitat complexity, each with their own benefits and drawbacks. This study aims to quantify and compare levels of morphological complexity of various marine macroalgal species, and determine correlations of complexity with epifaunal diversity. Dry biomass was used as a measurement of habitat availability, while fractal dimensions were used as a measurement of habitat architecture. Samples were collected from Key Largo, Crandon Park, and Deering Estate in south Florida. Individual samples were scanned using WinRHIZO software for image analysis of the macrophytes. Currently, 80 samples were collected, representing 3 species of macroalgae with differing morphologies. Significant differences were found in fractal dimensions among macroalgal species ($p < 0.05$). Multiple regression analyses found that epifaunal richness and abundance correlated well with macrophyte species richness and total dry biomass per habitat ($p < 0.001$), although the strength of those correlations varied ($R2 = 0.14 – 0.26$). Both diversity of macrophyte species and architectural forms should be considered as essential habitat components when conducting biodiversity assessment, especially for bioassessments related to macrophytes and invertebrate epifauna.

Keywords: subtropical ecosystems, associated fauna, epifauna

SYM06: Algae and biotic interactions: introducing the symbiome

Keynote lecture

THE MOLECULAR BASIS AND EVOLUTIONARY CONSEQUENCES OF VITAMIN EXCHANGE BETWEEN MICROALGAE AND THEIR BACTERIAL PARTNERS

Alison Smith, Andrew Sayer, Andre Holzer, Shelby Newsad, Ellen Harrison, Marcel Llavero Pasquina, Payam Mehrshahi

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Despite their photoautotrophic lifestyle over half of all microalgae require an external supply of vitamin B12 (cobalamin) for growth, and ~20% require vitamin B1 (thiamine). B-vitamins are essential enzyme co-factors and so the widespread nature of these traits is surprising. However, vitamin auxotrophy is common in the microbial world, and likely underpins many microbial communities. We have demonstrated that growth of algal auxotrophs can be supported by

coculturing with bacteria that synthesise the vitamins. Using information from sequenced genomes, together with defined laboratory co-cultures and modelling approaches, we are dissecting the molecular basis for B12 utilisation, including identifying a key protein involved in its uptake, understanding its role in regulating the central C1 pathway of metabolism, and revealing a potential role in epigenetic processes that might explain the evolution of B12-auxotrophy.
Financing: Research supported by BBSRC and Gates Cambridge Trust

Keywords: B-vitamins, genomics, C1 metabolism

Keynote lecture

THE ROLE OF MICROBES IN THE ECOLOGY OF HABITAT-FORMING SEAWEEDS

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Marine habitat-formers underpin critical ecosystem goods and services along the world's coastlines, but are declining globally due to multiple stressors. Such widespread declines, together with dire predictions of future environmental conditions, have prompted the development of management interventions to recover, conserve and/or enhance ecosystems now and into the future. Most of our understanding and management of coastal ecosystems is based on our understanding of the ecology and biology of macro-organisms. But we live in a 'microbial world'. Microbes are ubiquitous in the ocean, where they play critical roles in the health and functioning of habitat-forming 'hosts'. Understanding host-microbe interactions may thus allow harnessing the power of microbes to build resilience of habitat-forming 'holobionts' (host plus their microbiome) in the face of environmental change. However, the integration between studies of microbes and the well-established theory and practice of benthic 'macrobial' ecology remains a fundamental challenge. Using experiments on seaweed-microbe interactions, I demonstrate the need to move beyond simple descriptions of patterns to understanding mechanisms and processes, and propose possible ways forward. I argue that experimental ecology provides the tools necessary for the advancement of our understanding of holobionts and the development of future-proofing strategies.
Financing: Australian Research Council

Keywords: Microbes, holobiont, kelp

Oral presentation

CHARACTERIZING THE *ULVA* MICROBIOME WITH LONG-READS FROM NANOPORE SEQUENCING

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The green seaweed *Ulva* is a model to study algal-microbiome interactions. Bacteria particularly are known to play a crucial role in the morphological development during the host's various life cycle stages. Here, we present the diversity of bacteria associated with *Ulva* collected from different locations in the North Sea and from an aquacultural setting, using Oxford Nanopore MinION sequencing technology to obtain long-reads covering the whole 16S rRNA region. Despite the lower accuracy of Nanopore-derived reads compared to Illumina technology, prior microbiome studies showed that long reads increase taxonomic resolution. However, protocols for Nanopore sequencing of the seaweed microbiome have not been published before. Chloroplast contamination may pose a problem as the plastid DNA is highly similar to that of cyanobacteria, and the lack of bioinformatical tools designed specifically for long-reads further complicates analyses. We used two different bioinformatical pipelines: 1) Nanopore's cloud-based EPI2ME platform (which employs the NCBI 16S database), and 2) an in-house developed script using Kraken2 to assign taxonomy with the Silva or GreenGenes 16S databases. The *Ulva* microbiome, based on tissue and swab samples, was very different from the environmental microbiome (sediment and seawater), but the variation between individuals was high. Despite the high variation, we could detect significant differences in bacterial composition and relative abundance between sample sites, especially between natural rocky shores and artificial sites. Our results show that Nanopore sequencing can be used to characterise the *Ulva* microbiome and that the Kraken2 pipeline in combination with the Silva database is most accurate.
Financing: LM van der Loos has been granted a FWO PhD Fellowship fundamental research

Keywords: Microbiome, *Ulva*, archaea

Oral presentation

UNCOVERING DRIVERS OF HETEROTROPHIC BACTERIAL PRODUCTION AND HYDROGEN PEROXIDE IN MACROALGAL HABITATS

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Microbial communities are key players in carbon cycling and retention within in macroalgal habitats. Through the microbial loop, heterotrophic bacteria reintroduce biologically available carbon to the ecosystem after release by macroalgae. However, macroalgae simultaneously release hydrogen peroxide (H2O2), a known cellular stressor and inhibitor of heterotrophic bacterial production. To understand patterns in microbial community characteristics with changing habitat type and season, 4 sampling trips were carried out across 12 months, measuring in situ heterotrophic bacterial production, bacterial abundance, H2O2 concentrations, and light levels within beds of 2 habitat forming macroalgae, *Macrocystis pyrifera, Ulva* sp., and open water habitat. H2O2 concentrations were highest in summer and lowest in winter, varying between species. Contrary to hypotheses, bacterial production and H2O2 concentrations were found to be tightly coupled across both macroalgal species and season. It was hypothesized that algal-derived dissolved organic carbon (DOC) was the driving factor in both H2O2 formation and heterotrophic bacterial production. To understand what drives patterns seen across seasonal trips, an extra sampling event was carried out during Summer in which DOC, 16S rRNA amplicon, and Biolog Ecoplate™ analyses were carried out in addition to all previous parameters. Determining the drivers of bacterial community characteristics in beds of macroalgae will increase our understanding of how different species support diverse ecosystems and influence habitat quality.

Keywords: Hydrogen Peroxide, dissolved organic carbon, bacterial production

Oral presentation

EPIPHYTIC MACROALGAE CO-OCCURRENCE PATTERNS IN THE CUBAN MARINE SHELF

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The spatial distribution of species can be modulated by the existence of some spatial regulatory pattern or by existence of randomization. This study aimed to determine patterns of co-occurrence of epiphytic macroalgae in eight habitats of marine shelf of Cuba. A matrix of presence and absence was made based on values assigned with 1 to the presence and 0 to the absence. Data were obtained from a review of published literature from 1900 to the present. To estimate whether macroalgae species co–occurred more or less than expected by chance, we used the checkerboard score (C–score) index. Simulated matrices were generated under three null models that differ in the way row and column totals are treated, a fixed–fixed, fixed–equiprobable and external weight–external weights algorithm. Epiphytic macroalgae coexisted less frequently than expected by chance in the eight habitats by models fixed – equiprobable (observed score = 1.26, expected score = 1.74, $p \geq 0.001$) and external weight–external weights algorithm (observed score = 1.26, expected score = 1.94, $p = 0.02$). These results suggest that the epiphytic macroalgal assemblages are structured by negative interspecific interactions. However, the model fixed–fixed suggests that the assemblages are structured by species segregation mechanisms (observed score = 1.26, expected score = 1.15, $p \leq 0.001$). In conclusion, epiphytic macroalgal species co-occurred less frequently than expected by chance, although this pattern was not similar for all models. These results show the presence of regulatory factors in the structure of the epiphytic macroalgae associations.

Keywords: Algae co-occurrence, C-score index, species associations

Oral presentation

ZOOXANTHELLAE–CILIATE SYMBIOSES HAVE POTENTIAL AS MODELS FOR CORAL SYMBIOSES

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Although zooxanthellae occur in a diversity of symbioses on coral reefs, most importantly with scleractinian corals, very few have so far been reported in ciliates. Such relationships have potential for understanding host-symbiont relations in corals. The first such symbiosis was reported from Florida in 1943 and has apparently not been seen since. Two ciliates with zooxanthellae have been found together on coral reefs in Guam, and there is a high probability that these or other species occur on reefs around the tropics. *Maristentor dinoferus* is a very large heterotrich ciliate visible to the naked eye and contains 500–700 zooxanthellae in the same genetic clade as the Symbiodiniaceae in local corals. It has complex "cluster dynamics" behavior that was documented in the field, tending to form tight clusters but dispersing in the early morning before reclustering. It has an abundant hypericin-like pigment that likely works with clustering as a defense mechanism. This species has proven fragile and intractable to laboratory culture. In contrast, *Euplotes uncinatus* is a hypotrich ciliate bearing some 60 zooxanthellae. It has proven culturable, and the zooxanthellae can be knocked out. Preliminary experiments indicate that it is a powerful system for lab studies including cell biology, genetic screens, functional genetics, and systems biology.

Keywords: Euplotes, *Maristentor*, symbiosis

Oral presentation

EXPLORING THE MICROBIOTA OF *SACCHARINA LATISSIMA*

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Saccharina latissima is an abundant kelp-forming brown algae in Europe. Its current distribution ranges from Spain to Spitzbergen, although several populations are in decline. Despite its economic and ecological importance, little is known about the composition of its microbiome and the interactions of the latter with the host. To explore the microbiome of *S. latissima* and to determine if specific patterns in microbial communities are correlated with algal fitness, we sampled both healthy and diseased (signs of degradation, twisted stipe, etc.) individuals from different geographic locations (Brittany, Helgoland, Southern Norway, and Svalbard) and in different seasons. For each sampled individual, we assessed the microbiome composition by 16S metabarcoding and isolated live microbial cultures for future co-culture experiments. Amplicon Sequence Variant (ASV) analyses highlighted the Proteobacteria (Alpha- and Gammaproteobacteria) as dominant phylum and showed a separation between the apex and meristem bacterial communities for all samples. Furthermore, several ASVs were specific to either healthy or diseased individuals. Bacterial cultures (381 isolates in total, belonging to four phyla, 16 orders, 45 genera) were dominated by Firmicutes and Gammaproteobacteria. Among these isolates, 48 were found exclusively on diseased individuals and 37 exclusively on healthy ones. These data contribute to our understanding of the variability of the *S. latissima* microbiome, establish a basis for ongoing experimental evaluations of algal-bacterial interactions, and serve for comparisons with other model systems such as Ectocarpus.

Keywords: Holobiont, brown macroalgae, metabarcoding

Oral presentation

CO-OCCURRENCE PATTERNS BETWEEN *CHAETOCEROS* SPECIES AND THEIR ASSOCIATED BACTERIA

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Autotrophic phytoplankton and heterotrophic bacteria have been investigated in terms of taxonomy, physiology, metabolism and their role in biogeochemical cycles, however the relationship with one another is still little known. This relationship is often governed by microscale interactions played out within the region surrounding phytoplankton cells, called the phycosphere. Phytoplankton can interact with free bacteria but also maintain attached bacteria on their surface. We have analyzed phytoplankton samples from a fixed station in the Gulf of Naples (Italy) sampled weekly from October 2017 to September 2018 for qualitative analysis. Similarly, we have sampled marine bacterial communities with the aim of characterizing them by 16S rDNA sequencing and comparing bacterial communities free-living versus those attached to particles. We then explored interactions between the attached bacteria and the most abundant diatom species using a bipartite network. *Chaetoceros* spp. was the most abundant diatom species present and, of the 27 species present, only 10 formed statistically significant relationship with specific bacterial taxa. Bipartition network analysis highlighted the presence of 6 different networks, of which three were constituted by single species of *Chaetoceros* that interact with specific bacterial OTUs, namely, *C. vixvisibilis, C. tenuissimus, C. simplex*. Instead, the other three networks include multiple species of *Chaetoceros* with close relationships with specific OTUs but also with other bacterial OTUs common to the other species. Some bacterial phyla co-occurred with all *Chaetoceros* species while others were diatom-specific (e.g. Cyanobacteria co-occurred only with *C. pseudocurvisetus*, candidate-phylum-WPS with *C. simplex* and candidate-phylum-FBP with *C. vixvisibilis*).

Financing: ACT has been funded by a SZN-OU fellowship

Keywords: Diatoms, bacteria, co-occurrence

Oral presentation

MACROALGAL-BACTERIA INTERACTIONS: IRON MANAGEMENT IN THE CHEMOSPHERE OF THE GREEN TIDE FORMING MACROALGA *ULVA* (CHLOROPHYTA)

Cristina F. Morales-Reyes, Michael Deicke, Peter Bellstedt, Thomas Wichard

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The marine macroalga seaweed *Ulva* (Chlorophyta) is one of the most abundant representative genera in coastal-areas. *Ulva mutabilis* was established as a model organism to study algal growth, development, and morphogenesis, as well as mutualistic interactions. Most notably, axenic *U. mutabilis* develops into a callus, but the presence of two essential bacteria recovers morphogenesis, forming a tripartite community. With this, *Halomonas* sp. MS1 induces cell division, whereas *Maribacter* sp. MS6 promotes rhizoid formation and proper cell wall synthesis. Iron is essential to growth for Ulva and its associated bacteria; however, due to its low bioavailability, organisms have developed several strategies to recruit the micronutrient. One of the strategies used by bacteria is releasing siderophores to acquire iron from the environment. The "carbon for iron" hypothesis suggests the iron exchange against carbon between bacteria and algae within their chemosphere. As bacteria can support algal growth, we hypothesize that bacterial siderophores contribute to their algal host's

iron homeostasis. A bacterial siderophore released by *Halomonas* sp. MS1 was identified in the algal chemosphere using metal isotope-coded profiling (MICP) and isolated from the culture supernatant. Preliminary physiological tests showed that the gametes of *Ulva* could utilize the bacterial siderophores to uptake iron. Our study thus supports the hypothesis "carbon for iron," and it is a further example of cross-kingdom interactions. It strengthens the idea that bacteria and algae collaborate within their cross-kingdom interactions and benefit from each other by "public goods." The multiple functions of metallophores will be discussed in algal-bacterial interactions.

Financing: Becas Chile of the Chilean National Agency for Research and Development (ANID) and German Academic Exchange Service (DAAD) Scholarship

Keywords: *Ulva*, iron, siderophores

Oral presentation

HOST PROMISCUITY PROMOTES INVASIVENESS OF THE RHODOPHYTE *AGAROPHYTON VERMICULOPHYLLUM*

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Invasive species are holobionts and during the invasion process they are accompanied by associated microbiota. In the course of the introduction process extreme conditions during transport and exposure to different conditions in a novel environment may induce holobiont disturbance. Upon introduction, the macroalgal holobiont interacts with microbiota from the new environment and reconfigures new functional microbial communities. As not all microbes may have survived, microbiota from the new environment may replace certain microbes from the native environment. Therefore, flexibility of the seaweed host towards environmental microbiota –or host promiscuity– may be an important trait in macroalgal invasions. Here, we simulated an introduction event in an experimental setting, using the invasive macroalga *Agarophyton vermiculophyllum* as a model. Individuals from geographically distant populations were transplanted to a common garden in the lab and subjected to a holobiont disturbance treatment followed by exposure to a new source of microbes. This treatment induced strong changes in associated microbiota, which shifted irreversibly in terms of composition and diversity, but recovered functionally in most respects. Moreover, beta-diversity strongly decreased in treated holobionts, indicating that different populations configured more common microbial communities in the common garden. In non-native populations this decline was more rapid and more pronounced, while microbial communities of native populations remained more similar to communities observed in the field. These results demonstrate that non-native *A. vermiculophyllum* are more flexible to environmental microbes, suggesting that an intra-specific increase in host promiscuity may have promoted the invasion process of *A. vermiculophyllum.*

Financing: DFG grant number WE2700/5-1DFG grant number BA5508/2-1

Keywords: Invasive species, holobiont, host promiscuity

Oral presentation

WHY IS PRIMARY ENDOSYMBIOSIS SO RARE?

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Primary endosymbiosis gave rise to the organelles (mitochondria and plastids) within eukaryotes and is considered the driving force behind the development of complex multicellular life. Given their transformative nature, why is primary endosymbiosis so rare? Primary plastids exist only in the Archaeplastida and the rhizarian amoeba *Paulinella* (two independent events). Here, using a recently generated draft genome and gene expression data from *Paulinella micropora* KR01, we argue that the complex web of interactions and innovations that are needed to harness a cyanobacterial endosymbiont render such events predictably infrequent. Inspection of the data show the evolution of hundreds so-called "dark" genes (with unknown functions) that are recruited to the diurnal cycle to harness the endosymbiont, the origin of a novel protein import system to maintain organelle functions, dozens of horizontal gene transfer events to counteract endosymbiont genome reduction, and the evolution of mechanisms to mitigate the damaging impacts of reactive oxygen species that can accumulate under high light conditions. These results suggest that once plastids have become integrated into a eukaryotic host and the associated, complex mechanisms for plastid maintenance are established, that this organelle, and the genes required for its maintenance, can be more easily transferred from one species to another. Based on these observations, we propose a simple paradigm for thinking about primary plastid endosymbiosis, the engine and chassis model: the plastid is the engine and the host, the chassis. This perspective explains why primary plastid origin is fleetingly rare, yet secondary and tertiary plastid endosymbiosis are more common.

Financing: DB acknowledges support from the United States National Aeronautics and Space Administration (80NSSC19K0462) and a NIFA-USDA Hatch grant (NJ01170).

Keywords: Primary endosymbiosis, organelle integration, *Paulinella* micropore KR01

Oral presentation

LICHEN PHYCOBIONTS OF THE CANARY ISLANDS

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The Canary Islands are known for their unique and diverse fauna and flora. Recently, the algal genus *Vulcanochloris* (with three species) and one species of *Asterochloris* (*A. mediterranea*) were described from this area. However, lichen phycobionts remained unresearched in the majority of the area. The three lichen genera *Stereocaulon, Cladonia*, and *Lepraria* were sampled around the Canary Islands, Madeira, and the Aeolian Islands. The islands and individual areas varied in climatic conditions as well as in the occurrence and abundance of lichens. ITS rDNA sequences of more than 300 samples were analyzed. The goal of this study was to uncover entire phycobiont diversity and to investigate the effects of climatic conditions, location and surface area of the island, and mycobiont identity on phycobiont distribution. The algal genera *Asterochloris, Chloroidium, Vulcanochloris*, and *Myrmecia* were recovered as phycobionts. Their occurrence is primarily driven by the specificity towards the mycobionts. However, the mycobiont genera showed various patterns in the specificity towards the phycobionts, as well as in other factors investigated. Notably, the phycobiont pool differs significantly from that of outside the studied area.

Financing: Supported by Charles University Science Foundation project GAUK (no. 570313) and Primus Research Programme of Charles University (no. SCI/13).

Keywords: Symbiosis, lichen phycobiont, islands

Oral presentation

SARGASSUM EPIBIOTIC HYDROID DIVERSITY WORLDWIDE

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Brown algae of the genus *Sargassum* provide a habitat for many marine organisms, including invertebrates like the cnidarians. Hydroids (Cnidaria, Hydrozoa) species are common epibionts on benthic and pelagic Sargassum. To date, we are conducting a study that aims to compile the records of epibiont hydroids of *Sargassum* at a global scale. Thereto, we searched for peer-reviewed reports of epibiont hydroids on *Sargassum* from 1939 to 2020. For each hydroid report, the reported taxon name and actual status (both hydroids and *Sargassum*), taxonomic classification, type of reproduction, sex, country, ecoregion, hydroids life cycle, and type of sampling method were incorporated into a database. In addition, we added records obtained from sampling campaigns performed in La Paz Bay, Baja California Sur, Mexico, between 2018 and 2020. Epibiont hydroids have been reported in 19 of the more than 300 Sargassum species worldwide; nevertheless, in several studies, the *Sargassum* species is not specified. Approximately 90 species of epibiont hydroids have been reported on *Sargassum*; 62 species were epibionts of benthic *Sargassum* and 18 of pelagic *Sargassum*. *Sargassum* species more frequently reported in the literature with hydroids have been *Sargassum muticum, S. fluitans*, and *S. natans*. The *Sargassum* species with the maximum number of epibiont hydroids recorded was *S. cymosum*, with 24 hydroid species, while the species with the minimum number of hydroids was *S. micracanthum*, with one. Our results show the world's regions that need studies focused on describing the hydroid epibiota of *Sargassum*.

Keywords: Epibiotic communities, macroalgae, Medusozoa

Oral presentation

DECIPHERING MOLECULAR MECHANIMS OF KELP DEFENSES UPON BIOTIC STRESS

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Saccharina latissima (Laminariales, Phaeophyceae) is an important primary producer in temperate to cold northern hemisphere coastal ecosystems and an economically relevant seaweed with high industrial potential. Natural populations and cultured *S. latissima* are both susceptible to disease and parasitism, which could have strong ecological impacts and cause great economic losses in aquaculture. Nowadays, there is an increasing interest in understanding defense responses of *S. latissima* against biotic threats. To study endophytic infection, we developed a co-cultivation bioassay using *Laminarionema elsbetiae*, a filamentous brown algal endophyte, to infect its main natural host *S. latissima* and occasional host *Laminaria digitata*, and monitored some physiological responses such as growth and endophyte prevalence in kelp sporophytes. The reduced growth rate and low infection ratio in *L. digitata* after two weeks indicated that L. digitata might perform a more efficient defense strategy

than *S. latissima* against endophytes. A large-scale transcriptomic analysis confirmed significant differences between gene regulation of the two kelps species during early responses upon endophyte infection. In addition, we have analyzed and compared these transcriptomic regulations to those induced by oligogulуronate (GG) treatment in these two kelp species. Indeed, GG could act as endogenous elicitors, inducing some defense responses and reducing the pathogen infection. The comparison of transcriptomic regulation during endophyte infection and upon GG elicitation will help us to decipher the molecular defense mechanisms and specificities of kelp-endophytes interactions.

Keywords: Kelp, endophyte, RNA-seq

Oral presentation

ARE SYMBIOTIC DINOFLAGELLATES TOXIC?

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Rapid ocean warming is causing the demise of coral reef ecosystems by disrupting the mutualism between corals and endosymbionts in the family Symbiodiniaceae. Host-symbiont signaling via exchange of secondary metabolites may be an important component in dysbiosis, but is largely unexplored. Some free-living symbiodiniacean species produce secondary metabolites that appear to be toxic, however, no species capable of forming symbioses with animal hosts have been examined. Dinoflagellate toxin production typically varies with nutrient availability, temperature, and light; parameters that also influence maintenance of functioning symbioses. We sought to test whether five symbiotic and three non-symbiotic species of cultured Symbiodiniaceae exhibited toxicity under nutrient replete conditions, and whether production changed with nutrient availability, thermal stress, and light stress. We use hemolysis as a proxy for toxicity, and describe the functional activity and efficiency of photosystem II throughout each experiment. Our results showcase the diversity in response to stress of species within the Symbiodiniacean family, and make the case for future study in the function of these compounds as they pertain to cell survival and proliferation (i.e. allelopathy, defense, signaling or heterotrophy) in the water column or within a host.
Financing: The Phycological Society of America, International Phycological Society

Keywords: Symbiodiniaceae, coral, toxin

Oral presentation

CHANGES IN EPIPHYTIC DIATOMS IN THE COLORADO RIVER BELOW GLEN CANYON DAM, ARIZONA, FOLLOWING CHANGES IN DOMINANT MACROPHYTES

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A rich assemblage of epiphytic diatoms and other algae occur on submerged macrophytes in the tailwaters of the Colorado River downstream from Glen Canyon Dam, and constitute the primary foodbase for aquatic consumers. From 1970s through 1990s the filamentous green alga Cladophora glomerata was the dominant macrophyte supporting a highly productive assemblage of epiphytic algae. In the following 25 years, a shift in macrophyte dominance occurred, coincident with reduced daily flow fluctuations from the dam to control sandbar erosion downstream in Grand Canyon. The macrophyte assemblage is now dominated by *Zannichellia palustris, Chara cf. vulgaris, Fontinalis* cf. *hypnoides, Oscillatoria/Phormidium* spp., with limited cover by *Cladophora*. We sampled a 23-km longitudinal series of sites downstream from the dam between March and Dec 2020 to reassess the contemporary epiphyte assemblage. We recorded 194 sub-generic diatom taxa, of which 59 had been recorded in the late 1980s, but 135 taxa observed in 2020 had not been recorded when *Cladophora* dominated. Major species in earlier years, *Cocconeis pediculus, C. placentula, Diatoma vulgaris*, and *Rhoicosphenia abbreviata*, remain common. Important changes to the diatom flora include gelatinous mats of *Didymosphenia geminata*, increased frequency of erect species *Tabularia fasciculata* and *Ctenophora pulchella*, and adnate species *Amphora pediculus* and *Karayevia ploenensis* var. *gessneri*. We are assessing how a shift in epiphytic algal taxa and architecture, and links to different macrophyte substrata, may affect the dominant invertebrate primary consumers, consisting primarily of chironomid larvae and non-native amphipods and mollusks, as it influences the fisheries foodbase.
Financing: Supported by a grant from the Argonne National Lab

Keywords: diatoms, macrophytes, epiphytes

Oral presentation

DE NOVO GENOMES OF THE DINOFLAGELLATE *EFFRENIUM VORATUM* REVEAL HALLMARKS OF FREE-LIVING LIFESTYLE IN SYMBIODINIACEAE

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The dinoflagellates of the family Symbiodiniaceae are important photosynthetic symbionts in corals and other coral reef organisms. Whereas most research of these dinoflagellates has focused on symbiotic species, free-living species have been described in multiple genera. Current hypothesis posits that the symbiotic lifestyle of Symbiodiniaceae was derived from a free-living ancestor. Thus, free-living species in recently diverged lineages may have reverted to free-living. However, genomic resources for free-living Symbiodiniaceae taxa remain scarce. *Effrenium* is the earliest-diverging Symbiodiniaceae genus that is exclusively free-living. Genomes from these lineages provide a useful platform to assess evolutionary transition(s) between free-living and symbiotic in Symbiodiniaceae. Combining both short- and long-read sequence data, we generated de novo genome assemblies and full-length transcriptomes for two isolates of *Effrenium voratum* (rt383 and RCC1521). In total, we generated ~100x genome data using Illumina, PacBio Sequel II and Nanopore technologies. Preliminary genome assemblies are contiguous and consistent with other Symbiodiniaceae genome assemblies (estimated size=1.4 Gbp, N50=230 Kbp). Our results reveal how selective pressures of symbiosis, or the lack thereof, affects intra-species genome variation in this free-living symbiodiniacean species. Incorporating available genome data from other Symbiodiniaceae taxa in a comparative analysis, our results also reveal distinct functional (e.g., gene content) and structural (e.g., synteny) elements that are genus-specific and lifestyle-specific. These results provide novel insights into the evolutionary transition between free-living and symbiotic lifestyles in these ecologically important taxa. Data generated from this study provide a useful reference for comparative genomics of the highly diverse Symbiodiniaceae, and more broadly of dinoflagellates.

Financing: Australian Research Council, DP190102474

Keywords: Symbiodiniaceae, *Effrenium*, comparative genomics

Oral presentation

UNUSUAL MITOCHONDRIAL GENOME EXPANSION IN THREE *PORPHYRIDIUM* SPECIES (RHODOPHYTA)

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To advance understanding of mitochondrial genome (mitogenome) evolution, we studied the model unicellular red alga, *Porphyridium*. Analysis of mitogenomes in three closely related species in this genus revealed they were 3-6-fold larger (56 – 132 kbp in size) than in other red algae that contain genomes of size 21 – 43 kbp. This discrepancy is explained by two factors, group II intron invasion and expansion of repeated sequences in large intergenic regions. Phylogenetic analysis demonstrates that a massive family of group II introns are present only in *Porphyridium* mtDNA and many are closely related to sequences in fungi and in algae containing plastids derived from red and green algal secondary endosymbiosis. These results strongly support the lateral movement of group II introns among algae and invasion of group II introns into their own genome. The intergenic regions in *Porphyridium* mitochondrial genomes are likely expanded through the extensive increase of repeat sequences by replication slippage around the replication origin.

Keywords: Red algae, group II intron, replication slippage

Oral presentation

MY SEAWEED LOOKS WEIRD: A PARTICIPATIVE PORTAL TO SUPPORT THE DEVELOPMENT OF AN OPEN-ACCESS ONLINE ATLAS OF SEAWEED DISEASES

Martina Strittmatter[1,2], Pedro Murúa[1,3], Marie-Mathilde Perrineau[1], Paola Arce[1], QianYi Zhang[1], Carla Ruiz-González[1], Janina Brakel[1], Juliet Brodie[4], Elizabeth Cottier-Cook[1], Philippe Potin[2], Claire M.M. Gachon[1,5]

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Diseases are omnipresent in wild and cultivated macroalgae. Yet, there is no centralised resource on how to recognise disease symptoms and know the identity of pathogens causing them. In order to fill this gap, an open-access online atlas of algal diseases is currently under development which will contain a range of resources including literature, macroscopic and histology images, molecular data, (e.g. barcode sequences, microbiome information) and biogeographic data. In order to enable both greater participation and inclusion of algal species and geographic regions not currently covered, we have developed the online, multilingual portal [1] "My seaweed looks weird" (MSLW), where anyone who comes across seaweeds that look unusual, whether wild or cultivated, can report such observations. Symptoms, such as deformation, discolouration, galls, holes or rot are of interest. Additionally, abnormalities that might not be linked to disease, but could be mistaken for one, are also of interest. Here, we invite scientists, seaweed professionals or members of the public to submit pictures and/or physical samples of diseased algae using the MSLW portal. Using a combination of microscopy and, if appropriate, DNA analysis, we shall endeavour to send back an in-kind diagnosis for all samples received. With the permission of contributors, the resulting data will be integrated into the online atlas of algal diseases, alongside contributions and scientific outputs from the GlobalSeaweedSTAR, Genialg and algaBLISTER initiatives. We anticipate that this tool will be a valuable source of information in the future and will accelerate the development of disease management solutions for seaweed aquaculture. [1] https://www.globalseaweed.org/?page_id=889

Keywords: Atlas, diagnostics, diseases

Oral presentation

THE ROLE OF PHYTOHORMONE SIGNALING PATHWAY COMPONENTS IN (BACTERIA-DEPENDENT) DEVELOPMENT OF *ULVA MUTABILIS*

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The marine chlorophyte macroalga *Ulva mutabilis (Ulva)* is a common inhabitant of coastal ecosystems, where it interacts with both macro- and microbiota. Remarkably, *Ulva* requires the presence of specific mutualistic bacteria, or the compounds they produce, for its proper development. Although the chemical mediators that establish this cross-kingdom communication have been partly resolved, the molecular mechanisms that regulate it remain unknown. To get insight in the genetic network involved in bacteria-dependent morphogenesis, we performed comparative transcriptome analysis of *Ulva* grown in either the presence or absence of its microbial symbiont *Maribacter* sp. or the morphogenetic compound (thallusin) that is produced by *Maribacter*. Analysis of differentially expressed genes (DEGs) between these treatments showed that more than 1500 genes were misregulated in the absence of *Maribacter* and/or *thallusin*, and that, interestingly, the majority of DEGs were upregulated. Moreover, we found that some close homologs of land plant genes that are involved in phytohormone signaling were among the DEGs. Currently, we are elucidating to which extent these homologous signaling components play a role in bacteria-dependent morphogenesis.

Financing: Funded by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) - SFB 1127/2 ChemBioSys - 239748522.

Keywords: Cross-kingdom interaction, morphogenesis, genetic regulation

Oral presentation

THE PARADOXICAL ROLE OF THE ALGAL DMSP LYASE ENZYME DURING PREDATOR-PREY INTERACTIONS IN THE OCEAN

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Phytoplankton are key a component of the oceanic carbon and sulfur cycles. During bloom events, some species can emit massive amounts of the organosulfur volatile dimethyl sulfide (DMS) to the atmosphere, where it can modulate aerosol formation and affect climate. In aquatic environments, DMS plays an important role as a chemical signal, mediating diverse trophic-level interactions. Yet, the role of DMS during microbial predator-prey interactions remains elusive. Contradicting evidence suggested the involvement of DMS in algal chemical defense and in grazer's chemoattraction to prey cells. We investigated the signaling role of DMS during zooplankton-algae interactions by genetic and biochemical manipulation of the algal DMS-generating enzyme (Dimethylsulfoniopropionate lyase, DL) from the bloom-forming alga *Emiliania huxleyi* . We inhibited DL activity in live *E. huxleyi* cells by the novel DL-inhibitor 2-bromo-3-(dimethylsulfonio)-propionate (Br-DMSP) and overexpressed DL in the model diatom *Thalassiosira pseudonana*. We showed that algal DL activity did not serve as anti-grazing chemical defense, but paradoxically enhanced grazing by the model microzooplankton *Oxyrrhis marina* and other micro- and mesozooplankton. Consumption of algal prey with induced DL activity also promoted *O. marina's* growth. Overall, our results demonstrate that DMS-mediated herbivory may be ecologically important and prevalent during prey-predator dynamics in oceanic ecosystems. The role of DMS as an appetizing signal to grazers revealed here raises fundamental questions regarding the retention of its biosynthetic enzyme through the evolution of dominant bloom-forming phytoplankton in the ocean.

Keywords: DMS, grazing, infochemicals

Oral presentation

VISUALIZING ACTIVE VIRAL INFECTION REVEALS DIVERSE CELL FATES IN SYNCHRONIZED ALGAL BLOOM DEMISE

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Marine viruses, the most abundant entity in the ocean, are considered as major evolutionary and biogeochemical drivers of microbial life. Despite years of research in aquatic virology, we remain unable to resolve the true impact of viral infection on nutrient fluxes and microbial dynamics, because we cannot estimate viral-induced mortality in the ocean. Here, we provide the first assessment of active viral infection in *Emiliania huxleyi* algal single-cells by subcellular visualization of giant virus and host transcripts, exposing co-existence of infected and non-infected subpopulations. We revisit major assumptions in the life cycle of giant viruses, showing that cells produce virions without lysing, and lyse without producing virions. We reveal that only a quarter of cells were infected in a natural algal bloom highlighting the importance of other mortality agents, and show how characterizing viral-induced cell aggregates suggests potential host defense strategies by enrichment of infected cells in sinking aggregates. We further explore the impact of an *E. huxleyi* bloom and demise on microbial communities and biogeochemical processes during a large scale mesocosm experiment. We highlight how eukaryotic osmotrophes potentially compete with the prokaryotic microbial loop for algal lysis products, and mechanistically resolve the contribution of viral infection to carbon budgets of inorganic carbon and transparent exopolymers.

Keywords: Virus, *Emiliania huxleyi*, bloom

E-Poster

SPATIAL AND TEMPORAL VARIATIONS IN ANTIMICROBIAL ACTIVITIES OF SOME MACROALGAE OF THE RED SEA, EGYPT

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Spatial and seasonal variations in the antimicrobial activities of some macroalgae native to the Red Sea coast were assessed at three sites which represent different hydrographic habitats along the north-western coast of the Red sea during 2018. The selected macroalgae were *Caulerpa racemosa var. gracilis* (Chlorophyta), *Padina boergesenii, Polycladia myrica, Hormophysa cuneiformis* and *Sargassum aquifolium* (Phaeophyceae), and Digenea simplex (Rhodophyta). Antimicrobial activities tested were against *Enterococcus faecalis, Staphylococcus aureus, Pseudomonas aeruginosa, Candida albicans*, and *Aspergillus niger*. Spatial and temporal variations of the antimicrobial activities of the methanolic extract of the seaweeds showed a significant difference ($P<0.001$) among sites and seasons, and the correlation with the environmental parameters was established, while there are no variations in antifungal activity. Summer (August) and autumn (November) are the best seasons for high antimicrobial activities for the brown seaweeds, *Hormophysa cuneiformis, Padina boergesenii, Polycladia myrica*, and *Sargassum aquifolium*, and the red seaweed *Digenea simplex*. While winter is favorable for the green seaweed *Caulerpa racemosa*. The tested seaweeds had more biological activity at site I and II compared to site III. The crude extract of *H. cuneiformis* was more effective in summer than other species (inhibition zone diameters were 16.7±5.1, 18 ±6.9, and 19.5±3.6 mm in *E. faecalis, S. aureus*, and *P. aeruginosa*, respectively). The antimicrobial activity of the algal extracts tested during the present investigation against the tested pathogens suggests that these seaweeds could be promising sources of antibiotic substances useful in the treatment of diseases caused by these pathogens.

Keywords: Seasonal variations, Red Sea, antimicrobial activity

E-Poster

CHASING BACTERIA IN THE GREEN ALGA *BRYOPSIS PLUMOSA*

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Bryopsis (Codiales, Chlorophyta) is a common siphonous marine alga, consisting of a single, giant tubular cell, and home to a remarkably diverse bacterial community. Some of the endosymbiotic bacteria have recently been shown to produce secondary metabolites that protect *Bryopsis* against predation. Although the bacterial community varies between *Bryopsis* strains, it seems to be relatively uniform within algal populations. Vegetative reproduction of the algae through fragmentation and protoplast formation after wounding can *de facto* be expected to ensure vertical inheritance of the bacteria but with bacteria also observed in algal gametes, vertical transmission through sexual reproduction also seems plausible. We are using microscopy (FISH, TEM) to quantify the contribution of the different transmission routes across generations for the bacteria commonly found in *Bryopsis plumosa*. We expect that host fidelity and functional benefits will be relatable to relevance of the different transmission routes.

Financing: This work is funded by the Fund for Scientific Research – Flanders (1252821N, FWO-Flanders, Belgium)

Keywords: Bacterial acquisition, coevolution, *Bryopsis*

E-Poster

DEVELOPMENT OF QUANTITATIVE PHENOTYPING TECHNIQUES FOR DISEASE RESISTANCE IN BROWN ALGAE WITH THE MODEL PATHOSYSTEM *ECTOCARPUS – ANISOLPIDIUM*

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Seaweed aquaculture is growing exponentially worldwide, yet the genetic determinism and heritability of traits of interest (including disease tolerance) are virtually unknown. We used the model brown alga *Ectocarpus* to develop quantitative and parallelisable assays for disease resistance, against the oomycete *Anisolpidium ectocarpii*. Overall, we combined different techniques based on host's PAM fluorometry and chlorophyll autofluorescence, pathogen's chitin fluorescence (WGA-FITC) and DNA relative concentration (qPCR) in order to check detectable changes during the infection course. We tested two strains, Ec568f and Ec32m, which previously showed to have contrasting resistance against *A. ectocarpii* AnQU67-5. Preliminary results show that PAM fluorometry proxies normally used in physiology (e.g. quantum yield) are not very resolutive to capture subtle differences on infection progress. Contrarily, we found chlorophyll (F0 and Fm) and chitin stained fluorescence are excellent to track infection progress, as long as corrections for biomass (i.e. nephelometry) are performed. In a similar way, the pathogen DNA quantification needs to be weighted with the host DNA to obtain a sensitive relative abundance. In total, four of the tested proxies are applicable to the same set up in different time points, proxies that are extrapolable to other algal pathosystems. We are currently characterising the ca. 90 individuals

of a Ec568f x Ec32m progeny and correlate their outcome with their genetic maps, in order to identify potential loci conferring resistance against *A. ectocarpii.*

Financing: NERC IOF Pump priming (scheme NE/L013223/1), UKRI GCRF grant BB/P027806/1 (GlobalseaweedSTAR) and H2020 project GENIALG (Contract No 727892)

Keywords: qPCR, nephelometry, chlorophyll fluorometry

E-Poster

PHOTOBIONTS OF SEASHORE LICHENS

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Among the most prominent algal symbiotic interactions are the lichens. In addition to other hostile environments, they also cover rocky seashores all over the world. This lifestyle is probably enabled by a specific set of photobionts, however, their diversity is only little known. We sampled crustose *Verrucariaceae* at northern Patagonian Pacific coast in Chile. Using molecular markers, we identified both the mycobionts and photobionts. Solely *Ulvophycean* photobionts were found. *Pseudendoclonium submarinum* was the most common, but representatives of other, yet undescribed, lineages were also found. Notably, the genus *Urospora* is reported as a lichen photobiont for the first time here. To find out more about these fascinating symbioses, please visit our e-poster.

Financing: Primus Research Programme of Charles University SCI/13

Keywords: Lichen photobionts, *Ulvophyceae*, seashore

E-Poster

EFFECT OF THE STRUCTURAL COMPLEXITY OF MACROALGAL ASSEMBLAGES ON THE DISTRIBUTION OF AMPHIPODA FAMILIES

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This study aimed to establish whether amphipods associated with macroalgae depend on habitat dimension or on structural complexity. Taxonomic determinations of 108 macroalgal assemblages and their amphipod families at three locations. Coverage and assembly profiles (AP) were used to express the habitat dimension, while the habitat complexity of macroalgal assemblages was evaluated using functional-form group weighting (FFGW) and displaced volume (DV). Spearman's correlation coefficient was used to obtain reference values and significances. Seventy species of macroalgae and eleven amphipod families were identified. When comparing the amphipod densities and the number of families with the habitat dimension and habitat complexity, Spearman's coefficient showed significant correlations in all three locations the Mexican pacific coast. In Palmar beach, both the size and complexity of the habitat were important factors for amphipod distribution, but they were not considered essential factors. In contrast, in the municipal dock, habitat complexity was a significant factor. In Gatas beach, during the dry season, the most significant factor was the habitat dimension, while during rainy season, it was habitat complexity. The dependence on the habitat dimension or its structural complexity was not confirmed because the values of Spearman's coefficient were highly variable. The relationships between amphipods (density or number of families) and their habitat (dimension or complexity) are complex and not necessarily direct. It is essential to understand these relationships that may result from interaction multiple factors.

Keywords: Macroalgae, habitat complexity, amphipods

E-Poster

ANNOTATION PIPELINES IMPACT OUTCOME OF METABOLIC COMPLEMENTARITY-BASED COMMUNITY SELECTION OF *ECTOCARPUS* (BROWN ALGAE) - ASSOCIATED BACTERIA

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Like many macro-organisms, the brown alga *Ectocarpus* depends on its symbiotic microorganisms for its development and functioning. Genome sequencing and genomic analyses of these microorganisms provide opportunities to construct and analyze metabolic networks of a host and its microorganisms as a unit. Genome-scale metabolic networks rest on information gained from genome annotation. As there are multiple bacterial annotation pipelines accessible, the question arises to what extent differences in annotation pipelines impact outcomes of these analyses. Here, we estimated the differences between five commonly used annotation pipelines (Prokka, MaGe, IMG, DFAST, RAST) from predicted annotation features (coding sequences, Enzyme Commission numbers, hypothetical proteins) to the metabolic network-based analysis of symbiotic communities (biochemical reactions, producible compounds, and selection of minimal bacterial communities that complement the network of the algal host). Our results underline differences between the output of the tested pipelines at all examined levels, with small differences in the metabolic networks resulting in considerably different complementary microbial consortia. However, the consortia generated supplied similar predicted producible compounds and could therefore be considered functionally interchangeable. This contrast between selected bacterial communities and community functions depending on the annotation pipeline needs to be taken into close consideration when interpreting the results of metabolic complementarity analyses. On that account, experimental validation of bioinformatic predictions will likely be crucial to both evaluate and refine the pipelines and needs to be coupled with increased efforts to expand and improve annotations in reference databases.

Financing: This work was supported partially by the CNRS Momentum call and the ANR project IDEALG [ANR-10-BTBR-04] "Investissements d'Avenir, Biotechnologies-Bioressources"

Keywords: Functional annotation, genome-scale metabolic networks, holobionts

E-Poster

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

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The microbiome associated with an organism has been recognized as playing an important role in metabolic processes. In marine and freshwater algae, there have been a growing number of studies to ascertain the function and composition of the organisms forming the microbiome. Genera in the Batrachospermales have macroscopic filamentous gametophytes that undoubtedly have a diverse microbiome but have yet to be explored. This study examined the similarity in microbiome for three different combinations of gametophytes as follows: a single species in multiple streams, three species in the same stream and a single species over the growing season. The associated organisms were characterized through PCR of four barcodes (16S, 18S, UPA and *rbc*L) followed by high throughput amplicon sequencing. These data were parsed bioinformatically and taxonomy assigned to all amplicon sequence variants (ASVs) followed by exploratory statistics for ASV similarities. Virescentia viride-americana was sampled from three streams and shared 92 ASVs from the 16S marker in the Bacteroidia, Gammaproteobacteria. As well, *Stramenopilia, Alveolata, Rhizaria, Fragilariaceae,* Bacillariophyta, and cyanobacteria were identified with the other markers. *Lympha muscosa, Virescentia viride-americana* and *Tuomeya americana* from a single steam shared 149 ASVs in the Proteobacteria, Bacteroidia, and Verrucomicrobiae and also Stramenopilia, Alveolata, Rhizaria, Fragilariaceae, Cymbellaceae, Bacillariophyta, and cyanobacteria. *Tuomeya americana was* sampled twice during the growing season and shared 310 ASVs of Proteobacteria, Bacteroidia as well as members of the Stramenopilia, Alveolata, Rhizaria, Fragilariaceae, Cymbellaceae, Bacillariophyta, and cyanobacteria from the other markers. The importance of the core microbiome taxa among comparisons is discussed.

Keywords: Bacteria, diversity, Rhodophyta

E-Poster

USE OF 13C LABELLED *ULVA* (CHLOROPHYTA) TO DECIPHER BACTERIAL-MACROALGAL INTERACTIONS WITHIN THE CHEMOSPHERE

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The marine green macroalga *Ulva mutabilis* (Chlorophyta) fails to form its typical morphology in the absence of appropriate bacteria and develops into aberrant callus-like colonies. The complete morphogenesis of *Ulva* can be restored in the presence of *Roseovarius* sp. strain MS2 and *Maribacter* sp. strain MS6 by forming a tripartite symbiotic community. The study aimed to unravel mutualistic interactions by identifying biomarkers that are released by *U. mutabilis* or *Roseovarius* sp. in the chemosphere using 13C-labelled algae or bacteria. In particular, the effects of bacteria-induced stimuli on the metabolism of *U. mutabilis* were investigated. For 13C-labelling, axenic germlings of *Ulva* were cultivated with 13C-bicarbonate. In parallel, cultures were grown on non-labelled carbon sources under identical conditions. Upon cultivation for four months, 13C-labelled and non-labelled *Ulva* cultures were inoculated with *Roseovarius* sp. and *Maribacter* sp. After two more weeks, solid-phase extracted waterborne metabolites were analysed by GC-MS and LC-MS using DeltaMS, a tool to track isotopologues in mass spectrometric data. The comparative approach allowed us to identify 13C-labelled metabolites, which were released by *U. mutabilis* (exo-metabolome) upon induction of the bacteria stimulus. Our reductionist model system provides insights into the chemically mediated cross-kingdom interactions and the translocation of metabolites between the symbionts.

Financing: Funded by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) - SFB 1127/2 ChemBioSys - 239748522.

Keywords: Seaweed, cross-kingdom-interactions, infochemicals

SYM07: From reference genomes to population genomics

Keynote lecture

LARGE SCALE GENOME-WIDE INVESTIGATION OF THE EFFECT OF FARMING AND HUMAN-MEDIATED INTRODUCTION ON *UNDARIA PINNATIFIDA*

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Human activity is an important driver of ecological and evolutionary change on our planet. In particular, domestication and biological introductions have significant and long-lasting effects on species genomic architecture and diversity. However, only a handful of case studies offer the opportunity to simultaneously address human-driven evolutionary change due to domestication and introduction. The Pacific kelp *Undaria pinnatifida* (Harvey) Suringar (Laminariales, Phaeophyceae) provides such an opportunity. In its native range of Northeast Asia, this brown edible seaweed has been exploited for centuries, before being extensively cultivated for food consumption, abalone farming and for its extracts. Parallel to cultivation, *Undaria pinnatifida has* been intentionally and unintentionally transported by humans across the planet and is now reported from the coastlines of 14 countries including France and New Zealand. Therefore, this kelp presents the rare characteristic of being independently cultivated in its native range and introduced in four continents outside of its native range and is now reported from the coastlines of 14 countries including France and New Zealand. Here we report the genome sequence of a Korean cultivar of *Undaria pinnatifida* along with the whole-genome sequencing of multiple individuals sampled in native, cultivated, and introduced populations, we compared genome architecture across these different categories. Finally, using this database, we present future perspective to extend the genotyping and to develop of a new resource for the study of *Undaria pinnatifida.*

Keywords: Population genomics, SNP, *Undaria*

Keynote lecture

EXPLORING *PSEUDO-NITZSCHIA MULTISTRIATA* EVOLUTION AND STRAIN DIVERSITY THROUGH GENOME RESEQUENCING

Mariella Ferrante[1], Svenja Mager[1], Francesco Manfellotto[1], Maria Valeria Ruggiero[1], Viviana Di Tuccio[1], Monia Teresa Russo[1], Antonella Ruggiero[1], Lisa Campbell[2], Marina Montresor[1], Remo Sanges[3]

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The planktonic diatom Pseudo-nitzschia multistriata represents an ideal model system to investigate the regulation of life cycle transitions and the mechanisms of sex determination. Thanks to a long term monitoring station in the Gulf of Naples (Italy), its populations have been followed for over a decade, allowing a multiyear population genetics study. The availability of the P. multistriata genome now allows to explore diversity and genome evolution through population genomics. We resequenced the genome of 26 strains of different mating type (MT+ and MT-), collected at different locations and including two strains whose genotype dominated an atypical bloom in 2013. The variant information was used to produce phylogenetic trees to investigate relationships between the strains. Scaffolds diverging in the level of heterozygosity between groups of strains were identified. Genes under selective pressure were identified by non-synonymous to synonymous nucleotide diversity estimations. Preliminary analyses highlighted the presence of one specific scaffold with higher heterozygosity in MT- with respect to MT+ strains, and a few specific scaffolds diverging in heterozygosity levels in the two strains responsible for the clonal expansion event in 2013 with respect to other strains collected in the Gulf of Naples. Variant analyses in a diverse set of diatom strains will allow identifying fast evolving genes and mutations that correlate with specific properties of groups of strains. Further analyses will include the determination of the functional categories of these genes, validation in additional strains and ultimately identification of the processes that drive functional differences between strains.

Financing: This work was supported by the Gordon and Betty Moore Foundation through grant #7978

Keywords: Diatom, population genomics, variations

Keynote lecture

BROWN ALGAL GENOMICS AND EPIGENOMICS

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The brown algae are an important group of eukaryotic organisms from evolutionary, ecological and economic perspectives. They independently evolved complex multicellularity and many of the larger members of this lineage are dominant species of rocky coastal ecosystems and/or intensively grown aquaculture crops. However, these seaweeds remain understudied compared to other multicellular lineages such as the animals, green plants and fungi1. The establishment of model organisms for this group, particularly the filamentous brown alga *Ectocarpus*, and the sequencing of several complete brown algal genomes2 represent significant steps towards an improved understanding of this lineage. Currently, two key challenges are i) to build on these advances to understand how genomes function to direct key features of brown algal biology and ii) to generalise information about model organisms to other brown algae. Ongoing functional genomics efforts applied to *Ectocarpus* aim to provide an increasingly detailed and dynamic description of the genome, including characterisation of non-coding loci and analysis of epigenetic processes3, and to develop methodologies to experimentally investigate gene function4. In parallel, the Phaeoexplorer project aims to significantly extend genome resources for the brown algae, facilitating transfer of information to other species and providing an overview of brown algal genome evolution and diversification. References: 1. Coelho, S. & Cock, J. (2020). Ann Rev Genet 54, 71–92//2. Cock, J. M. et al. (2010) Nature 465, 617–621//3. Bourdareau, S. et al. (2020) Genome Biol. in press//4. Arun, A. et al. (2019) eLife 8, e43101

Financing: Funding: CNRS, Sorbonne University, ANR Epicycle ANR-19-CE20-0028-01 and Idealg ANR-10-BTBR -04-01, ERC 638240 and ANR France Genomique Phaeoexplorer ANR-10-INBS-09

Keywords: Brown algae, genomics, epigenomics

Oral presentation

IS TWO BETTER THAN ONE? THE MOLECULAR DIFFERENCES BETWEEN EVOLVING HAPLOID AND DIPLOID POPULATIONS

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Ploidy shifts are omnipresent and occur at different levels of biological organization, as part of the eukaryotic success formula of sexual reproduction, as endopolyploid cell lineages during development, in polyploid species complexes, etc. The accompanying increase in genetic material can affect the phenotype e.g. via the well-established correlation between cell and genome size, altering surface area to volume ratios and other nucleotypic effects. But more importantly the presence of an extra genome copy that is free to evolve is supposed to increase the genomic and epigenetic flexibility and therefore the evolvability. As such whole genome duplication is a major evolutionary force contributing to the increasing complexity and diversity of life over time. In order to gain insight in the differences in molecular changes between evolving haploid and diploid populations we allowed haploid and autodiploid clonal populations of the unicellular green algae *Chlamydomonas reinhardtii* to adapt for hundreds of generations to a benign and stressful saline environment. We sequenced the ancestral and evolved populations (pool-seq) and used a combination of coverage analysis, SNP-calling and TE-detection to test whether the theoretical expectations of a higher genetic diversity, a higher frequency of deletions and an increased activation of transposable elements are fulfilled.

Financing: Research was funded by the Research Foundation Flanders (PhD fellowship fundamental research nr:1168418N) and the ERC (Advanced Grant: DOUBLE-UP)

Keywords: Genome evolution, Whole genome duplication, Polyploidy

Oral presentation

PHYLOGEOGRAPHY OF ARCTIC AND NORTH ATLANTIC RIBBON KELP *ALARIA ESCULENTA* AS REVEALED BY WHOLE GENOME SEQUENCING DATA

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Continued warming of the Arctic marine environment highlights the need to better understand species assemblages, how they historically reacted to changes in climate, and whether populations are adapted to local (Arctic) conditions. Genetic analysis and ecological niche modelling of marine macroalgae have revealed unique population structure in the East Canadian Arctic relative to globally distributed conspecifics, suggesting populations survived the Last Glacial Maximum at high latitudes and may indeed be tailored to the Arctic marine environment. Our work seeks to test this hypothesis by investigating 1) phylogeographic patterns and 2) selection regimes using genomic data in Arctic and North Atlantic ribbon kelp, *Alaria esculenta* (Linnaues) Greville. Specimens of A. esculenta were collected from the East Canadian Arctic, Greenland, the Bay of Fundy (Northwest Atlantic), and Norway, and whole genome sequencing (short-read) datasets were produced. Patterns in phylogeography and selection regimes were inferred from single nucleotide polymorphism datasets, individually for the mitochondrial, chloroplast, and nuclear genomes. Arctic specimens of *Alaria* are genetically distinct from Atlantic populations, and are possibly a separate species. We hypothesize Arctic populations represent the deep-water ecotype *Alaria grandifolia*, currently a synonym of *A. esculenta*. Meanwhile, clear phylogeographic signal is present among Northwest Atlantic, Norwegian, and Greenlandic populations. Selection analyses are ongoing at the time of abstract submission. Our work continues to highlight the unique nature of Arctic marine macroalgae, the need to take stock of endemic biodiversity in the Arctic using genomic datasets, and leads the way to functional genomic investigations of climate-change responses in Arctic kelp.

Keywords: Genomics, kelp, phylogeography

Oral presentation

ASSOCIATION GENETICS WITHIN A CLONAL DIVERSITY OF *TISOCHRYSIS LUTEA*

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Development of next generation sequencing (NGS) technologies allowed us to study marine microorganisms and, in particular, to identify millions of genes expressed in open ocean (Carradec et al. 2018). Among referenced genes in microalgae, 75% encode for unknown proteins (i.e. sequences have no detectable similarity with known genes) (Caputi et al. 2019). DyNAlgue project aims at identifying genetic basis of traits of interest, without prior information, in *Tisochrysis lutea* by using a genome-wide association study approach (GWAS). Working from 15 strains of *Tisochrysis lutea* isolated from different ecosystems in the ocean, we cytometrically isolated 100 clones from these strains on the basis of their size, their fluorescence and their lipid content. We precisely characterized each clone individually through two controlled culture conditions in photobioreactors, nitrogen-limiting and phosphorus-limiting. We will present results of GWAS to localize genes which play a role in variation of traits of interest, as pigment production.

Financing: French National Research Agency

Keywords: Quantitative genetics, microalga, phenotyping

Oral presentation

TIGHTLY CONSTRAINED GENOME REDUCTION AND RELAXATION OF PURIFYING SELECTION DURING SECONDARY PLASTID ENDOSYMBIOSIS

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Endosymbiosis, the establishment of a former free-living prokaryotic or eukaryotic cell as an organelle inside a host cell, can dramatically alter the genomic architecture of the endosymbiont. Plastids, the light harvesting organelles of photosynthetic eukaryotes, are excellent models to study this phenomenon because plastid origin has occurred multiple times in evolution. Here, we investigate molecular processes acting through secondary plastid endosymbiosis – the origination of a new plastid from a free-living eukaryotic algal ancestor. We used phylogenetic comparative methods to study gene loss and changes in selective regimes on plastid genomes, focusing on the green lineage, which has given rise to three independent lineages with secondary plastids (euglenophytes, chlorarachniophytes, *Lepidodinium*). Our results show an overall increase in gene loss associated with secondary endosymbiosis, but this loss is tightly constrained by retention of genes essential for plastid function. The data show that secondary plastids have experienced temporary relaxation of purifying selection during secondary endosymbiosis, but that this process is tightly constrained as well, with the relaxation being relative to that in primary plastids, and purifying selection continues to dominate other evolutionary forces during the endosymbiosis events. Selection intensity rebounds to pre-endosymbiosis levels after secondary endosymbiosis, demonstrating the changes in selection efficiency during different phases of secondary endosymbiosis. The three independent events differ in the degrees of relaxation of selection, highlighting the different evolutionary contexts of these events. This study reveals the selection-drift interplay during secondary endosymbiosis, and evolutionary parallels during the process of organelle origination.

Keywords: Secondary endosymbiosis, plastids (photosynthetic organelle), selection efficiency variation

Oral presentation

FIRST IDENTIFICATION OF FUCOXANTHIN-CHLOROPHYLL A/C BINDING PROTEIN OF *TISOCHRYSIS LUTEA*, INFLUENCE OF NITRATE CONCENTRATION AND LIGHT INTENSITY ON ITS EXPRESSION

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Tisochrysis lutea is a haptophyte producing high amounts of fucoxanthin (Fx), a major carotenoid pigment of interest to the cosmetic and pharmaceutical industry. To assess the biological levels to understand the production of fucoxanthin by *T. lutea*, we researched the genes coding for the Fucoxanthin Chlorophyll a/c binding Protein (FCP) of its light harvesting antenna, composed of three protein families (Lhcf, Lhcr, Lhcx) binding different photosynthetic and photoprotective pigments such as Fx, Chl a, Chl c, diatoxanthin and diadinoxanthin. Though this complex is well described in diatoms, it is still quite unknown in haptophytes. By assuming its light harvesting system was close to that of diatoms and other well described brown algae, we found fifty-two protein sequences forming the FCP in *T. lutea*. Based on this result, we found the putative binding sites of the main photosynthetic pigments Fx and Chl a/c in *T. lutea* by comparing with *Phaeodactylum tricornutum* binding sites (Wang et al. 2019). Our results highlight an efficient energy transfer *in T. lutea* photosynthetical process, and allow us to make hypotheses to understand how to increase the intrinsic amount of fucoxanthin in *T. lutea*. We also observed the influence of NO_3 concentration and of a day/night cycle on the expression of the FCP genes in continuous culture. NO_3 depletion induces a great decrease of the majority of those genes. Day light induces an increase of lhcf and lhcr genes and of the Fx production, meaning cells form more light harvesting antenna during the day to perform photosynthesis.

Keywords: Haptophytes, fucoxanthin, transcriptomics

Oral presentation

SEASONAL GENOTYPE DYNAMICS OF A BALTIC DINOFLAGELLATE – PELAGIC POPULATIONS ARE HOMOGENEOUS AND AS DIVERSE AS BENTHIC SEED BANKS

Jacqueline Jerney[1,2], Karin Rengefors[3], Satoshi Nagai[4], Bernd Krock[5], Conny Sjöqvist[6], Sanna Suikkanen[1], Anke Kremp[7]

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Genetic diversity is the basis for evolutionary adaptation and selection under changing environmental conditions. Phytoplankton populations are genotypically diverse, can become genetically differentiated within small spatiotemporal scales and many species form resting stages for seasonal survival. Resting stage accumulations (seed banks) are expected to serve as archives for genetic information, but so far, their role in phytoplankton diversity and evolution has remained unclear. In this study we used the toxic Baltic dinoflagellate *Alexandrium ostenfeldii* (Dinophyceae) as a model organism to investigate if (1) the benthic seed bank is more diverse than the pelagic bloom population and (2) if the pelagic population is seasonally differentiated. Cysts and bloom samples were collected in the Baltic Sea, followed by cell isolation and genotyping using microsatellites and restriction site associated DNA sequencing. High clonal diversity (98 – 100%) combined with intermediate to low gene diversity (0.58 – 0.02 depending on the marker) was found. Surprisingly, the benthic and pelagic fraction of the population were equally diverse, and the bloom was temporally homogenous, despite seasonal fluctuation of potential selection pressures. The persistence of linkage equilibrium throughout the year indicates frequent genetic recombination. Results of this study suggest that continuous benthic-pelagic coupling, combined with sexual reproduction prevent the establishment of a single clonal lineage in a dynamic environment. Together they harmonize the pelagic with the benthic population and thus prevent seasonal population differentiation. At the same time frequent sexual reproduction and benthic-pelagic coupling maintain high clonal diversity in both habitats.

Financing: Academy of Finland, Walter and Andrée de Nottbeck Foundation, Japan Society for the Promotion of Science

Keywords: Seed bank, sequencing, resting stages

Oral presentation

DRIVERS AND SPATIAL SCALES OF LOCAL ADAPTATION AND CONNECTIVITY IN THE SUGAR KELP, *SACCHARINA LATISSIMA*

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Environmental and oceanographic features drive processes of genetic differentiation and adaptation over species distributions. Understanding these influences can offer valuable insights that can feed in to the effective management and maintenance of genetic diversity and adaptation potential in marine ecosystems. Here we investigated how oceanographic connectivity and environmental heterogeneity affect local adaptation and genetic diversity in the cosmopolitan brown macroalgae *Saccharina latissima* across an environmental transition zone between the North Sea and Baltic Sea. A genome-wide marker set of 9,222 SNPs was combined with environmental data and a hydrographic model of spore dispersal to give insights into the complex relationship between population connectivity and local adaptation. The results showed hierarchical structuring amongst populations with stations in the southern Kattegat demonstrating clear genetic differentiation from central and northern populations. Tests for spatial genetic influences showed the significant effects of asymmetric oceanographic processes on genetic distance. Candidate loci from GEA analysis additionally highlighted the presence of strong putative adaptation gradients along the transition zone. Investigations into separate drivers of putative adaptation showed contrasting patterns and spatial scales of temperature and salinity adaptation. The results pointed to combined effects of oceanographic isolation and environmental selection in driving genetic differentiation across the region. The findings highlighted potential sources of unique adaptation as well as highlighting increased levels of putative adaptive diversity towards the centre of the transition zone. Insights gained will inform the management and conservation of macroalgal ecosystems in the Skagerrak-Kattegat region as well as the emerging seaweed cultivation industry.

Financing: SFSER MISTRA grant no. 2013/75, SRCF grant no. 213-2013-92, the NRC MACROSEA project 254883

Keywords: Seascape genomics, adaptation, kelp

Oral presentation

PRIMARY ENDOSYMBIOSIS OF PHOTOSYNTHETIC *PAULINELLA* REVEALED BY GENOMICS

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Eukaryotic photosynthetic organelles, plastids, are the powerhouses of many aquatic and terrestrial ecosystems. The canonical plastid in algae and plants originated >1 billion years ago and therefore offers limited insights into the initial stages of organelle evolution. To address this issue, we focus here on the photosynthetic amoeba *Paulinella micropora* strain KR01 that underwent a more recent (ca. 124 Mya) primary endosymbiosis, resulting in a photosynthetic organelle termed the chromatophore. Analysis of genomic and transcriptomic data resulted in a high-quality draft assembly of size 707 Mbp and 32,361 predicted gene models. A total of 100 and 26 well-supported HGT and EGT events, respectively, were identified in a phylogenomic analysis, suggesting a greater role for foreign gene acquisition than EGT in the evolution of this lineage. A total of 291 chromatophore targeted proteins were predicted in silico, 206 of which comprise the ancestral organelle proteome in photosynthetic *Paulinella* species with functions, among others, in nucleotide metabolism and oxidative stress response. The biggest portion of the chromatophore targeted proteins was derived from the host, suggesting dominant host contribution to plastid endosymbiosis. Gene co-expression analysis identified networks containing known high light stress response genes as well as a variety of genes of unknown function.

Keywords: Chromatophore, photosynthetic amoeba, primary endosymbiosis

Oral presentation

PATTERNS OF ADAPTIVE SELECTION ON SYMBIOTIC DINOFLAGELLATE LINEAGES WITHIN THE GENUS *SYMBIODINIUM*

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Dinoflagellates from the family Symbiodiniaceae are well-known for their ecologically-important symbioses that have evolved with reef-building corals. While previous studies have investigated patterns of positive selection on the Symbiodiniaceae family as a whole, the recent expansion of genomic data for both free-living and symbiotic species from this family enables examinations at finer resolutions. In this work, we employ genomic data for free-living and symbiotic representatives of the genus *Symbiodinium* to conduct a lineage-specific probe of genes experiencing adaptive selection due to symbiotic lifestyle, while controlling for taxonomic bias. We inferred 43,832 homologous protein sets from fifteen Suessiales species, identifying 6,580 protein sets for inference of adaptive selection. We conducted tests for adaptive selection, varying initial parameter estimates (i.e., transition/transversion, dN/dS ratios) and selecting the model with the highest log-likelihood for both the null and alternative models to prevent errors resulting from local optima. Additionally, we employed a complementary approach to identify signatures of adaptive selection evident not only through the fixation of specific nucleotide changes (i.e., branch-site models), but also through sites exhibiting divergent levels of sequence conservation between groups due to changes in purifying selection over evolutionary time (i.e., clade models). Although rarely used and never within Symbiodiniaceae, we found clade models to highlight distinct patterns of evolutionary divergence in gene functions compared to previously used branch-site model approaches. Our results through this comprehensive investigation of selective pressures on *Symbiodinium* genomes illustrate the complex evolutionary histories and selective pressures experienced by genes integral to the coral-algal symbiosis.

Financing: Australian Research Council DP190102474

Keywords: *Symbiodinium*, adaptive selection, symbiosis

Oral presentation

REVISED GENOME ASSEMBLY OF THE CORAL SYMBIONT *CLADOCOPIUM GOREAUI* REVEALS GENES WITH INTRICATE EVOLUTIONARY HISTORIES

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Dinoflagellates belonging to the family Symbiodiniaceae are crucial photosynthetic symbionts in corals and other coral reef organisms. Among Symbiodiniaceae taxa, *Cladocopium goreaui* is the most dominant in the Indo-Pacific including Australia's Great Barrier Reef, found in diverse coral hosts. An earlier genome study of *C. goreaui* SCF055-01 (isolated from the coral *Acopora tenuis*) revealed adaptive gene functions related to the establishment and maintenance of coral symbiosis. However, the origin and evolution of these genes remain to be systematically investigated. Here, we present a revised genome assembly of *C. goreaui* SCF055-01 incorporating long-read data (8877 scaffolds, N50 297.8 Kb), and improved gene models guided by full-length transcriptome (recovery of BUSCO eukaryote genes: 78%). Using the 42,367

C. goreaui genes, we assessed the evolutionary history of these genes at the protein level in a comprehensive phylogenomic approach using proteomes from broadly sampled taxa. Of the identified *C. goreaui* homologous protein sets, over half are specific to *C. goreaui* and/or to dinoflagellates, indicating lineage-specific functional innovation including conserved gene functions yet to be characterised. We identified a substantial proportion of *C. goreaui* genes that were potentially impacted by lateral genetic transfer involving both prokaryote and eukaryote lineages. Many of these genes encode photosynthetic functions, likely reflecting multiple endosymbioses implicated in plastid evolution of dinoflagellates. These results lend support to the complex evolutionary history of dinoflagellate genes and demonstrate for the first time how lateral genetic transfer contributed to the ecological success of Symbiodiniaceae as symbionts critical to corals and coral reefs.

Financing: Australian Research Council DP190102474

Keywords: Dinoflagellate, phylogenomics, coral reef symbionts

Oral presentation

INSIGHT INTO PELAGOPHYTES: NOVEL ALGAL GENOMES AND STRAIN LEVEL GENOME VARIATION IN THE HARMFUL ALGAL BLOOM CAUSING SPECIES *AUREOCOCCUS ANOPHAGEFFERENS*

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The Pelagophyceae are marine stramenopile algae that include *Aureoumbra lagunensis* and *Aureococcus anophagefferens*, two microbial species notorious for causing harmful algal blooms. Despite their ecological significance, relatively few genomic studies of pelagophytes have been carried out. To improve understanding of the biology and evolution of pelagophyte algae, we produced new high-quality reference genomes using Oxford Nanopore long-read sequencing technology for *A. lagunensis* (CCMP1510) (43 Mbp) and *Pelagomonas calceolata* (CCMP1756) (34 Mbp), and re-sequenced *A. anophagefferens* (CCMP1984) (53 Mbp). This includes a fully resolved telomere-to-telomere genome assembly for *P. calceolata*, with 6 chromosomes ranging from 4 to 6 Mbp in size. Furthermore, to investigate intra-species variation we produced high-quality draft genomes for four additional *A. anophagefferens* strains (CCMP1707, CCMP1708, CCMP1850, and CCMP3368). The pan-genome refers to the sum of genes across all strains of a given species, only a subset of which reside in the genome of any given strain. The pan-genome concept readily applies to prokaryotes, where lateral gene transfer (LGT) can lead to enormous intra-species gene-content variability. However, the extent to which LGT-driven pan-genomes exist in eukaryotes is uncertain. Our comparative genomic investigation indicates significant strain level variation in gene content in *A. anophagefferens*, including genes predicted to be related to bloom conditions, providing insight into both bloom dynamics and how microbial eukaryotes adapt and diversify.

Keywords: Genomics, Pelagophyceae, Stramenopiles

Oral presentation

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

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The photosynthetic plastid in eukaryotes putatively arose ca. 1.5 Ga from a single cyanobacterial primary endosymbiosis in the Archaeplastida ancestor. The only other known case of primary plastid origin occurred more recently (ca. 100 Ma) in the rhizarian amoeba *Paulinella*. The transition of *Paulinella* from a heterotrophic to a photosynthetic lifestyle has resulted in significant remodeling of both the host and endosymbiont genomes. Understanding this process using genomic techniques underpins our research efforts. The host genome shows significant levels of genome instability, with a plethora of unannotatable “dark” genes, many of which are differentially expressed over the light-dark cycle, and novel regulatory mechanisms that have evolved to accommodate the endosymbiont, potentially as a response to the damaging reactive oxygen species produced during photosynthesis. On the other hand, the endosymbiont genome has undergone significant genome reduction when compared to the free-living ancestor lineage. The high light inducible (*hli*) genes which were transferred to the host genome from the endosymbiont comprise a large multigene family, many members of which are encoded in conserved outward facing (head-to-head) pairs flanked by conserved repeat motifs. The two genes in these pairs, that may have arisen from different ancestral sequences, appear to have undergone gene duplication independently in different lineages, and may play different roles in the stress response of the host. The dynamic evolution of *hli* genes in *Paulinella* demonstrates how important these loci are to the host that is still under strong selection to manage the novel organelle.

Financing: United States National Aeronautics and Space Administration (80NSSC19K0462)

Keywords: Endosymbiosis, evolution, *Paulinella*

Oral presentation

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

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Seaweed farming in the Gulf of Maine has expanded rapidly over the past decade. As part of ARPA-E's MARINER program, we are pursuing a selective breeding program to improve the productivity and composition of sugar kelp, *Saccharina latissima*, which could serve new markets for food, animal feeds, bio-products and eventually biofuels. Understanding the population genetics and diversity of sugar kelp is key both for conservation and for planning breeding improvements for farming. We recently published the first genomic characterization of the genetic diversity of sugar kelp from 13 wild populations in the Northeastern US. We used genome-wide single nucleotide polymorphism data to identify the finer population structure of kelp in the Gulf of Maine and Southern New England. Our assessment revealed distinct genetic variation between the Gulf of Maine and Southern New England populations, confirming that Cape Cod acts as a barrier to gene flow. Furthermore, based on the analysis of molecular variance (AMOVA), we found the largest variance (58%) was found within populations. Given this information, we have conducted field trials within two different biogeographic regions with hundreds of parental crosses from our wild sporophyte collections. These crosses were planted in "common garden" farm arrays over two seasons. Analysis of our phenotypic and genotypic results will be presented. A project goal is to develop methods to predict offspring performance based upon genotype and breeding values of parents for a rapid-cycle breeding approach, and to improve dry matter yield per unit area >10% per generation.

Financing: Funded by U.S. Department of Energy's ARPA-E MARINER program; contract number DE-AR0000915 awarded to Woods Hole Oceanographic Institution. Marc. VonKeitz@hq.doe.gov

Keywords: *Saccharina*, population genetics, breeding

E-Poster

A MAGIC DESIGN TO STUDY MINERAL NUTRITION IN *CHLAMYDOMONAS REINHARDTII*

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Natural trait variation is present across all domains of life. Individuals of the same species often present differences in response to environmental stress or in adaptation. Some traits, such as biomass production, have economical interest in the industrial, pharmaceutical or agricultural sectors. Identifying the genetic variants affecting these processes is, therefore, fundamental. *Chlamydomonas reinhardtii* is the reference unicellular photosynthetic eukaryote model organism. This haploid unicellular green alga is capable of sexual reproduction, has a high recombination rate and a very short generation interval. Furthermore, *C. reinhardtii* can metabolize alternative carbon sources and grow under nutrient deficiency. Studying its mineral nutrition is essential to understand adaptation to the environment. A Multiparent Advanced Generation Inter-Cross (MAGIC) design is used to study genetic variation. Eight founder lines presenting phenotypic variation were intercrossed in a determined design where each founder line contributes equally, for 8 generations. A total of 768 terminal lines, consisting of a genetic mosaic of the founder lines, were obtained. Mineral nutrition of the terminal lines is explored using mixotrophy as control condition, and 10 conditions were tested: autotrophy, 5 macronutrient deprivation, and 4 micronutrient deprivation. Cells are pre-cultured in control media for 2 days, transferred to treatment media, then harvested after 4 days. Phenotypic variation in the terminal lines of the MAGIC design largely exceeds the variability observed in founder lines, indicating that new diversity has been obtained. Together with genome sequencing of the terminal lines, the dataset will enable Quantitative Trait Loci mapping for mineral nutrition in *C. reinhardtii.*

Financing: This project is funded by a University of Liège fellowship under the ARC project Green MAGIC

Keywords: *Chlamydomonas reinhardtii*, mineral nutrition, MAGIC design

E-Poster

PHYLOGEOGRAPHIC GENOMICS OF *SARGASSUM POLYCYSTUM* C. AGARDH (FUCALES, PHAEOPHYCEAE) IN THAILAND

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Thailand is situated in the Indo-Pacific transition zone. The west coast borders the Andaman marine province (Western Indo-Pacific biogeographic realm) and the east coast borders the Sunda Shelf province (Central Indo-Pacific realm). They are connected via the southern tip of the Thai-Malay Peninsula. The Sunda Shelf was emersed during the Last Glacial Maximum (LGM) and must have been repopulated by marine organisms after it became inundated again. This geographic pattern leads us to hypothesize two contrasting evolutionary scenarios: spatial isolation vs. genetic introgression. The present study aims to reveal phylogeographic patterns along the Thai-Malay Peninsula in the seaweed *Sargassum polycystum*. We sequenced complete chloroplast and mitochondrial genomes of this species from populations along the Thai-Malay Peninsula to gain insight in their population genetic diversity and connectivity between populations. The intergenic spacer content in the chloroplast is ± threefold the percentage in the mitochondrion. However, the mutation rate in the latter is ± three times higher than in the former. Their suitability as molecular marker is comparable, because the chloroplast genome (124,493 nt) is more than three times larger than the mitochondriome (34,825 nt). Both markers revealed two main lineages in the Gulf of Thailand. However, a clear phylogeographic pattern did not emerge. We will discuss how the LGM and geographical processes interacted to shape the contemporary distribution and genetic variation patterns.

Financing: Thailand Research Fund (National Research Council Thailand) grant RDG6130002 National Natural Science Foundation (China) grants 31971395 and 41761144057

Keywords: Phylogeography, mitochondriome, Sunda Shelf

SYM08: Physiological and ecological responses of algae and their ecosystems to ocean acidification

Keynote lecture

CELLULAR MECHANISMS UNDERLYING THE RESPONSE OF COCCOLITHOPHORES TO FUTURE CHANGES IN OCEAN CARBONATE CHEMISTRY

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Coccolithophores are a group of unicellular marine phytoplankton that are characterised by their ability to generate a cell covering of intricate calcium carbonate platelets, known as coccoliths. Coccolith production has an important influence on the global carbon cycle, making a major contribution to carbon fluxes to the deep ocean. Calcification by coccolithophores is predicted to be detrimentally affected by future changes in ocean pH (ocean acidification). However, as coccolithophores calcify intracellularly, the mechanisms through which this process is affected by changes in seawater pH remain unclear. Our research has examined the cellular mechanisms of calcification in coccolithophores. We have found that lower seawater pH impairs coccolith formation by disrupting intracellular pH homeostasis. In particular, the activity of voltage-gated H+ channels in the plasma membrane of *Coccolithus braarudii* is greatly reduced in cells acclimated to low pH. This impairs the ability of *C. braarudii* to remove H+ generated by the calcification process and leads to specific coccolith malformations. The results demonstrate that H+ channels are required for intracellular calcification in *C. braarudii* and that these mechanisms are sensitive to low pH environments. We will discuss how these findings may allow us to better predict the response of coccolithophores to future changes in ocean carbonate chemistry.

Keywords: *Coccolithus braarudii*, calcification, ocean acidification

Keynote lecture

CORALLINE ALGAL CALCIFICATION PHYSIOLOGY UNDER OCEAN ACIDIFICATION

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Coralline algal are highly susceptible to the impacts of ocean acidification, with their calcification rates especially impacted. Here I will discuss recent syntheses of these impacts on calcification, as well as outlining some of the physiological mechanisms responsible for these declines. There are also a raft of physiological and morphological traits that have been proposed to give a handful of coralline algal species tolerance to ocean acidification. These include differences in morphology, size, metabolic rates and abilities to control their calcifying fluid chemistry. The hardest traits to quantify are those involving the calcifying fluid chemistry, where δ11B, B/Ca and raman FWHM has been used to infer pH, dissolved inorganic carbon and saturation state of calcium carbonate in corallines and corals. Though there are uncertainties in their quantification for high magnesium calcite, these uncertainties are lower for aragonite. I present the results of environmental controls on these in coralline algae and directions for future research.

Financing: Rutherford Discovery Fellowship from The Royal Society of New Zealand Te Apārangi, ARC CoEfor Coral Reef Studies

Keywords: Coralline algae, calcification, multiple stressors

Oral presentation

CARBON METABOLISM RESPONSES IN ACCLIMATED AND PERTURBED *EMILIANIA HUXLEYI* CULTURES UNDER OCEAN ACIDIFICATION CONDITIONS

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Carbon metabolism related variables in *Emiliania huxleyi* show variable responses to ocean acidification (OA). However, most of the studies converge on the statement that OA has negative effects on calcification. In this study we hypothesize that carbon metabolic responses to OA differ between CO2 acclimated and perturbed phytoplankton cultures. Hence, responses of *Emiliania huxleyi* cultures acclimated to future CO2 concentrations (1000 ppmv, High Carbon: HC) and present CO2 concentrations (406 ppmv, Low Carbon: LC, Control) were assessed under acclimated and perturbed conditions, the last one promoted by stopping the CO2 supply in the culture media for 4 hours. Gene expression of three genes related to CCMs (Carbonic anhydrase (CA): αca1, αca2) and carbon fixation (RuBisCO: rbcL) were quantified as well as rates of photosynthetic carbon incorporation, DOC release and calcification. The results revealed two different patterns in both, molecular and physiological responses, depending on culture conditions and CO2 treatment: acclimated conditions performed a down-regulation of the carbon metabolism in HC cells compared to LC cells while under perturbed conditions, HC cells showed an up-regulation of most of the photosynthetic carbon metabolic pathways studied. In addition, the calcification rates under HC concentrations revealed a more conservative response than the other tested variables and always showed lower values than under LC conditions. These results highlight the relevance of considering previous growth conditions to appropriately interpret the response of calcifying phytoplankton to future OA scenarios.
Financing: This work has been funded by the Spanish Ministry of Economy, Industry and Competitiveness and by the Xunta de Galicia

Keywords: Carbon metabolism, ocean acidification, *Emiliania huxleyi*

Oral presentation

DISSOLVED ORGANIC CARBON RELEASE BY SEAWEEDS UNDER CO2 ENRICHMENT: IMPLICATIONS FOR CCM AND NON-CCM SPECIES UNDER OCEAN ACIDIFICATION

Ellie R. Paine[1], Matthias Schmid[1], Catriona L. Hurd[1], Philip W. Boyd[1], Guillermo Diaz-Pulido[2]

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Concentrations of dissolved carbon dioxide (CO2) in the ocean are predicted to increase by 200% by the year 2100 due to anthropogenic activity, causing ocean acidification. The responses of seaweeds to increased CO2 is difficult to predict but may depend on whether their growth/productivity is currently limited by dissolved inorganic carbon (DIC) supply, and the mechanism by which they take up DIC. In natural seawater, DIC is primarily available as bicarbonate which cannot pass through the seaweed plasmalemma via diffusion; 65% of seaweeds possess mechanisms which aid its uptake, termed CO2 concentrating mechanisms (CCMs). However, 35% of seaweeds do not possess CCMs and solely use CO2 as their source of DIC (non-CCM species). As DIC levels increase in the ocean, seaweeds which are currently limited for DIC may utilise this additional carbon for growth. Once DIC is assimilated into organic carbon via photosynthesis, seaweeds may release dissolved organic carbon (DOC) into the surrounding seawater depending on local environmental conditions such as light and nitrogen. Diaz-Pulido et al. (2020) found a greater DOC release with an increase in seawater DIC i.e. increasing ocean acidification. We tested the effect of ocean acidification on DOC release by three temperate seaweed species with differing DIC uptake mechanisms: *Hemineura frondosa* (Rhodophyta, non-CCM), *Lenormandia marginata* (Rhodophyta, CCM) and *Ecklonia radiata* (Ochrophyta, CCM). I will discuss the experimental design, results and implications of our findings for future ocean acidification experiments.

Keywords: Ocean acidification, dissolved organic carbon, macroalgae

Oral presentation

CORALLINE ALGAE AT INCREASED CO2: A GLOBAL RESPONSE TO OCEAN ACIDIFICATION

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Coralline algae are an ecologically important part of benthic communities worldwide and there is growing concern that ocean acidification can severely impact their calcite skeletons. Laboratory studies of coralline algae in simulated ocean acidification conditions have revealed wide response variability, making it difficult to assess their future biodiversity and contribution to ecosystem function. Here, we used natural gradients in seawater carbonate chemistry in widely separated biogeographic regions (Mediterranean, NW Pacific) to investigate the effects of ocean acidification on coralline algal

biodiversity, abundance and skeletal mineralogy. Molecular identification showed a decrease in the taxonomic diversity of coralline algae with increasing acidification and more than half of the taxa were lost in high pCO2 conditions. The success of some coralline species in acidified conditions may relate to their ancient evolutionary history as well as their present-day exposure to environmental variability. The Sporolithales is the most ancient order and evolved when ocean chemistry favoured low Mg-calcite deposition, although it has survived past ocean acidification events is less diverse today and was intolerant of ocean acidification in our molecular surveys. The Corallinales is the most recent order, it evolved when ocean chemistry favoured aragonite and high Mg-calcite deposition, it had the highest diversity at our high pCO2 sites. The CO2 gradients we surveyed did not affect the skeletal mineralogy of the coralline algae but the cover of coralline algae declined with the increasing pCO2, as did the thickness of their carbonate deposits, highlighting the lower fitness of this group as a whole under future high pCO2.

Keywords: Biodiversity, climate change, evolutionary history

Oral presentation

ENVIRONMENTAL DRIVERS OF CALCIFICATION IN TROPICAL CORALLINE ALGAE

Guillermo Diaz-Pulido[1], Ellie Bergstrom[1], Tessa Page[1], Rocio García-Urueña[3], Soyoung Jeong[1], Emma Kennedy[1,2], Bonnie Lewis[1], Merinda Nash[4], Alexandra Ordonez[1,2], Ulrike Troitzsch[4]

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In this talk, we will provide an overview of the research we are currently undertaking to understand the influence of the environment, particularly ocean acidification, on the growth and calcification of crustose coralline algae (CCA) in the Great Barrier Reef (GBR) and the Caribbean. A first step towards this goal is to understand the mechanisms and patterns of calcification, growth and mineralogical composition. We are making significant progress to unravel the molecular basis of CCA calcification and have now identified RNA molecules (transcriptomes) involved in biomineralization and other key processes (T. Page work). Because biomineralization in the CCA occurs in the cell walls, we are studying the monosaccharide constituents of the cell wall and their potential role in calcification (E. Bergstrom work). Understanding the influence of environmental variability on the calcification process requires fundamental research on species boundaries and phylogeny of the corallines, as well as knowledge of the distribution of species across reef habitats. This knowledge allows us to examine in more detail the influence of water quality, seasonality and upwelling (Caribbean) on CCA calcification and mineralogical composition and to obtain growth and calcification estimates of CCA along the GBR. There is considerable variability in CCA responses to ocean acidification and our recent experiments suggest that this variability may also be explained by their evolutionary history. This work is critical for advancing our understanding of anthropogenic influences on CCA ecology and the critical roles they play in reef ecosystem functioning, in particular their contribution to reef framework construction.

Financing: Australian Research Council Discovery Grant (ARC-D) DP160103071

Keywords: Coralline algae, ocean acidification, coral reefs

Oral presentation

CONNECTING MACROALGAL O2, PH, AND CARBONATE THALLI SURFACE DYNAMICS TO CALCIFICATION AND DISSOLUTION ON FUTURE CORAL REEFS

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While ocean acidification (OA) can negatively affect calcification in tropical reef macroalgae, the mechanisms remain elusive. We examined 4 dominant calcifying macroalgae (*Halimeda, Udotea, Jania, Neogoniolithon*), for the effects of OA on calcification, dissolution and thalli surface dynamics (O2, carbonate, and pH) under ambient (8.1) and low (7.7) pH using radioisotopes (45Ca) and microsensors. Additional experiments were conducted in light and dark with/without a photosystem II (PSII) inhibitor to examine photosynthesis and light-triggered proton pumps. At low pH in the light, all species maintained gross calcification rates and most sustained net calcification rates relative to controls. Further, there was greater Δ pH (2-3 times) between the thalli surface and bulk seawater compared to ambient. In contrast, all species had lower net calcification rates in the dark at low pH with some exhibiting net dissolution. Only *Udotea*, which exhibited dissolution in the light, also had lower daily calcification rates integrated over 24 h. *Udotea* also exhibited the least thalli surface pH increase under OA and no pH dynamics independent of PSII. Conversely, species that showed biotic control of thalli H+ dynamics without PSII, also maintained 22-34% of their calcification rates independent of PSII at ambient pH. However, calcification independent of PSII was not sustained at low pH. Therefore, a combination of light-triggered proton pumps and photosynthesis promote calcification in the light, but are dependent on photosynthesis at low pH. Species with the capacity to calcify in the light under OA can compensate for low net calcification or dissolution in the dark.

Financing: Funded by NSF OA Program CRI-OA Grant #1416376. The IAEA is grateful for support from Government of Principality of Monaco.

Keywords: Calcification, coral reef, dissolution

E-Poster

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

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The Levantine basin in the eastern Mediterranean Sea is a naturally oligotrophic marine ecosystem. This region has experienced multiple local species extinctions and a 3°C increase in seawater temperature over the past 40 years. The Israeli coastline has also been colonized by a multitude of non-native species, mostly via the Suez Canal, including the calcifying red alga *Galaxuarar ugosa*. This non-native was first found on the Syrian coastline in the late 1990s, and since then is becoming dominate in the shallow reef ecosystem alongside native coralline algal turfs. In previous investigations, a native coralline called *Ellisolandia elongata*, but now likely representing several Corallina sp., responded poorly to high temperatures (>27 °C). In contrast, G. rugosa only becomes stressed in temperatures over 33 °C, which is still rarely experienced in high summer in the region, suggesting it may have an advantage under future ocean conditions. Often overlooked in macroalgae in general, the unique physiology of each ploidy stage in these calcifying haplodiplontic algae has not been quantified. Here, we test the variable response of haploid and diploid stages to a range of temperatures reflecting pre-industrial, present day, and near-future ocean conditions in one experiment, and to combined increased pH and temperature conditions reflecting the same conditions in both species in a second experiment. The maintenance of alternative generations in these haplodiplontic life cycles indicates they have unique, though likely subtle, ecophysiology, therefore we expect variable responses in haploid and diploid *G. rugosa* and *Corallina* sp.

Financing: Binational Science Foundation 2017276 to SAKH and GR

Keywords: Haplodiplontic life cycle, invasion, gametophyte and tetrasporophyte

E-Poster

EFFECTS OF RISING CO2 ON ALGAE IN JAPAN

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Shimoda Marine Research Centre has set up a platform for international research to assess the benefits of reducing multiple stressors for sustainable development of the Blue Economy. A closely monitored gradient in seawater CO2 is available to assess ocean acidification, deoxygenation, eutrophication, warming and harmful species. We welcome collaborations as CO2 seep show profound effects of acidification on micro- and macroalgae, as well as the ecological tipping points that drive shifts in coastal systems1. Recent sea surface warming has killed-off kelp forests around Shikine island. Here, coralline algae decline as CO2 levels rise from 300 ppm to 900 ppm near seeps and perennial macroalgae are replaced by opportunistic turf algae and summer diatom blooms2. Benthic carbon fixation is increased at high CO2 - but most of it is exported offshore and the resilience of coastal communities to typhoons is diminished3. In the UN Decade of Ocean Science, data from this field facility will be used help inform people that need to adapt to global changes affecting aquaculture, fisheries and coastal tourism. References: 1. Hall-Spencer J.M., Harvey B.P. (2019) Ocean acidification impacts on coastal ecosystem services due to habitat degradation. Emerging Topics in Life Sciences 3 197–206//2. Harvey, B. P. et al. (in press) Feedback mechanisms stabilise degraded turf algal systems at a CO2 seep site. Communications Biology.//3. Wada, S. et al. (in press). Ocean acidification increases phytobenthic carbon fixation and export in a warm-temperate system. Estuarine, Coastal and Shelf Science

Financing: 'International Educational and Research Laboratory Program', University of Tsukuba. JSPS KAKENHI Grant 17K17622, Ministry of Environment, Japan (Suishinhi: 4RF-1701)

Keywords: Global change, marine ecology, CO2 seeps

SYM09: A future for algal taxonomy: challenges and prospects

Keynote lecture

MOLECULAR TAXONOMY AND PHYLOGENOMICS OF CERAMIALES (RHODOPHYTA) HIGHLIGHT CHALLENGES AND ADVANCES IN UNDERSTANDING THE DIVERSITY AND SYSTEMATICS OF ALGAL TURFS

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Algal turfs are ecosystem engineers receiving growing attention in relation to their expansion on temperate reefs as a consequence of global change. However, their species diversity and taxonomy are still poorly understood. Turfs are composed of densely entangled small seaweeds, in which the red algal order Ceramiales is commonly a major component. The advent of classical molecular taxonomy and -omic approaches has revolutionized investigations of seaweed diversity and systematics. These approaches have been applied to the study of the Ceramiales, facilitating the discovery of new species and resolving classification issues. A molecular diversity survey using the rbcL gene and involving the study of ca. 400 specimens of turf-forming *rhodomelacean* species in Macaronesia detected impressive amounts of newly discovered diversity. A total of 67 species were identified, of which half corresponded to undescribed species presumably endemic to this bioregion. Likewise, the application of molecular species delimitation methods to widely distributed records of *Polysiphonia scopulorum* (>150 samples collected in Australia, South Africa, southern Europe and Macaronesia) revealed that it is a complex in which 13 species were resolved. These 13 cryptic species range from endemics with narrow known distributions to a species found in all studied regions. At taxonomic levels above species, the use of plastid phylogenomics has produced well-resolved phylogenies that have been applied to the resolution of classification issues in the Ceramiales. These studies illustrate how classical and newer evolving molecular techniques facilitate the understanding of seaweed diversity and systematics, and provide new insights into the complexity of turf assemblages.

Financing: PDT acknowledges support by GAIN, Xunta de Galicia, Spain (grants 03-IN858A-2019-1630129 and ED481D/2017/011)

Keywords: Classification, High Throughput Sequencing, molecular species delimitation

Keynote lecture

THE RECENT EVOLUTION OF PROTIST CLASSIFICATION SYSTEMS: LESSONS FOR THE NEXT DECADE

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I address continuing conflicts in protistology between different traditions of naming lineages. The introduction of phylogenetics and parallel developments in molecular biology caused a collapse of a historical classification tradition. The algal classification was already in continuous flux in decades prior to the 1990s. The disagreements of the late 1990s are legendary. It was a period of wild speculation by some, and cautious synthesis by others, with rivalries and personality differences that made a synthesis difficult. The 2005 synthesis emerged from several years of quiet diplomacy managed by email, with well-respected authorities. It was meant to sort through the confusion of multiple names for each taxon introduced by different labs, and to sketch a synthesis of the overall picture. In the 2012 revision most disputes shifted to rooting the tree of eukaryotes, and how the main lineages were linked. Agreements on the phylogenetic information were not matched by agreements on naming lineages. Traditional practice, discipline-specific culture, and modernizing trends remain in conflict. Since then, we have seen developments in PR2 towards the EukRef database, fewer conflicting classification systems for the same sequence information, and increased phylogenetic thinking by taxonomists. The 2019 revision was less combative, with agreements on phylogenetics along many more branches, towards orders and families in many lineages. We provided a guide for primer selection, functional group assignment, and to modernize the vocabulary in Chinese script. Since, PhyloCode (2020) has come into effect. We must continue to strive for name stability despite shuffling of lineages that will continue.

Keywords: Classification, nomenclature, systematics

Oral presentation

MOLECULAR ASSESSMENT OF *ULVA* (ULVOPHYCEAE, CHLOROPHYTA) DIVERSITY IN VIETNAM REVEALS MARKED DIFFERENCES WITH TRADITIONAL UNDERSTANDING OF SPECIES DIVERSITY

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We investigated *Ulva* diversity in Vietnam based on extensive sampling along the entire coast. DNA sequence data of three commonly used markers, including the nuclear encoded rDNA internal transcribed spacer (ITS), the chloroplast genes RuBisCO large subunit (*rbcL*), and elongation factor Tu (*tufA*), were analyzed using different methods of sequence-based species delimitation, including the Generalized Mixed Yule Coalescent (GMYC), Automatic Barcode Gap Discovery (ABGD), and Poisson tree processes (PTP). From 199 specimens, we identified 18 molecular species hypotheses. Subsequent analysis comparing these candidate species with available sequences in GenBank revealed a species diversity of *Ulva* in Vietnam that is largely incomparable to the current species inventory based on morphology. Only three names, *U. lactuca*, *U. reticulata*, and *U. flexuosa*, matched our DNA-based species list. 11 species, mainly with an Indo-Pacific distribution, are newly reported from Vietnam. Among these, *U. ohnoi*, *U. limnetica*, *U. meridionalis*, *U. tepida* and *U. chaugulii*, have been described relatively recently based on molecular data. The identity of the other six species was rather uncertain because they fall in either clusters bearing more than one accepted species names or clusters having invalid names. Four species clades could not be attributed to existing species names. Our study advances our understanding of *Ulva* diversity in

tropical seas, and emphasizes the need for detailed taxonomic studies, combining morphological and molecular data to study species diversity in these regions, and gain better insights in global *Ulva* diversity pattern.

Keywords: *Ulva*, Vietnam, DNA-assisted alpha taxonomy

Oral presentation

DIVERGENCE TIMES AND PLASTID PHYLOGENOMICS WITHIN THE ORDER ERYTHROPELTALES (COMPSOPOGONOPHYCEAE, RHODOPHYTA)

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The advent of high-throughput-sequencing (HTS) has allowed for the use of large numbers of coding regions to produce robust phylogenies. The Erythropeltales are an order in the Compsopogonophyceae, a group with unusual plastid genomes but with low taxon sampling. We use HTS to produce near complete plastid genomes of all genera, and multiple species within some genera, to produce robust phylogenies to investigate character evolution, dating of divergence in the group, and plastid organization, including intron patterns. Our results produce a fully supported phylogeny of the genera in the Erythropeltales, and suggest that morphologies (upright, crust) have evolved multiple times. Our dated phylogeny also indicates that the order is very old (~ 800 Ma), with diversification occurring after the ice ages of the Cryogenian period (750-635 Ma). Plastid gene order is very congruent with phylogenetic relationships and suggest that genome architecture does not change often. Our data also highlight the abundance of introns in the plastid genomes of this order. The use of plastid genomes clearly produces robust phylogenetic relationships that can be used to infer evolutionary events, and increased taxon sampling, especially in less well-known red algal groups, will provide additional insights into their evolution.

Keywords: Phylogeny, divergence times, chloroplast genomes

Oral presentation

TRACKING GENE LOSS IN PLASTID GENOMES OF PARASITIC RED ALGAE

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Red algal parasites are often closely related to their red algal hosts but have different levels of divergence from their hosts. The majority of the ~120 known parasites are not well studied and there is a high number of undescribed diversity, for example in New Zealand. The nuclear genome of parasitic red algae has not been studied yet and only a few mitochondrial and plastid genomes have been investigated so far. Present knowledge indicates that mitochondrial genomes of red algal parasites have no major architectural changes compared to their hosts or other related red algae. On the other hand, plastid genomes may show major rearrangement and massive gene loss in comparison to free-living red algae. These annotated plastid genomes are from *Pterocladiophila hemisphaerica, Harveyella mirabilis* and *Choreocolax polysiphoniae*. The three characterized red algal parasite plastid genomes have highly reduced gene content, with the loss of almost all photosynthetic genes, but they share the majority of the remaining genes. High-throughput-sequencing was used to sequence plastid genomes of mainly undescribed red algal parasites from New Zealand. Preliminary results indicate that there are plastid genomes that are similar in size to non-parasitic red algal but with high numbers of pseudogenes, including photosynthetic genes. These results indicate that red algal parasites can be used to track plastid genome reduction during the evolution of parasitism. This highly diverse group, red algal parasites, may be an important study system to understand the processes of genome evolution in parasites.

Financing: This research was supported by the Marsden Fund Council from Government funding, administered by the Royal Society of New Zealand

Keywords: High-throughput sequencing, plastid genome evolution, parasitism

Oral presentation

LITHOTHAMNION SPECIES (HAPALIDIALES, RHODOPHYTA) IN THE ARCTIC AND SUBARCTIC: PROVIDING A SYSTEMATICS FOUNDATION IN A TIME OF RAPID CLIMATE CHANGE

Viviana Peña[1], David Bélanger[2], Patrick Gagnon[3], Joseph L. Richards[4], Line Le Gall[5], Jeffery R. Hughey[6], Gary W. Saunders[7], Sandra C. Lindstrom[8], Eli Rinde[9], Vivian Husa[10], Hartvig Christie[9], Stein Fredriksen[11], Jason M. Hall-Spencer[12], Robert S. Steneck[13], Kathryn M. Schoenrock[14], Janne Gitmark[9], Ellen Sofie Grefsrud[10], Marc B. Anglès d'Auriac[9], Erwann Legrand[10], Jacques Grall[15], Thomas M. Mumford[16], Nicholas A. Kamenos[17], Paul W. Gabrielson[18]

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Coralline red algae in the genera *Clathromorphum, Phymatolithon* and *Lithothamnion* are important benthic ecosystem engineers in the photic zone of the Arctic and Subarctic. In these regions, the systematics and biogeography of *Clathromorphum* and *Phymatolithon* species have mostly been resolved whereas *Lithothamnion* species have not. Seventy-three specific and infraspecific names have been given to Arctic and Subarctic *Lithothamnion* specimens, the vast majority by Mikael H. Foslie in the late 19th and early 20th century. From the type specimens of 38 of these names, partial rbcL sequences were obtained that enabled us to correctly apply the earliest available names and to correctly place the remainder in synonymy. Three of the four Arctic and Subarctic Lithothamnion species, *L. lemoineae, L. soriferum* and *L. tophiforme* were distinct based on all three sequenced genes, two plastid encoded, *rbc*L and *psb*A, and the mitochondrial encoded COI-5P; rbcL and COI-5P also segregated *L. glaciale* from *L. tophiforme* but psbA did not. Based on DNA sequences, morpho-anatomy and biogeography, we recognize all four species. It is difficult to identify these species based on morpho-anatomy and they can all occur as encrusting corallines, as rhodoliths or as maerl. We demonstrate the importance of sequencing these historical type specimens by showing that the recently proposed northeast Atlantic *L. erinaceum* is a synonym of one of the earliest published Arctic species of *Lithothamnion, L. soriferum*, itself incorrectly placed in synonymy under *L. tophiforme* based on morpho-anatomy. Based on sequenced specimens, we update the distributions and ecology of these species.

Financing: Norwegian Biodiversity Information Center (project nº 70184235), Ministry of Trade, Industry and Fisheries of Norway (AKVAKYST III), family trust (P.W.G.)

Keywords: Biogeography, coralline red algae, taxonomy

Oral presentation

HIDDEN CYANOBACTERIA BIODIVERSITY IN THE CANARIAN LAUREL FOREST

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Epiphytes in the Canarian laurel forest are abundant wrapping the trees, although until now studies on this topic have focused mostly on lichens and bryophytes but not on microalgae. However, in tropical forests colonization of the phyllosphere has been studied in some depth, highlighting the appearance of cyanobacteria and other microalgae. The present study dealt with heterocyst-forming cyanobacteria epiphyllous on leaves in the laurel forests of the Canary Islands. A culture collection of 102 strains of heterocyst-forming cyanobacteria was established using an enrichment culture medium lacking combined nitrogen. Therefore, the leaf of the laurel forest trees is described here for the first time in the Canary Islands as a singular habitat for nitrogen-fixing cyanobacteria of the order Nostocales. The study was performed combining morphological (LM) and molecular (16S rDNA) analyses and revealed an unprecedented genotypic diversity of the strains isolated. None of the 102 strains was identical to any 16S RNA sequence deposited in GenBank. Morphologically, most strains were represented by either of two morphotypes, here termed "*Nostoc-type*" and "*Tolypothrix-type*" but strains belonging to genera *Brasilonema* and *Nodularia* were also encountered. In conclusion, the current study highlights the novel genetic diversity of heterocyst-forming cyanobacteria in the laurel forests of the Canary Islands with general implications for cyanobacterial taxonomy and ecology.

Keywords: Canary Islands, laurel forest, Nostocales

Oral presentation

BIODIVERSITY AND DISTRIBUTION OF HALIMEDA SPECIES IN MALAYSIAN WATERS

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The genus *Halimeda* is a well-known tropical benthic genus of green algae and plays an important ecological role in marine ecosystems. *Halimeda* species are also recognized as a type of carbon sink due to their ability to capture CO2 for photosynthesis and bicarbonate for calcification. High intraspecific polymorphism complicates species identity in *Halimeda* and few studies have focused on the taxonomy in Malaysia. This study aimed to investigate the biodiversity and distribution of *Halimeda* species using morpho-anatomical examinations and molecular analysis of the chloroplast tufA and rbcL genes. We collected 62 samples of *Halimeda* from Malaysian coastal areas. Fifteen species were identified: *H. borneensis, H. cuneata, H. cylindracea, H. discoidea, H. gigas, H. hederacea, H. heteromorpha, H. macroloba, H. macrophysa, H. micronesica, H. minima, H. opuntia, H. taenicola, H. velasquezii* and *H. xishaensis*. Five new species were recorded, namely *H. gigas, H. hederacea, H. micronesica, H. minima* and *H. xishaensis*. Of the 15 recognized morphospecies, we confirmed four species using molecular data: *H. discoidea, H. gigas, H. macroloba* and *H. xishaensis*. Species diversity was greater in Sabah and Labuan. In Peninsular Malaysia, the west coast showed greater species diversity compared to the east coast. The most abundant species were *H. opuntia* and *H. macroloba*. These results may assist future studies on species variation and geographic distribution of *Halimeda* in Malaysia by utilizing morphological and molecular analysis.

Keywords: Taxonomy, phylogeny, species richness

Oral presentation

RESOLVING CRYPTIC SPECIES COMPLEXES IN MARINE PROTISTS: PHYLOGENETIC HAPLOTYPE NETWORKS MEET GLOBAL DNA METABARCODING DATASETS

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Marine protists have traditionally been assumed to be lowly diverse, with each taxon having a cosmopolitan distribution because of an apparent lack of barriers to dispersal and morphological homogeneity as perceived in light microscopy. Yet, several recent studies have shown that many protistan morphospecies actually consist of cryptic species complexes whose members often show more restricted distributions. Detection of cryptic species is usually hampered by incomplete sample coverage and by use of methods (e.g. phylogenetics) not well suited to spotting recent divergence and ongoing gene-flow. To overcome these issues, we infer phylogenetic haplotype networks from global metabarcoding datasets to investigate a cryptic species complex of marine planktonic diatoms, namely that of *Chaetoceros curvisetus*. We show that haplotype networks inferred from two complementary metabarcoding datasets, the predominantly coastal one of Ocean Sampling Day (18S rDNA V4 + V9 regions) and the mostly oceanic one of Tara Oceans (18S V9 region) equally resolve the cryptic complex in terms of number of species. New hypothetical species are detected in both datasets. Gene flow is absent between most of the species. Geographic information contained in the two datasets reveals that some species have restricted distribution patterns whereas others are widely distributed. Closely related taxa occupy contrasting biogeographic regions, suggesting that geographic and ecological differentiation drive speciation.

Keywords: Haplotype networks, cryptic species, metabarcoding

Oral presentation

UPDATES ON CORALLINE ALGAE DIVERSITY FROM SUB-ANTARCTIC AND ANTARCTIC REGIONS

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Coralline algae are recognized for their critical roles in marine communities as ecosystem engineers and the provisioning of ecosystem services. Unfortunately, taxonomy and species occurrence of coralline algae from sub-Antarctic and Antarctic regions are still poorly understood, and there is a gap of information and updates in the modern context of DNA-based approaches. In this study, we focus on these regions to evaluate the diversity of coralline algae using three gene markers (COI, psbA, and rbcL). Our results validated the genus *Carlskottbergia*, sister taxa of *Synarthrophyton patena*, containing the generitype *Carlskottbergia antarctica*, and a new lineage from the Antarctic Peninsula. Our study also revealed a candidate of new species in the genus *Arthrocardia* from southern Chile and a report of this species in the Antarctic Peninsula, representing the first finding of a geniculate species as a non-native species in this continent. Additionally, our data showed that the distribution of the newly described *C. chamberlainiae* exceeds the southern Atlantic (Falkland and Tristan da Cunha Islands) and New Zealand, including our additions from central and southern Chile. Species *Lithothamnion glaciale* and *Pneophyllum discoideus* were found in southern Chile as well. Taxonomic identifications of other observed lineages require further examination: *Pneophyllum* sp. and *Clathromorphum* spp. from the Antarctic, *Lithophyllum* from southern Chile, and several lineages in *Hapalidiales* from both regions. Sequencing of type specimens is essential to correctly apply names and critical for truly understanding the morphological variation and biogeography of species.

Financing: Fondecyt N° 3180539 and Conicyt PIA Apoyo CCTE AFB170008 through the Instituto de Ecología y Biodiversidad (IEB).

Keywords: Sequencing, taxonomy, type specimen

Oral presentation

TAXONOMIC IMPEDIMENT OR OPPORTUNITY: DOCUMENTING THE FALKLAND ISLANDS SEAWEED DIVERSITY AS A CASE HISTORY

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In Britain, we take an up to date seaweed checklist for granted and that provides a baseline for fundamental and applied research. For many other parts of the world, no such lists exist and if they do, they may be based on limited sampling and outdated species concepts. Nevertheless, there is a huge amount of diversity to discover, describe or taxonomically resolve, our seaweed flora study of the Falkland Islands being a case in point. Despite two centuries of seaweed collections from the islands, it is only now that we are constructing a checklist based on historical and contemporary material. In 2018 and 2019 we undertook two sampling trips to the Falkland Islands, collecting over 1,500 specimens, and used a molecular approach to identify species, particularly for some of the key ecological (e.g. habitat-forming) groups, notably in the reds the Bangiales, Gigartinales and Corallinophycidae, in the greens the Ulvophyceae and in the browns the Fucophycidae. Of the approximately 300 species listed, based on the samples we tested, c. 30% are thought to be undescribed; further, this is primarily for the intertidal, whereas the subtidal remains comparatively under-sampled. The Falkland Islands are not alone in this regard, but this study highlights the scale and necessity of the task to document diversity in a time of rapid environmental change. By considering the Falklands seaweed flora in the context of the wider South Atlantic, we will address this taxonomic imperative including a strategy to resolve the global taxonomy of key seaweed groups.

Financing: UKRI GlobalSeaweedSTAR project (BB/P027806/1)

Keywords: Habitat-forming, taxonomic imperative, global taxonomy

Oral presentation

DETECTION OF *ULVA* SPP. AND RELATED SPECIES WITH BETTER RESOLUTION: A TUFA METABARCODING APPROACH FOR ULVOPHYCEAE

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Ulva-like green algae are notoriously difficult to distinguish because of their great morphological variability and/or similarity, and DNA barcoding approaches are currently indispensable for their identification. However, such approaches often fail if rare or inapparent species are to be detected in large mixed green algal stands. We therefore developed a detection method based on next generation DNA sequencing, suitable for analysis of DNA traces in conserved water samples. A primer pair was developed that allows for amplification of a 475 bp long section within the *tufA* marker gene. The primers are relatively group specific, as 79.6 % of all reads obtained after quality filtering represented Ulvophyceae. The relatively short target amplicon still allows for good differentiation of Ulvales and Ulothrichales at the species level. Using a database containing tufA sequences of 879 species – thereof 281 Ulvophyceae – we detected predominantly species that were previously observed in our study area in Northern Germany. However, the number of species detected in single sites was generally higher than in earlier barcoding studies, which may be due to drifting genetic traces: Samples collected offshore appeared influenced by Ulvophyceae present within a radius of up to about 1 km in winter and less than 100 m in summer. Nonetheless, this new approach can be used to detect rare species: In one site an undescribed Blidingia species not yet known from our study area was repeatedly detected. Based on these findings the species was discovered and its identity was confirmed by traditional *tufA* barcoding.

Keywords: Ulva, metabarcoding, *tufA*

Oral presentation

CRYPTIC SPECIES COMPLEXES IN THE MARINE DIATOM *PSEUDO-NITZSCHIA* EXPLORED BY METABARCODING

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Pseudo-nitzschia H. Peragallo is a cosmopolitan marine diatom genus that encompasses more than 50 species, many of which producing the toxin domoic acid. Because of several cryptic and pseudocryptic species-complexes, species identification is tricky while inter- and intra-specific phylogenetic relationships are intriguing. To explore the genetic structure of the genus, we analysed meta-barcoding data of the 18S-V4 region from 48 environmental DNA samples collected along three years at the LTER Station MareChiara (LTERMC) in the Gulf of Naples (Mediterranean Sea). Reference *Pseudo-nitzschia* sequences were used as queries in blast analysis, phylogenetic building, SWARM clustering and amplicon sequence variants (ASV) to assign metabarcode haplotypes to species. The V4 barcode showed a good resolution power in most cases. Within individual taxa, many low frequency haplotypes were retrieved along with a single abundant one, which was easily assigned to known species. While SWARMS and ASV detected comparable genetic structures among and within taxa, OTUs and phylogenetic methods were not always successful. Signs of incomplete lineage sorting and/or introgression between species were observed within the "*P. galaxiae*" and "*P. delicatissima*" species-complexes. Almost all taxa showed a regular seasonal pattern among years, with cryptic species occurring in distinct periods and suggesting ecophysiological differences among sister taxa. Overall, V4 metabarcoding coupled with adequate analytical approaches proved to be valuable to address intraspecific variability, while intricate phylogenetic relationships and enhanced ecological diversity point at fast evolutionary processes that are probably at the basis of the success of *Pseudo-nitzschia* in coastal areas of the world's seas.

Keywords: *Pseudo-nitzschia*, meta-barcoding, seasonality

Oral presentation

PHAEOSACCIOPHYCEAE, A NEW ALGAL CLASS RELATED TO THE PHAEOPHYCEAE AND XANTHOPHYCEAE

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The ancestors of the multicellular brown seaweeds and the sexually reproducing xanthophytes remains a mystery even though the PX clade is well established. The Phaeothamniophyceae, Aurearenophyceae and Chrysoparadoxophyceae are small classes within the PX clade. Using a five gene phylogeny (SSU rRNA, *atpB, psaA, psaB, rbcL*), we discovered a new class, the Phaeosacciophyceae, consisting of macroscopic marine algae and microscopic freshwater algae that are the closest known relatives of the Phaeophyceae and Xanthophyceae. We examined the marine *Phaeosaccion collinsii* collected from the type locality and type material for the freshwater *Tetrasporopsis fuscescens* collected in 1846. The class also *includes Antarctosaccion applanatum, Phaeosaccion stellifera, P. okellyi, Psammochrysis cassiotisii*, and *Tetrasporopsis moei*. Morphologically, the marine taxa form macroscopic thalli up to 20 cm in size and the freshwater taxa form small colonies barely visible to the naked eye. We also studied the marine *Nematochrysis sessilis var. vectensisfrom* from its type locality but it belongs to the Chrysoparadoxophyceae. The taxonomic positions of *Chrysomeris ramosa* (Chrysomerophyceae) and the invalid "*Giraudyopsis*" are involved. Chrysomeris ramosa was described by Nellie Carter as a uniflagellate alga whereas members of the SI clade, including the PX clade, have two obvious flagella. Culture strains identified as "*Giraudyopsis*" are closely related to *Phaeosaccion collinsii* and are described as new *Phaeosaccion* species.

Keywords: *Chrysomeris, Phaeosaccion, Tetrasporopsis*

Oral presentation

DISCOVERIES OF NEW PEYSSONNELIOID ALGAE SPECIES FROM HAWAII'S MESOPHOTIC CORAL ECOSYSTEMS

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

Financing: U.S. National Science Foundation (DEB-1754117), U.S. National Fish & Wildlife Foundation (0810.18.059023), and National Oceanic and Atmospheric Administration

Keywords: Hawaii, mesophotic, red algae

Oral presentation

HAPALOSPONGIDION HOLLENBERGII (RALFSIALES, PHAEOPHYCEAE), A NEW SPECIES OF CRUSTOSE

BROWN ALGAE FROM THE MEXICAN TROPICAL PACIFIC

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The genus *Hapalospongidion* De A. Saunders (Ralfsiales) has been little studied worldwide, despite their wide distribution in tropical and subtropical areas on the American Pacific coast. Species are characterized by having mucilaginous crusts, presenting free filaments, subterminal plurilocular, and terminal unilocular reproductive structures. The morphological similarity at the macroscopic level and simple anatomy of *Hapalospongidion* complicates differentiating between species, as they are defined by a few characters. Reproductive structures are essential for recognizing species, but these features are rarely observed. The use of molecular tools in combination with morphological data has confirmed that *H. gelatinosum*, a type species of the genus, is found throughout the Mexican Tropical Pacific and is part of the recent family Hapalospongidiaceae, which is genetically distant from the Mesosporaceae family, but with whose species it shares a great morphological similarity. In this work, a new species is described: *Hapalospongidion hollenbergii* sp. nov., from morphological characters and sequences of the *rbcL* and *Cox1* genes of specimens from four locations in the Mexican tropical Pacific. The phylogenetic analysis shows a new clade within the genus, different and distant from *H. gelatinosum*, which also have different morphological characters that distinguish it from the seven currently accepted species, and of which only two have been registered in the region: *H. gelatinosum* and *H. pangoense* (Setchell) Hollenberg. This study contributes to the clarification of the phylogenetic relationships within the order Ralfsiales and at the same time envisions a diversity of species that have been underestimated until now.

Financing: Financial support was partially provided by DGAPA, UNAM, PAPIIT IN214115 project

Keywords: Hapalospongidiaceae, Mexican Tropical Pacific, Ralfsiales

Oral presentation

RED ALGAL DIVERSITY (RHODOPHYTA) FROM PERU BASED ON MOLECULAR ANALYSIS

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In Peru, an ongoing project is to document the macroalgal biodiversity because the Peruvian marine flora has been mostly characterized on the basis of morphological observations. We herein report on red algae collected along the coast of Peru including at historical collections sites in order to provide a better understanding of Peruvian red algal diversity. Analyzing *rbcL* sequences, for the first time we report the occurrence of *Nothogenia chilensis, Porphyra mumfordii*, and *Schizymenia dubyi* from Peru. The *rbcL* sequences of seven taxa did not match previously published sequences in GenBank; *Acrosorium* sp., *Neoharaldiophyllum* sp., *Hypnea* sp., *Chondrus canaliculatus, Pyropia* sp.1, *Pyropia* sp. 2. Analysis of topotype materials proposes that Chondracanthus glomeratus (M.Howe) Guiry is conspecific with *C. chamissoi* (C.Agardh) Kützing. Both *Rhodymenia howeana* E.Y.Dawson and *R. multidigitata* E.Y. Dawson, Acleto & Foldvik are proposed to be later taxonomic synonyms of *R. corallina* (Bory) Greville. Further studies are needed to reveal more diversity of red algae from Peru.

Financing: MSC by Fondecyt 3180539 and SMB by Korean Government's Ministry of Oceans and Fisheries.

Keywords: DNA-barcoding, Pacific South America, Peru

Oral presentation

THE CHLOROPLAST GENOME OF *CHONDRIA TUMULOSA*, A NEW RED ALGA OF UNKNOWN ORIGIN INFESTING THE PAPAHĀNAUMOKUĀKEA MARINE NATIONAL MONUMENT, HAWAII

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A mysterious red alga was first observed in 2016 by National Oceanographic and Atmospheric Administration (NOAA) researchers at Pearl and Hermes Atoll forming considerable mat-like growth and distinct entangled thalli. In 2019, a survey in August reported a massive spread of the same species, reaching 19 meters depth, comprising eastern, western and northern sides of Pearl and Hermes Atoll. The alga was recently identified as belonging to *Chondria*, a rhodomelacean genus within the red algal order Ceramiales. Herein, we present the newly sequenced plastid genome of *C. tumulosa*. The NGS data analysis resulted in the assembly of the complete chloroplast genome, as a circular molecule of 172,617 bp and containing 231 genes, including 197 protein-coding genes, 29 tRNAs, 3 rRNAs, 1 tmRNA, and 1 ncRNA. The overall GC content of the plastid genome is

27.4%, which is slightly lower than average for the Rhodomelaceae, Ceramiales. A phylogenomic analysis with previously published plastid genomes of members of the Rhodomelaceae showed *C. tumulosa* positioned as an early divergent branch with 3 other *Chondria* spp., forming a sister clade with species from the Laurencieae with full support values. Although *C. tumulosa* cannot be considered an invasive species given that it has not been confirmed as introduced to Pearl and Hermes Atoll, its complete plastid genome will be helpful in efforts to understand this species that is threatening the Hawaiian archipelago, and possibly other unexplored parts of the Pacific.

Financing: U.S. National Science Foundation, U.S. National Fish & Wildlife Foundation, National Oceanic and Atmospheric Administration (NOAA) Papahānaumokuākea Marine National Monument.

Keywords: *Chondria tumulosa*, Papahānaumokuākea Marine National Monument, plastid genome

Oral presentation

CORALLINA OFFICINALIS VAR. CHILENSIS (CORALLINACEAE, RHODOPHYTA) IS NOT A VARIETY, BUT A CONGENERIC SPECIES WITHIN A PUZZLING GENUS

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Geniculate coralline algae are notoriously challenging to identify in the field due to confusing morphological variation. Consequently, former species delimitations based exclusively on morphology are often unsupported by sequence-based phylogenies. The purpose of this research was to determine whether *Corallina chilensis* Decaisne, basonym of *C. officinalis var. chilensis*, was a distinct species or should be considered a variety of *C. officinalis*; and consequently whether *C. chilensis* was distributed in two hemispheres. In order to answer these questions, *psbA*, CO1, and *rbcL* genes were sequenced from 76 voucher specimens representing *Corallina* collections from ~2000 to 2019. Names were applied by comparing these sequences with published sequences and type specimen sequences, including an *rbcL* sequence from the specimen collected by Darwin (#2151 from Valparaiso, Chile), the holotype specimen for *C. chilensis* designated by Harvey. DNA from the Chilean *C. chilensis* holotype matched an unnamed coralline species commonly found in the Northeast Pacific, and C. chilensis specimens formed a separate clade from *C. officinalis* specimens in phylogenetic analyses. *Corallina chilensis* is a distinct species, not a variety of *C. officinalis*, and it is present in both hemispheres. Going forward, the name *C. officinalis var. chilensis should* be discontinued, and the older name *C. chilensis* should be used in its place. Incidentally, our results also revealed rampant incongruence across all three individual phylogenetic gene trees, including between the two plastid genes (*psbA* and *rbcL*) presumably on the same chromosome.

Keywords: coralline algae, systematics, *Corallina*

Oral presentation

THE GENOME AS A TAXONOMIC MARKER: INSIGHTS GAINED FROM DINOFLAGELLATES OF THE FAMILY SYMBIODINIACEAE AND GENUS *SYMBIODINIUM*

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Modern algal taxonomy generally relies on the use of single marker genes (e.g. rDNA and *rbcL*) or sets of concatenated genes from nuclear or organellar genomes. Yet classification systems over time have evolved to utilise more, not fewer, data. A classic example, combining morphological and molecular data, is the recent systematic revision of the dinoflagellates commonly found as coral symbionts from a genus to the family Symbiodiniaceae, comprising 15+ clades with nine named genera. Our recent work comparing whole-genome sequences uncovered extensive divergence among 13 Symbiodiniaceae genomes, and revealed that the genus *Symbiodinium* could be further divided into new genera or subgenera. These results underscore the rapid evolution of these dinoflagellates that comprise a massive genomic diversity hidden behind subtle morphological differences. It is clear that genome data are needed to gain a more-comprehensive view of taxonomic relationships within the Symbiodiniaceae family. However, the question remains as to how we can best use these data and associated features (e.g. gene duplication, repeats, and conserved dark genes) to guide taxonomic classification of Symbiodiniacean taxa. Here we explore the fundamental question posed by the era of "sequence everything": are genomes good taxonomic markers, and if so, how do we interpret genome-wide changes to capture phylogenetic diversity of microbial eukaryotes? Genome data provide a comprehensive view of genetic inheritance at the molecular level, but we need to soon decide how this genomic information could be used to inform taxonomy as the data continue to accumulate.

Financing: Australian Research Council Discovery Projects DP150101875 and DP190102474

Keywords: Genomes, taxonomy, dinoflagellates

Oral presentation

A NEW CLASSIFICATION SYSTEM OF THE CYANIDIOPHYCEAE (RHODOPHYTA) BASED ON ORGANELLE GENOME DATA

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Cyanidiophyceae is a class of unicellular red algae that thrives in acidic (pH 0.5-3.0), high temperature and heavy-metal reich extreme environments in volcanic region around world. These unicellular red algae are primarily photo-autotrophic but some of these species (i.e. *Galdieria*) have mixotrophic growth. Previous classifications of Cyanidiophyceae class that were based on morphological, physio-ecological misidentification had conflicts. The problem also occurred in recent molecular phylogenetic analysis. To better and wider understand its evolutionary history and clarify relationship within the Cyanidiophyceae class, five complete mitochondria and eight plastid genomes (*Cyanidiococcus yangmingshanensis* ACUF 8.1.23, *Cyanidium caldarium* ACUF 063, Mesophilic *Cyanidium* Italy and Taiwan, *Galdieria sulphuraria* SAG 108.79, *Galdieria sulphuraria* DBV 011, *Galdieria phlegrea* ACUF 629 and Cyanidium sp. OTU2) were constructed in this study. We compared them in terms of genome characteristic (i.e. CDS, GC contents, skewness and repeat frequency), gene synteny, different gene transfer pattern and genome rearrangement events among Cyanidiophyceae organelle genomes. Also, we secure robust phylogeny by using their organelle gene data. As a result, we found and propose several generic and genomic evidences of major separation between the Galdieriales order and each three families of Cyanidiales order (Cyanidiaceae, Cavernicoliaceae and Cyanidioschyzonaceae). Based on these organelle genome data, we solve phylogenetic incongruence between species tree and gene tree and propose new classification system of Cyanidiophyceae.

Financing: National Research Foundation of Korea (NRF-2017R1A2B3001923)

Keywords: Classification, organelle genomes, Cyanidiophyceae

Oral presentation

UNVEILING THE *PSEUDO-NITZSCHIA* BIODIVERSITY IN THE NORTHWESTERN ADRIATIC SEA

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Several species belonging to the genus *Pseudo-nitzschia* are common representatives of the northern Adriatic diatom communities occurring throughout the year often causing intense blooms (abundances up to 106 cells/l). As some species are potentially harmful due to the production of the neurotoxin Domoic Acid (DA), their identification at the species level is crucial, although hampered due to the presence of several cryptic and pseudocryptic species. The aim of this study is to unveil the diversity of the *Pseudo-nitzschia* species in the coastal station of the LTER Senigallia-Susak transect (NW Adriatic Sea), through an integrative approach, combining morphological analysis and molecular methods over a 2-year study period, and to describe the mean annual cycle of species or groups in a 30-year (1988-2019) long time series. Phytoplankton and environmental parameters have been sampled with monthly frequency. Light microscopy analysis allowed to identify six morphotypes and to reveal their mean annual cycle: *P. fraudulenta* and *P. pungens* (occurring in winter). *P. delicatissima* and *P. pseudodelicatissima* complexes (both mainly in spring-summer), *P. multistriata* and *P. cf. galaxiae* (mainly in autumn). In 2018-2019, net samples were collected at the surface to set up monoclonal cultures for molecular, ultrastructural and toxin analyses. Molecular (LSU and ITS1-ITS2 markers) and transmission electron microscopy analyses confirmed the presence of *P. pungens, P. fraudulenta, P. delicatissima, P. calliantha* and *P. mannii*. Furthermore, a new cryptic species *Pseudo-nitzschia* cf. *arenysensis* within the *Pseudo-nitzschia delicatissima* complex was recorded. DA was never detected in detectable amount.

Financing: This research was partially funded by the Italian Ministry of Health (Ricerca Finalizzata 2016), grant number GR-2016-02363211

Keywords: LTER long-term ecological research, integrative taxonomy, domoic acid

Oral presentation

MORPHOLOGICAL VARIABILITY AND MOLECULAR TAXONOMY OF THE *CYSTOSEIRA* S.L. TAXA IN THE BLACK SEA

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Brown algae of the genus *Cystoseira sensu lato* form the most diverse and productive marine ecosystems throughout the Mediterranean Sea, and have equal roles also in the Black

Sea where they have been decreasing in recent years. The taxonomy of *Cystoseira s.l.* taxa from the Black Sea is still not well understood, and questions arise when close taxa have to be delimited. In addition to morphological descriptions, we provide molecular data of the Black Sea *Cystoseira s.l.* distinct morphologies as an additional tool to clarify their identities and phylogenetic affinities. The analysis of two mitochondrial markers (cytochrome oxidase subunit 1 — COI, and 23S-tRNAVal intergenic spacer — mt-spacer) showed that *Cystoseira s.l.* specimens from the Black Sea belong to two recently resurrected genera, namely, *Ericaria* and *Gongolaria*. Molecular data confirm the morphological identification of *Gongolaria barbata*, which is characterized by high morphological plasticity in the Black Sea. Our morphological data support the transition of *G. barbata* to the genus *Gongolaria*, which was previously proposed based only on the genetic data. For the Black Sea endemic taxon *Cystoseira bosphorica*, sequence divergence suggests conspecificity with Mediterranean Sea species *Ericaria crinita* and *Ericaria barbatula*. However, considering original morphological characteristics of the taxon, its geographical isolation, and endemism, the new combination *Ericaria crinita f. bosphorica* (Sauvageau) S.S. Sadogurska, J. Neiva et A. Israel was proposed. Degradation of *Cystoseira s.l.* communities and the reduction of their density in the Black Sea stress the need for their protection and restoration, in particular for rare and endemic taxa, such as *E. crinita f. bosphorica.*

Keywords: *Cystoseira*, taxonomy, Black Sea

Oral presentation

BLADE-FORMING *ULVA* SPECIES IN THE GALÁPAGOS ARCHIPELAGO ASSESSED BY DNA SEQUENCING

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During February and July 2019, specimens of blade-forming Ulva species were collected from four islands in the Galápagos Archipelago, Fernandina, Isabela, Floreana and San Cristobal. Three DNA loci were sequenced, plastid encoded *rbc*L and *tufA*, and nuclear encoded ITS1. Based on BLAST analyses, three species were found, *Ulva lactuca, U. ohnoi* and what appears to be an undescribed species. Type material of *U. lactuca* and *U. ohnoi* has been sequenced; those names can be applied with confidence in the archipelago. The undescribed species was collected most commonly and was also the most widespread, occurring on all four islands. *Ulva lactuca* and *U. ohnoi* were only found on the more easterly islands, Floreana and San Cristobal. Both the green sea turtle, *Chelonia mydas*, and the endemic marine iguana, *Amblyrhynchus cristatus*, were observed to feed on the widespread and apparently undescribed species of *Ulva.*

Financing: University of North Carolina, Chapel Hill Ideas Grant and Galápagos Seed Grant

Keywords: DNA sequencing, Galápagos Archipelago, *Ulva* species

Oral presentation

PHYCOLOGICAL COLLECTIONS IN THE DIGITAL AGE

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Phycological collections provide a permanent record of global algal diversity, and contain unique reference material that documents the evolutionary history of algae. Collected over centuries of field exploration, collection specimens are historical records, providing a biodiversity baseline that enables us to track geographic and temporal changes in algal species and communities, and to correlate those patterns with changes in the environment. Collection specimens also serve as vouchers for research activities, ranging from taxonomic studies to monitoring and genome projects. Although knowledge derived from specimens has made important contributions to phycological research, collections are significantly underused due to the difficulty of obtaining data within and across collections. Thousands of herbariums specimens, microscope slides, and other types of collections are housed in hundreds of institutions worldwide, with data stored in many separate databases. Some of these phycological collections are well-known and their data readily accessible, while the content of many other collections remains largely obscure. Digitisation and mobilisation of specimen and associated data removes this obstacle of untraceability. Technical advances with imaging systems have significantly increased the rate of digitization, now making it feasible to digitize large collections in a reasonable time. The new European initiative DiSSCo (Distributed System of Scientific Collections) offers new perspectives for the digitization of phycological collections. DiSSCo works for the digital unification of all European natural history assets, and aims to ensure that all collection data is easily findable and accessible. As such, DiSSCo will transform a fragmented landscape of collections into an integrated knowledge base.

Keywords: collections, digitization, DiSSCo

Oral presentation

ARE SINGLE-LOCUS SPECIES AUTOMATED DELIMITATION MODELS (ABGD; PTP) USEFUL TO IDENTIFY BACILLARIOPHYCEAE SPECIES?

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Multiple automated single-locus computational models have emerged to assist molecular taxonomy. The Automatic Barcode Gap Discovery for primary species delimitation (ABGD) distinguishes species using pairwise genetic divergence, while the Poisson Tree Processes (PTP) is a coalescent model, that delimit species through identification of the points at which alleles and lineages diverged. A few studies have applied these models to species of microalgae, including dinoflagellates, rhodophytes, trebouxiophytes, bacillariophytes and chlorophytes. However, questions remain about the efficiency and accuracy of these models. We applied both models to *rbc*L (540 - ~1000 bp), 5.8S + ITS2 (334 - 362 bp) and ITS1 + 5.8S + ITS2 (420 - 880 bp) molecular markers for species of several pennate diatom groups and compared the results to species delimitations based on published sexual reproductive isolation data. The ABGD and PTP both delimited species of *Eunotia, Seminavis* and *Pseudo-nitzschia* corresponding to sexual isolation. Both methods also seemed robust to marker length (~300 bp to 1000 bp). Species overestimation for *Tabularia fasciculata* sequences occurred with both methods, possibly due to diversification rate differences between araphid (*Tabularia*) and raphid genera (*Eunotia, Seminavis, Pseudo-nitzschia*). Additionally, the PTP requirement for sequence data of closely-related taxa outside of the target clade is problematic, as there are still many missing data across the diatom phylogeny.
Financing: This work was supported by Brazilian funding agencies National (CNPq Proc. 203883/2017-9; CAPES; BR LTER PELD FAPERGS-CNPQ Proc. 403805/2012-0)

Keywords: Microalgal species, coalescent methods, molecular systematics

Oral presentation

A PERSPECTIVE ON THE EVOLUTION OF SEX IN *VAUCHERIA*

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Vaucheria (Xanthophyceae) are coenocytic filamentous algae which inhabit various aquatic habitats such as freshwater streams, lakes, and salt marshes. Most of the species in the class Xanthophyceae are predominantly asexual but *Vaucheria* is the only genus which performs oogamous sexual reproduction in the class. Species delimitation of *Vaucheria* has been conducted with morphological shapes of their sexual organs and former molecular analyses justified the classification of *Vaucheri*a according to the organ morphology. However, the exact phylogenetic relationships between various clades of *Vaucheria* remained to be discovered. In this study, we collected *Vaucheria* spp. from 40 sites in Korea and U.S. and did a phylogenetic analysis using multiple genes. The analysis revealed that *Vaucheria* shows serial changes in their breeding systems, from hermaphroditism, monoecy, to dioecy. In addition, there are apparent reversions of the sexual organ arrangement to earlier forms (e.g. dioecy to monoecy) in three phylogenetically independent lineages within *Vaucheria* genus. This study suggests that *Vaucheria* can be a promising model for studying evolutionary transitions between various sexual systems.
Financing: Samsung Science & Technology Foundation

Keywords: *Vaucheria*, evolution of sex

Oral presentation

UNRAVELLING MARINE MACROALGAE FROM THE PACIFIC COAST OF CENTRAL AMERICA

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In the last 10 years, a great effort has been made to clarify the taxonomy and diversity of species of marine macroalgae in the Pacific of Central America. This region has shown to have a more diverse marine flora than what it was described by the first researchers who made reports between the 50s and 60s. Recent studies have shown that the Tropical Pacific has a flora of indigenous species and there are still many new species to report and to describe in this area. The aims of this work are to elucidate the diversity of algae in this region and to update the taxonomy using molecular methods and morphology. For this, intensive collection efforts have been made in more than 200 sites on the Pacific coast of this region and at several depths up to 60 m. In total, more than 2000 specimens have been collected (intertidal and subtidal): 54% of reds, (Rhodophyta) 24% of greens (Chlorophyta), 22% of browns (Phaeophyceae). We carry out DNA sequence analyzes of several genes (nuclear, mitochondrial and chloroplast) and morphological evaluations. Many records in the literature were found to be synonymous with other species, in total more than 150 new records and approximately 28 new species have been identified. The species accumulation curve analyzed showed us that there is still much to discover, especially in the flora that forms algae mats (turfs), and it was found that there are very particular species in deep areas (more than 30 m) that must be analyzed.
Financing: CIMAR-Vicerrectoría de Investigación-Universidad de Costa Rica, Universidad de El Salvador, Universidad Autónoma de Honduras, DAAD-Alemania, Smithsonian Institute, CONACYT-México

Keywords: Taxonomy, diversity, Eastern Tropical Pacific

Oral presentation

DNA BARCODING OF ATLANTIC *CYSTOSEIRA SENSU LATO* SUPPORTS TAXONOMIC RE-ARRANGEMENTS AND REVEALS NOVEL BIOGEOGRAPHIC INSIGHTS

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NE Atlantic endemic *Cystoseira* s.l. marine forests are extremely diverse when compared to other foundation seaweeds, such as Fucus and Laminaria, but their systematics and biogeography remain far less well understood. *Cystoseira* are easy to recognize but challenging to identify due to high morphological plasticity and convergence, plus many regional floras remain insufficiently investigated. Consequently, species boundaries and geographical ranges remain imprecise for many taxa. Molecular approaches are less confounded by intra-specific plasticity and taxonomic expertise and can help overcome persisting taxonomic difficulties. Recent studies demonstrated the polyphyly of *Cystoseira* (presently divided into *Treptacantha, Carpodesmia* and *Cystoseira* s. s.) but at species level have been limited by low marker resolution and narrow taxonomic/geographic scope. We sequenced a diverse collection of *Cystoseira* s.l. for a standard barcode marker to delimit (and tentatively map) major genetic entities, their appropriate genus, and identify major conflicts with current (largely) morphology-based taxonomic and biogeographical literature. Barcode/phylogeographic data recovered at least 27 operational taxonomic units (OTUs, as proxies for species) and pinpointed multiple instances of overlooked cryptic diversity and over-splitting, but more frequently mis-identification/classification, with interesting taxonomic, biogeographical and evolutionary implications. Several species were re-instated or redefined, with endemism apparent in many regions. Inter-specific divergence was very variable and particularly low in some *Treptacantha* complexes, but in general a barcode gap was observed. Intra-specific diversity within some *Carpodesmia* and *Cystoseira* s.s. revealed substantial phylogeographic signal. Representative samples of each OTU were sequenced for additional markers to investigate with greater resolution diversification within each genus.

Financing: Portuguese FCT through projects MARFOR Biodiversa/0004/2015, UID/Multi/04326/2020 and DL 57/2016/CP1361/CT0010. H2020 (EU) grant agreement No 730984, Assemble Plus.

Keywords: *Cystoseira*, barcoding

E-Poster

DNA BARCODING OF CERAMIALES (RHODOPHYTA) AROUND THE MALTESE ISLANDS REVEALS HIDDEN BIODIVERSITY IN THE CENTRAL MEDITERRANEAN

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The genetic biodiversity of Mediterranean macroalgae is generally understudied, a fact which is especially important in the case of morphologically cryptic taxa. As a result, it is often challenging to compare DNA barcodes from Mediterranean samples to references in online databases since, very often, no close hits are available. At a regional scale, of around 1124 records of algae in the Mediterranean Sea, only 114 species have been barcoded. This makes it difficult to discuss the biogeography of algae from the central Mediterranean, especially in the case of morphologically cryptic species. Malta's macroalgal species checklist, based on morphological data spanning the last 23 years, contains 339 species, of which 204 belong to the Rhodophyta: 194 Florideophyceae, 4 Bangiophyceae, 3 Compsopogonophyceae and 3 Stylonematophyceae. Our study aims to barcode red algae from 5 sites in the North of the Maltese islands. Different samples were taken, both from the substratum and also of mature algal specimens. Substratum samples were processed via the germling emergence method, with subsequent culturing *in vitro*. Segments of the thallus of mature red algae were dried to be preserved in an herbarium that was documented photographically. DNA extraction and barcoding of both types of sample via COI biomarkers confirmed the presence of *Laurencia* and *Palisada* spp. The study aims to contribute to macroalgal genetic data from the central Mediterranean and provides new records of Ceramiales (Florideophyceae) for this region. *Palisada tenerrima* is recorded from the Maltese islands for the first time.

Keywords: Algae, Rhodophyta, Florideophyceae

E-Poster

WHERE INDIGENOUS KNOWLEDGE AND TAXONOMY MEET: DISCOVERING, DOCUMENTING AND NAMING RIMURIMU/SEAWEEDS IN NEW ZEALAND

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Ngāti Kuri are descended from the original inhabitants of the northernmost peninsula of Aotearoa/New Zealand. The tribal lands of Ngāti Kuri hold high biodiversity and endemism, in particular the islands of Manawatāwhi/Three Kings Islands and Rangitāhua/Kermadec Islands. As kaitiaki (guardians/stewards), Ngāti Kuri seek to understand and protect the biota dwelling on land and waters around these islands, regarding the biota as taonga (treasures) and tūpuna

(ancestors). Recognising the national and international significance of the unique diversity and assemblages of these offshore islands, Ngāti Kuri prioritise science partnerships in the documentation of species and Ngāti Kuri knowledge. In doing so, their capacity to engage and contribute to the processes of knowledge making is transformed. A collaboration began in 2017 to develop protocols for naming rimurimu (seaweed) species endemic to Ngāti Kuri lands and waters. From this collaboration grew a partnership that mobilises and articulates Ngāti Kuri autonomy: locally, nationally, and globally. The partnership has enabled a two-way exchange of knowledge, language, values, principles and science between taxonomists and Indigenous peoples. This process is transforming the formal authority in the description of species. While tribal authorship was not, perhaps, envisaged in the development of the Code of Nomenclature, there is no restriction written into the code that excludes group authorship. Ngāti Kuri as science leaders and with science allies name seaweed through high-trust and ethical partnerships. This poster examines the processes of co-authorship to better understand the collaborative processes and challenges of naming our worlds.

Financing: Tāmaki Paenga Hira Auckland Museum; School of Biological Sciences, University of Auckland; Strategic Science Investment Fund, NIWA

Keywords: Transformation, indigenisation, partnership

E-Poster

EPIPHYTIC DIATOMS ON THE RED ALGA *LAURENCIA SAITOI* FROM KOMINATO, CHIBA PREFECTURE, JAPAN

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Not enough studies have been carried out on the diversity of marine benthic diatoms in Japan. The epiphytic diatom flora on the red alga *Laurencia saitoi* was examined to understand the diatom species living on the seaweed. The sample was collected in Kominato, Chiba Prefecture, Japan on 19 June 2019. 23 taxa in 16 genera were observed using light microscopy (LM) and scanning electron microscopy (SEM). The epiphytic diatom flora mostly consisted of common species in temperate habitats and cosmopolitans. Among them, we especially found several significant taxa: *Cocconeis californica, Druehlago cuneata, Nagumoea africana* and *Falcula* sp. Abundantly growing in cold regions, *C. californica* slightly occurred in the temperate coast, Kominato. The occurrence of *C. californica* indicates that the species can grow in warm environments or the epiphytic diatom flora in this site is marginally influenced by cold water. We newly discovered *D. cuneata* from Japan, which is also the first report after the original description. *N. africana* was dominant (15.3% out of all diatom cells) in the present study. *N. africana*, morphologically resembling *N. neritica* in LM which has been commonly reported from Japan, was distinguishable by the number of areolae per stria on valve and the presence/absence of silica ridges connecting fibulae with SEM. These results show that the SEM observation is required for the identification and classification of *Nagumoea* species. *Falcula* sp. is possibly a new species because of the smaller cells and rectangular girdle.

Keywords: Diatom flora, marine diatom, morphology

E-Poster

TAXONOMY, NOMENCLATURE AND MOLECULAR SYSTEMATICS: IMPLICATIONS ON NON-NATIVE SEAWEEDS FROM PACIFIC MEXICO

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Non-native organisms have been proposed for Mexico, among them marine algae. Pacific Mexico has 30 species recorded among this kind of taxa. Most of them are the result of floristic studies and morphological traits have been the foundation for these proposals. Extensive review including all historic records since 1930 showed three different kinds of problems in interpreting these assumptions: a) changes in nomenclature, b) misapplied names due to lack of experience by some researchers, c) insufficient molecular evidence. Conclusions from this study revealed that seven species are along the Pacific coast, 17 are exclusive of one geographical area (12 Pacific Baja, 4, Gulf of California, 1 Tropical Pacific Mexico) and the rest five are common to Pacific Baja and the Gulf of California. Of the 30 species, only 14 species have strong molecular evidence to be considered alien species. Besides, using two chloroplast markers, one of these records should be eliminated and another taxon considered a Mexican subspecies could be a possible new invader. These cases are *Codium fragile* (Suringar) Hariot and *Codium latum* subsp. *palmeri* (Dawson) Silva. Genetic and molecular studies are necessary to confirm the nature of the other considered also alien species. A rigorous taxonomic treatment should be applied during the florist studies and careful training in new phycologists is strongly recommended.

Financing: Universidad Autónoma Metropolitana - LermaUC-MEXUS Programa Universidad Autónoma de Baja California

Keywords: Non native, marine, algae

E-Poster

SUBTIDAL SEAWEED DIVERSITY AND DISTRIBUTION IN HONG KONG

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A territory-wide comprehensive study on the distribution and diversity of subtidal seaweeds in Hong Kong was conducted between 2018 and 2019. Twenty sites across Hong Kong waters were selected based on previous records of seaweed diversity in the literature, including marine parks and marine reserve. The modified belt transect method was used in each site with six 10 m transects laid parallel to the shore in two depth zones (Shallow: 0m to -3m; Deep:-3m to -6m). Seven to 15 photos of 0.25 m x 0.25 m quadrats randomly placed on each transect were taken. A total of 442 transect data of two depth zones in 20 sites from four seasons were analyzed. The total number of recognizable seaweed species recorded is 86, covering 24, 40 and 22 species of brown, red and green algae respectively. Among these species, 10 are new geographical records for Hong Kong. Significant differences in seaweed community structures were observed in different water depths, water regions and seasons. Extensive *Sargassum* bed in Tung Ping Chau Marine Park and *Ulva* bed in Cape D'Aguilar Marine Reserve exhibit high ecological values in supporting many marine organisms. This is the most extensive study on seaweed diversity and distribution to have been carried out in Hong Kong.

Financing: Agriculture, Fisheries and Conservation Department, Hong Kong, China

Keywords: Subtidal seaweed, diversity, distribution

E-Poster

UNDESCRIBED SPECIES OF *NODOSILINEA* (CYANOBACTERIA) ISOLATED FROM TERRESTRIAL HABITAT IN RYUKYUS CAMPUS AREA, OKINAWA

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Terrestrial cyanobacteria undoubtedly have important ecological roles in carbon, oxygen and nitrogen cycles. Despite their importance, the taxonomy of cyanobacteria is far from complete, reflection on diversity studies. We are intensively studying terrestrial cyanobacteria especially black stains growing on the surface of urban structures in Okinawa, Japan. In the previous study, we reported very high diversity of the isolates from even a small area like the campus of the University of the Ryukyus. In this study, we focus on the simple filamentous strains with narrow width. They were characterized by a polyphasic approach based on morphology and molecular phylogeny (16S rRNA and 16S-23S ITS region) as well as secondary structure analysis of ITS region. The strains were simple thin filaments, with slightly longer than wide or isodiametric cells, enclosed in thin sheaths. The filaments consistently formed nodules under nitrogen depleted medium. These morphological characters agreed well with the genus *Nodosilinea*. Based on molecular phylogenies of 16S rRNA and ITS regions, all strains were distributed in two genetic clusters, and the most closely related species were *N. signiensis* and *N. bijugata*, respectively. However, phylogenetic differences of 16S rRNA gene and ITS region, as well as secondary structures of ITS region are sufficient evidence to establish new species, well-separated from these most closely related known species. Hence, we conclude that these two genetic clusters are two undescribed species of the genus *Nodosilinea*. These findings may help to reveal further species diversity of the genus *Nodosilinea*.

Keywords: *Nodosilinea*, undescribed species, polyphasic approach

E-Poster

THE GENUS *SARGASSUM* IN THE CANARY ISLANDS: PRELIMINARY ASSESSMENT OF ITS DIVERSITY

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The genus *Sargassum* C.AGardh, with over 500 described species and around 350 of them accepted taxonomically, represents almost one sixth of the species in the class *Phaeophyceae*. Species are distributed worldwide, being an especially important component of tropical and subtropical regions where they play the role of habitat forming species. Identification can be specially challenging, as they show great morphological variability. Only in the north Atlantic Ocean more than 30 species are recognized. Recent molecular studies combined with extensive morphological assessments are clearing up the relationships and actual diversity of this genus. The aim of this study was to assess a preliminary diversity of Sargassum in the Canary Islands based on bibliographical compilation, morphological examination of herbaria material and extensive field collections to characterize the distribution and morphological variability of the different species, as a first step to clarify the actual diversity of this

genus using molecular techniques. From the species considered accepted for the region, only 6 have been confirmed with recent field collections and from the examined herbaria material, and 1 species has been found for the first time in the Canaries. Also, new morphotypes have been found that are not consistent with any species described for this region, and further studies will allow us to assess it identification.

Financing: D. Álvarez Canali is funded by the Canarian Agency for Research, Innovation and Information Society, Gobierno de Canarias (TESIS2020010084)

Keywords: *Sargassum*, diversity, Canary Islands

E-Poster

MONITORING OF PHYTOPLANKTON IN A SUBTROPICAL ESTUARINE SYSTEM THROUGH TRADITIONAL TAXONOMIC, FUNCTIONAL DIVERSITY AND MICROSCOPY-IMAGED-BASED CLASSIFICATION TOOLS

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Estuarine systems are under human activities pressure that may lead to changes in the structure of planktonic community. Given its importance as the basis of food webs and their rapid responses to environmental changes, phytoplankton is fundamental to understanding the effects of these changes on the general plankton community. The Santos Estuarine System (SES), Brazil, receives a high load of pollutants from petrochemical and fertilizer industries, as well as hosts one of the largest ports in Latin America. The present study aims to establish the bases for the implementation of long-term monitoring programs in this ecosystem combining classical monitoring methods (variation of chlorophyll biomass and taxonomic composition), with methodologies based on functional diversity (Convex hull) and on Microscopy-Imaged-based Classification Tools of plankton. Considering previous dataset from SES, computer vision techniques were employed to perform steps of object identification, filtering and feature extraction in order to obtain the final dataset. The developed software is open-source and available under the MIT license. From March 2020 (except in April and May due to COVID-19 pandemic), monthly surveys are being performed in four stations through the navigation channel of SES. Preliminary results showed dominance of filamentous cyanobacteria during raining/freshwater-influence periods and of diatoms under brackish and seawater-influence conditions. Salinity gradient was also a stressor condition resulting in changes in functional diversity index (FDis, FEve and FRic). Microscopy-Imaged-based Classification first results obtained a mean accuracy of 83.88% considering 4 classes, and 76.67% considering 13 classes.

Financing: Fundação de Apoio à Pesquisa do Estado de São Paulo (FAPESP), Process Nº 2018/25816-7

Keywords: Ecosystem monitoring, functional trades, phytoplankton image classification

E-Poster

FRESHWATER RED ALGAE (RHODOPHYTA) OF THE WORLD BOOK PROJECT HIGHLIGHTS THE DIVERSITY OF THESE TAXA

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The Rhodophyta are probably best known as charismatic marine seaweeds. Nevertheless, approximately 5% of the Rhodophyta can be considered non-marine taxa occurring in typical freshwater habitats such as lakes, bogs, rivers, streams and springs as well as hot springs, soils, and epizoic. Although most genera are confined to these habitats, approximately 20% have species reported from brackish or marine habitats as well as freshwater. The morphologies are diverse ranging from unicells, microscopic filaments, crusts, macroscopic filamentous branched thalli and tube-like thalli that can be pseudoparenchymatous. Three-quarters of the genera form growths that can be considered macroscopic as they can be seen with the naked eye, but most are diminutive (< 5 cm). These red algae are phylogenetically divergent occurring in all seven Rhodophyte classes and within those, 15 orders with a total of 49 genera. More than half (55%) of the genus level diversity is within the subclass Nemaliophycidae and is housed in four orders. Three orders are exclusively freshwater: Balbianiales, Batrachospermales and Thoreales. Two-thirds of the species diversity for all freshwater red algae is in the Batrachospermales. Within Batrachospermales, rectifying the paraphyly of *Batrachospermum* has been the recent focus and new genera have been proposed in the last few years to accommodate sections of the genus as well as clades of taxa that previously had no sectional designation. These 'Batrachospermum-like' new genera include *Acarposporophycos, Lympha, Montagnia, Nocturama, Paludicola, Sheathia, Torularia, Virescentia, Visia and Volatus*. These proposals raised the total number of genera in the order to 21.

Keywords: Phylogeny, Rhodophyta, biodiversity

E-Poster

EXPLORING THE DIVERSITY OF THE BROWN ALGAE (PHAEOPHYCEAE) FROM THE ATLANTIC COASTS OF MEXICO USING MOLECULAR-ASSISTED ALPHA TAXONOMY

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Molecular-assisted alpha taxonomy is a promising tool for species identification and exploration of diversity. Although this approach has increased during the last decade for the study of Phaeophyceae in Mexico, several taxa still lack molecular assessments. Here, we contribute to the understanding of the Phaeophyceae species occurring in the Atlantic Coasts of Mexico (ACM) analyzing DNA sequences of *psb*A, COI, and *cox*3. A total of 141 samples from 22 morphotaxa were collected. Other sequences previously reported from Mexico and similar sequences (through BLAST search) were downloaded from GenBank. Sequences were analyzed calculating p-distances and Bayesian Inference. Nearly 200 new sequences were obtained, many of them of taxa not found in GenBank. The analysis corroborated 22 species, which combined with other works, represent nearly half of the species reported for ACM. Besides, species recovered as polyphyletic and others that are likely to be new records or new species for Mexico were revealed. One of the main challenges for species identification and delimitation in Phaeophyceae is the lack of a universal marker as different genes are used at species level, even in closely related taxa. Another obstacle was the differential amplification success of these three genes in several taxa and more specific primers are required. However, this work will help to the construction of a sequence library that will be useful as a reference for the study of the brown algae in Mexico, as well as providing an overview of the group to detect taxonomic conflicts and gaps in knowledge.

Financing: UNAM PAPIIT IN225416; UNAM PAPIME PE-207819

Keywords: Barcodes, new records, Phaeophyceae

E-Poster

MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF A NEW *GELIDIUM* (GELIDIALES, RHODOPHYTA) SPECIES FROM THE MEXICAN TROPICAL PACIFIC: *GELIDIUM NAYARITENSE* SP. NOV.

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Gelidium pusillum is a species reported from the northern Gulf of California to the tropical region of the Mexican Pacific, but there is wide morphological variation among populations. The objective of this research is to evaluate this species using a morphological and molecular approach, with the molecular markers *rbc*L and COI-5P. This study examined eight samples from five sites in the Mexican tropical Pacific. Phylogenetic analyses resolved these specimens within a clade separated from the type of *G. pusillum*. The main differences with other species were size, branching pattern, branching order, distribution of internal rhizoidal filaments, and shape of the tetrasporangial sori. The sequence divergences between these two clades and the morphological differences support their representation of two separate species so proposed here that *Gelidium nayaritense* sp. nov. for tropical specimens of the Mexican Pacific.

Keywords: *Gelidiaceae*, molecular markers, phylogeny

E-Poster

MAZZAELLA CANALICULATA COMB. NOV. BASED ON *CHONDRUS CANALICULATUS* (C.AG.) GREVILLE (GIGARTINACEAE, RHODOPHYTA) FROM PERU AND CHILE

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Chondrus canaliculatus, endemic to Peru and Chile, currently represents the only *Chondrus* species from the southern hemisphere. Based on previous phylogenetic analyses, *C. canaliculatus* is polyphyletic with respect to *Chondrus* and possesses unique morpho-anatomical features that distinguish it from other genera in the Gigartinaceae. In this study, we expanded phylogenetic analyses using *rbc*L and COI sequences and morphological details were further examined to address the taxonomy and evolutionary systematics of *C. canaliculatus*. Genetic analyses placed *C. canaliculatus* within a well supported clade *Mazzaella membranacea, M. convoluta, M. laminarioides*, M. ‘*affinis*’ and *Mazzaella* sp. The species named *C. canaliculatus*, therefore belongs in *Mazzaella*, and *Mazzaella canaliculata* comb. nov. is proposed. *Mazzaella canaliculata* is distinguished from the other *Mazzaella* species from the southern hemisphere by its dichotomous branching, secondary filaments that persist and leave a well-defined involucre, the absence of terminal tubular cells, and tetrasporangia that are borne from secondary filaments from inner cortical and outer medullary cells. The distributional range of *M. canaliculata* is extended from the central coast of Peru, from Bahía de Pucusana (12°S) to Marcona (15°S).

Financing: Convenio de Cofinanciamiento 017-2016-FONDECyT, CONCYTEC-Perú

Keywords: COI-5P, phylogenetics, rbcL

E-Poster

AN INCREASE IN THE DIVERSITY OF CONTINENTAL ALGAE IN MEXICO. THE CASE OF TABASCO

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There are currently 5071 names of specific and infraspecific microalgae taxa reported from Mexico. About a third are dubious or synonymous names, which leaves us with a figure close to 3380 valid names. These names have been documented from 1843 to 2021, with the latest added (88 species). Although the country has a considerable amount of natural and built water bodies, the continental phycoflora is little known. The state of Tabasco (1.3% of the surface of Mexico) has 200 lakes. From the collections made by our laboratory, in 9 of those lakes, we have obtained 88 new records for Mexico, representing 16% of the flora so far known to the state (2019-2020). Tabasco results signify 553 taxa. Many species are from groups little studied in the country: xanthophytes and coccoid chlorophytes. Some of these records are also new for the continent, and there are examples of species with a very restricted worldwide distribution that we have seen in Tabasco. These records make Tabasco the third state in the country with the most records of continental microalgae and with only the analysis of 4.5% of existing water bodies. This work signifies the importance of floristic studies in the country and the Latin American region.

Keywords: Lakes, phycoflora, Tabasco

E-Poster

A NEW SPECIES OF *COLPOMENIA* (SCYTOSIPHONACEAE, PHEOPHYCEAE) FROM HOKKAIDO, JAPAN AND MAGADAN, RUSSIA

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A putative new species of *Colpomenia* is reported herein from Hokkaido, Japan and Magadan, Russia based on molecular analyses using mitochondrial cox3 and chloroplast *rbc*L genes and on morphological observations. This species can be distinguished from other *Colpomenia* by its small globular to vesicle-like thallus of 5 cm in diameter, thin thallus composed of a cortex of one to two-cell layers and a colorless medulla of up to three layers. This species was epiphytic on *Stephanocystis* in protected areas against waves. Our phylogenetic analyses supported that the new species is a distinct species from congeners. The life history of the species was investigated in culture, where its pseudodiscoid sporophytic thalli formed plurilocular sporangia and unilocular sporangia.

Keywords: Brown algae, *Colpomenia*, molecular and morphological analyses

E-Poster

A NEW GENUS *ROSEOLITHON* (HAPALIDIALES, RHODOPHYTA) WITH SEVEN NEW SPECIES FOR THE WESTERN SOUTH ATLANTIC

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Lithothamnion is the only known genus of Melobesioideae with flared epithallial cells. However, many studies have revealed the traditional morphological characters used to identify the genera and species of non-geniculate coralline algae are inconsistent. Recent molecular studies have been showing the cryptic diversity and polyphyly in the genus of *Lithothamnion*. In this study, we aimed to investigate the diversity and phylogeny of specimens morphologically described as *Lithothamnion* based on extensive collections along the coast of Brazil using an integrative taxonomic approach. Our results led to the proposal of *Roseolithon* gen. nov. belonging to the subfamily Melobesioideae. This new genus is described from tropical northwestern Atlantic and warm temperate southwestern Atlantic, based on phylogenetic analyses of *psb*A, SSU rDNA, COI-5P and *rbc*L-3P molecular markers, species delimitation methods, genetic divergence, and morpho-anatomical observations. *Roseolithon* is distinguished by the following suite of morpho-anatomical characters: (i) flared epithallial cells, (ii) subepithallial varying in size being shorter, approximately equal to or longer than those subtending them, (iii) tetra/bisporangial conceptacle chambers multiporate with rosette cells differing from sunken to disintegrated, (iv) cells linked by cell fusions, (v) thallus organization monomerous with plumose hypothallus (non-coaxial). The new genus *Roseolithon* is composed of at least 18 species, of which we describe seven new species.

Financing: FAPESP (Biota 2013/11833–3), CNPq (301491/2013–5), Biota–FAPERJ (E–26/110.019/2011)

Keywords: Coralline algae, taxonomy, classification

E-Poster

COMPLETE PLASTID GENOME OF *OEDOGONIUM* CF. *CALCAREUM* FROM NEW ZEALAND

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Oedogonium Link ex Hirn is a genus of fast-growing filamentous green algae that are good candidates for algal bioremediation, including polishing of effluent from municipal wastewater treatment plants. The genus is speciose, and identification using morphological and anatomical characters can prove difficult. We used a genome skimming approach to obtain sequence data for the plastid and nuclear ribosomal cistron of a recently collected New Zealand *Oedogonium* strain morphologically identified as *Oedogonium* cf. *calcareum*, in order to characterize this strain and to increase the suite of DNA sequence-based markers available for this genus. Phylogenetic analyses based on nuclear ribosomal ITS regions and on plastid *rbc*L sequence data show that the New Zealand strain is closely related to *Oedogonium* fragile. The complete plastid sequence has the same quadripartite structure as that of *Oedogonium cardiacum*, with two inverted repeat regions of 23kbp separating two single copy regions, and a similar gene complement. The *Oedogonium* cf. *calcareum* plastid is 166kbp in size, slightly smaller than that of *O. cardiacum* at 196kbp.

Keywords: Plastid sequencing, Oedogoniales, Chlorophyta

SYM10: Life history trait variation: evolutionary and ecological consequences

Keynote lecture

ARE COMPLEX LIFE CYCLES MAINTAINED BY CRYPTIC DIFFERENCES IN PHASES?

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The complexity of life cycles within the marine realm, where alternation of generations amongst haploid and diploid phases are common, are simultaneously both baffling and intriguing. The diversity of life cycles amongst the algae are particularly fascinating. Understanding these complex life cycles is essential for understanding the distributions and abundances of species, conservation and management, domestication through aquaculture production, and in understanding the evolutionary origins and ecological consequences of the complexity exhibited. In this keynote presentation, I will lead you on a journey from the Pacific coast of Japan to the lab on a quest to understand how the complex life cycles of isomorphic red algae (using *Chondrus verrucosus* as a model) can be maintained by cryptic ecological and ecophysiological differences, and the possible ecological consequences of these subtle differences.

Financing: Australian Academy of Science, Japan Society for the Promotion of Science, Monbusho, Deakin University

Keywords: Ecological niche partitioning, evolutionary ecology, macroalgae

Keynote lecture

MICROEVOLUTIONARY VARIABILITY OF A COMPLEX LIFE CYCLE IN A COSMOPOLITAN MICROALGAE

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Complex life cycles are well known in macroalgae, but poorly recognized in microalgae. One of the most wide-spread and successful microalgae in the ocean is *Emiliania huxleyi*, which became a dominant or co-dominant coccolithophore from tropical to polar seas and from highly productive to oligotrophic waters since appearing only 291000 years ago. Strikingly, none of its closest relatives, taxonomically classed in the genus *Gephyrocapsa*, share this cosmopolitanism. The *Emiliania-Gephyrocapsa* genus is therefore intriguing for exploring what permits adaptation and colonization of new environments. The most mysterious aspect of the genus is the haplo-diplontic life cycle: The diploid calcified phase is well-known and easily observed in nature, but the motile non-calcified haploid phase is known almost exclusively from culture. Genome analysis revealed that *E. huxleyi* strains from low latitude and offshore waters of the South Pacific and Mediterranean tend to lose key haploid-specific genes related to motility, which are conserved in strains from higher latitudes. We recently isolated and sequenced the genomes of *G. muellerae, G. parvula*, and *G. ericsonii*. Genomic and phylogenomic analyses offer evidence of the history and possible consequences of life cycle variability observed in *E. huxleyi*. Do ideas of life cycle evolution from macroalgae, confined to a very narrow coastal strip, extend to the vast populations of planktonic microalgae from coastal to open oceans?

Financing: Instituto Milenio de Oceanografía ICN12_019; FONDECYT

Keywords: Life cycle, coccolithophore

Oral presentation

DIVERSE MECHANISMS OF CARBON ACQUISITION IN THE COMMERCIALLY-IMPORTANT RED ALGA *PYROPIA*

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Pyropia ("zi-cai in Chinese", "nori" in Japanese, "gim" in Korean) is a commercially important red alga that is eaten throughout the world. The two phases of the *Pyropia* life history inhabit distinctive niches; gametophytic blades in the intertidal zone experience frequent emersion to the air while the filamentous sporophyte (conchocelis-stage) lives inside mollusk shells and similar calcareous substrates. Comparative genomic analyses between red algal genomes belonging to the Bangiophyceae (e.g., *Porphyra*, *Pyropia*) and Florideophyceae (e.g., *Chondrus* ["Irish moss"] revealed expanded gene families in Bangiophyceae that protect against reactive oxygen stress and provide carbon concentrating mechanisms (CCMs). These features explain their robust adaptation to intertidal stresses. Conchocelis can utilize mollusk shell carbonate as a carbon source using extracellular carbonic anhydrase. I will also share our recent work on asexual reproduction of *Pyropia yezoensis* by archeospores, which is relevant to aquaculture.

Financing: National Key R&D Program of China (2018YFD0900106)

Keywords: *Pyropia*, carbon acquisition, carbon anhydrase

Oral presentation

EFFECT OF GENETIC AND ENVIRONMENTAL FACTORS ON *AGAROPHYTON CHILENSE* PRODUCTIVITY

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In Chile, as a result of unconscious selection and domestication process based on asexual reproduction, farmed populations of the red alga *Agarophyton chilense* (previously known as *Gracilaria chilensis*) have experienced a reduction in the genotypic diversity and a modification of life history traits when compared to natural populations. In 2015, the *Agarophyton* farmers reported a sharp decrease in productivity in the southern part of the country that were associated to various possible causes, including the effect of environmental and genetic factors. Lab and field experiments were set up to evaluate how the genetic factors and environmental variables affect the species productivity. Lab experiments showed a contrasting response of farmed and wild populations to temperature. Thalli from natural populations were significantly affected by low and high temperature while the response of farmed thalli was more homogeneous along the temperature gradient tested. The field experiments show that farmed thalli grow better when planted in monoclonal stands than in polyclonal ones. We hypothesized that fishermen could have selected general-purpose-genotypes, tolerant to a wide range of environmental conditions and that these genotypes could be high-quality clones well suited for high biomass production when grown in monoclonal culture. Even if aquaculture has impoverished the *A. chilense* pools of genotypes in farms, it seems that selection have retained genotypes well adapted to anthropogenic and seasonal stressors. Nevertheless, this short-term advantage could lead to long-term negative consequences if clonally farmed thalli are confronted to extreme events of heat stress or nutrient pollution in a near future.

Keywords: *Agarophyton chilense*, genotypic diversity, environmental factors

Oral presentation

MACROCYSTIS PYRIFERA LIFE HISTORY: UNWRAPPING THE RELEVANCE OF MICROSCOPIC STAGES FOR BIOMASS PRODUCTION

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We review our latter work with *Macrocystis pyrifera* deciphering how the development of microscopic stages impact the sporophytes' performance. The microscopic gametophytic phase has been a "black box" that requires attention and further research, as it is a critical stage for the survival of kelp under stressful scenarios (i.e. increase in sea temperature). By following the development of those microscopic stages under standardized laboratory conditions, we have found female gametophytes with different number of oogonia, and those with a higher number produced a "sporophytic unit" (multiple frond morphotype) united by a single not coalescent holdfast: the fertilized oogonia and their subsequent sporophytes remained attached to the original gametophyte. These sporophytic units proved genetically diverse, suggesting that oogonia were fertilized by antherozoids from different male gametophytes. Thus, female gametophytes growing under controlled conditions produce juveniles with different number of fronds, i.e. few (≤2) or multiple fronds (≥3) that showed different responses under controlled laboratory experiments combining temperature and N-NO3 availability: the multiple fronds morphotype can withstand better nitrogen limiting conditions at 12°C (higher growth rate), and nitrate reductase activity increased independent of temperature. *M. pyrifera* multiple frond morphotype out-planted to a natural kelp bed and an on-growing site also showed a significant higher biomass. These results indicate that morphotype is defined earlier during development, and it is as important as genetic management when pursuing kelp growth. The use of gametophytic development traits to produce a more productive and environmentally resistant sporophyte may prove to be a novel and powerful tool.

Financing: Funded by ANID-FONDECYT 1180647 and Basal CeBiB (FB-0001)

Keywords: *Macrocystis*, life cycle, morphotype

Oral presentation

INBREEDING AND OUTBREEDING DEPRESSION AND ITS IMPORTANCE FOR GENETIC RESTORATION

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Environmental changes and human activities seem to critically threat kelp marine forests resulting in wide populations' declines and distribution shifts. Such degradations have major ecological and socio-economic consequences. There is then an urgent need to tackle this crisis and to develop approaches for the conservation and restoration of marine ecosystems. Here we address the question on how knowledge on intra-specific diversity, and in particular mating system, can help to define conservation and restoration practices. Kelps are characterized by a haplo-diplontic life cycle. A direct consequence of this type of cycle is the effect of selection that will tend to purge rapidly the deleterious alleles within the haploid generation. The question that arises here is that of the variation of the compatibility of crossbreeding between individuals according to their similarity and of the selective value of their descendants since the reproduction between genetically too similar individuals would suffer from an accumulation of deleterious mutations (Inbreeding depression) whereas the crossing between too different individuals would cause a rupture of the adaptive complexes (outbreeding depression). While the effect of genetic distances between parents on reproductive success is commonly studied in higher plants, this is still very little known in algae despite its important consequences on the management of natural resources and on the development of aquaculture.

Financing: This work was funded by the IDEALG project (France: ANR-10-BTBR-04), the H2020 project GENIALG (Grant Agreement No 727892)

Keywords: Life cycle, mating system, genetic diversity

Oral presentation

HAPLOID AND DIPLOID ADVANTAGES OF THE *AGAROPHYTON CHILENSE* LIFE CYCLE

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Conditional differentiation is considered the driver of the evolutionary stability of biphasic life cycles. For this stability, gametophytes and tetrasporophytes must differentiate enough in niche exploitation to not inevitably eliminate one of them. Though differentiation in heteromorphic life cycles (e.g., kelp) is readily perceptible, this is not the case for isomorphic life cycles (e.g., most red algae), where differentiation is invisible and only unveiled in short-term experiments. We followed all individuals of *Agarophyton chilense* in five rock-pools within the Valdivia river estuary for 28 months to assess the *in situ* differentiation between gametophytes and tetrasporophytes. We observed that gametophyte adults generally grew and survived better than tetrasporophytes. Gametophytic females grew 15% faster to twice as large and out-survived tetrasporophytes in about 63%, both under intense competition and under stress from desiccation. This advantage may result from gametophytes (haploids) spending fewer resources on DNA production and maintenance than the tetrasporophytes (diploids), thus having more resources available for growth and survival - the resource limitation hypothesis. Also, fertile gametophytic females survived 20% better than fertile tetrasporophytes, while their diploid carpospore progeny also survived more (usually 2-10 times) than haploid tetraspores. This may be due to gametophytic females allocating part of their spared resources to maternal care. Haploid maternal care was the only advantage to the diploids that we identified in the *A. chilense* life cycle. The resource limitation hypothesis together with maternal care may be responsible for the conditional differentiation sustaining the evolutionary stability of *A. chilense.*

Financing: CONICYT (FONDECYT) grant number 1090360 and 117054, and FCT funding UIDB/EEA/50009/2020, SFRH/BPD/63703/2009, SFRH/BPD/107878/2015 and UID/Multi/04326/2020.

Keywords: Conditional differentiation, evolutionary stability, life cycle

Oral presentation

PHEROMONE SIGNALING IN PENNATE DIATOMS TO PREVENT DEATH

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Marine benthic diatoms shape the ocean floors and contribute substantially to biofilm formation. Due to their silica cell wall diatoms possess a unique life cycle, including a sexual phase initiated when cells become small after repeated mitotic divisions (Chepurnov et al., 2002). Since sex is a costly event it is often guided by pheromones but little is known about pheromone involvement during mating of pennate diatoms. In *Seminavis robusta* a two-step pheromone system is activated during sexual reproduction and involves a cell cycle arrest to increase mating efficiency (Gillard et al., 2013). Here we address the question whether this strategy is conserved among pennate diatoms. The benthic diatom *Cylindrotheca closterium* equals other pennates in its heterothallic mating system (Vanormelingen et al., 2013). We found that the two mating types (mt) can be differentiated in mt+ and mt⁻ with distinct functions. By establishing a novel capillary assay, we proved the involvement of a pheromone that attracts the opposite mating partner and provokes chemokinetic response. Further, two more pheromones produced by mt⁻ promote the sexual events. One temporarily arrests the cell cycle progression of mt+ while the other induces gametogenesis. We suggest that *C. closterium* shares a functionally similar pheromone system with other pennate diatoms like *Seminavis robusta* and *Pseudostaurosira trainorii* which synchronize sexual events and mate attraction.

Keywords: Pennate diatoms, pheromones, attraction assay

Oral presentation

GAMETOPHYTE KINSHIP RECOGNITION AND INBREEDING IN *MACROCYSTIS PYRIFERA*

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Inbreeding, the mating between genetically related individuals, often results in reduced survival and fecundity of offspring, relative to outcrossing. Yet, high inbreeding rates are commonly observed in seaweeds, suggesting compensatory reproductive traits may affect the costs and benefits of the mating system. We experimentally manipulated inbreeding levels in controlled crossing experiments, using gametophytes from 19 populations of *Macrocystis pyrifera* along its Eastern Pacific coastal distribution (EPC). The objective was to investigate the effects of male-female kinship on female fecundity and fertility, to estimate inbreeding depression in the F1 progeny, and to assess the variability of these effects among different regions and habitats of the EPC. Results revealed that the presence and kinship of males had a significant effect on fecundity and fertility of female gametophytes. Females left alone or in the presence of sibling males express the highest gametophyte size, number and size of oogonia, suggesting they were able to sense the presence and the identity of their mates before gamete contact. The opposite trend was observed for the production of embryos per female gametes, indicating higher costs of selfing and parthenogenesis than outcrossing on fertility. However, the increased fecundity compensated for the reduced fertility, leading to a stable overall reproductive output. Inbreeding also affected morphological traits of juvenile sporophytes, but not their heatwave tolerance. The male-female kinship effect was stronger in high latitude populations, suggesting that females from low latitude marginal populations might have evolved to mate with any male gamete to guarantee reproductive success.

Financing: ANID/CONICYT FONDECYT de Iniciación 11170699 ANID/CONICYT FONDECYT 1160930

Keywords: Fecundity, fertility, *Macrocystis*

Oral presentation

VARIABILITY IN PHYSIOLOGICAL PERFORMANCES OF THE REPRODUCTIVE PHASES IN *GRACILARIOPSIS TENUIFRONS* (GRACILARIALES, RHODOPHYTA) CULTIVATED AT DIFFERENT TEMPERATURES

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The knowledge about physiological adaptations between haploids-diploids, and unfertilized-fertile phases in red algae is still incipient. Hypothesis models have indicated that diploids are superior to haploid phase, and vice-versa, depending of laboratory conditions; proceeding, energy-cost in fertile phases are used to sexual structure and maintenance. *Gracilariopsis tenuifrons* has a wide distribution along the Brazilian coast, São Paulo state is the population limit of distribution to the species. This work aimed to elucidate distinct physiological adaptation of unfertilized female gametophytes (FG), fertile male gametophytes (MG), fertile tetrasporophytes (T), and cystocarpic plants (CP) cultivated in different temperatures (20, 25, and 30°C), evaluating growth rates (GRs), photosynthesis (Fv/Fm), pigment content (phycoerythrin, PE; phycocyanin, PC; allophycocyanin APC; chlorophyll-a, CLOa; carotenoids, CAR), thallus length (TL), and number of differentiated branches. Evaluating the differences between T (diploid) and FG (haploid) at stressed temperatures (20 and 30°C), T showed higher GR and PE, when compared to FG. However, intermediate (25°C) temperature promoted higher GRs, TL, PC, and APC in FG when compared to T. Evaluating the differences between FG (unfertilized) and CP (fertile), we could observe that FG presented higher TL, number of differentiated branches, GRs, Fv/Fm, PE, PC, and APC, when compared to CP, at 25°C. These results suggest that haploids and diploids have different adaptations and enable different physiological performances depending on temperature. Fertile plants showed reduced physiological performance.

This study allowed us to observe different physiological performances of the reproductive phases in Gp. *tenuifrons*.

Financing: FAPESP-2017/13983-3

Keywords: Triphasic life cycle, haploid-diploid, climate change

E-Poster

EVIDENCE OF SEXUAL REPRODUCTION IN *PROBOSCIA* BLOOMS

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Many diatoms exhibit valve size reduction with successive cell divisions, which results in a higher percentage of smaller valve sizes. To return to larger valve sizes, diatoms must undergo sexual reproduction. But observations on auxospores and post-auxospore frustules (initial cells) in natural populations of marine diatoms are rarely recorded, since most species do not form blooms and thus the chances of witnessing sexual reproduction events are low. However, if the population has a high percentage of large valve sizes, one may assume that sexual reproduction has taken place. In this study we measured valves in *Proboscia* blooms from the Southern Ocean and subarctic Pacific. In at least two of the samples, there is evidence of auxospores, supporting the assumption that these are post-auxospore assemblages. Measurements of valve length, valve width and proboscis tip diameter were made on 300 specimens, and plotted as histograms using size ranges. The data reveals that the percentage of larger sizes is higher than would be expected if only asexual reproduction was taking place. For example, in the case of a *P. alata* bloom from the Southern Ocean, the average valve width is 15.1 µm, with the maximum value (41.4 µm) over 7 times larger than the minimum one (5.5 µm). The small (<10 µm) valves account for 19% of the population, while the larger (>20 µm) ones represent 20%. There are 2 peaks in the histogram, a large one at 8.5-11.5 µm and a smaller one at 20.5-23.5 µm.

Keywords: Proboscia, auxospore

E-Poster

MORPHOLOGICAL DIFFERENCES OF *MAZZAELLA LAMINARIOIDES* (RHODOPHYTA, GIGARTINALES) BLADES IN RELATION TO SAND ABRASION

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The high morphological variability in macroalgal species can make morphological identification difficult, especially of species with simple morphology. In low intertidal rocky zones exposed to high sand abrasion, individuals of *Mazzaella laminarioides* tend to have longer fronds (some exceeding 50 cm in length) than those inhabiting rocky shores with no sand effect, which attain a maximum of 30 cm in length. Molecular analyzes using the COI marker confirmed that the long-frond individuals corresponded to *M. laminarioides*. Frond morphology of gametophytes and sporophytes collected from four sites with, and four without sand scouring, at equivalent low intertidal levels in the Biobío region (southern Chile), was evaluated with traditional morphometry. Results showed that fronds from sites with sand influence were longer and wider than those from sites without sand abrasion, regardless of the life cycle phase. Results also indicated that seasonality and vertical height did not explain the occurrence of long blades. The accompanying biota of *M. laminarioides* was characterized by evaluating relative cover. In sand affected rocky areas where long-frond individuals occur, sand tolerant species and bare rock were more abundant than in areas without sand effect. We propose that, in *M. laminarioides*, the larger fronds would originate from sand-abraded disks after tissue regeneration. This is comparable to the mechanism proposed to explain frond differences within *Chondracanthus chamissoi*. Thus, morphological variability may be related to changes during regeneration of the damaged tissue.

Keywords: Morphometry, regeneration, fronds

E-Poster

A POTENTIAL MECHANISM TO EXPLAIN THE OCCURRENCE OF TWO SYMPATRIC FORMS OF *CHONDRACANTHUS CHAMISSOI* (RHODOPHYTA, GIGARTINALES)

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Intraspecific morphological variability is common in red seaweeds. Two forms (*f. lessonii* and f. chauvinii) have been described for *Chondracanthus chamissoi* based mainly on the width of blades central axes. In this study, morphological characters were quantitatively evaluated from sporophytic, and male and female gametophytic blades from three localities in southern Chile in autumn-winter; one locality was resampled in spring-summer. PCA analysis using morphological characters separated two groups: one with narrow, thick, and canaliculated central axes, with few or no spines, consistent with *f. lessonii*, and another with broad, thin, flat central axes and many spines, consistent with *f. chauvinii*. Potential explanations were considered. Blades of both forms and phases shared a single *rbc*L and two COI haplotypes, supporting they correspond to the same species. Also, forms were not related to phase or sex. Furthermore, thalli of both forms occur in sympatry (side by side) at all sites (reports confirm sympatry through its geographical distribution in Chile-Perú), so they do not correspond to ecotypes. We propose that thalli originating from spores (primary origin) may differ from those originating after differentiation of cells when apexes produce secondary attachment discs (secondary origin). Spores and fragments (apexes) were cultivated to obtain primary and secondary discs, respectively. Cells of secondary discs were more than twice the length than those of primary discs, indicating morphological differences at the cellular level. The adaptive significance of sympatric forms remains to be determined. Morphological variability of other *Gigartinaceae* could be explained by a similar mechanism.

Financing: CONICYT PFCHA/MAGISTER BECA MAGISTER NACIONAL/2016–22162094; MAGÍSTER EN ECOLOGÍA MARINA, (UCSC) CENTRO DE INVESTIGACIÓN EN BIODIVERSIDAD Y AMBIENTES SUSTENTABLES

Keywords: Morphological variability, secondary attachment, life history

E-Poster

SPATIAL HETEROGENEITY AND TEMPORAL STABILITY: KEYS EFFECTS ON A RED ALGA REPRODUCTIVE SUCCESS

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Male and female fertilization success depends on successful gamete encounters. In red seaweeds, the available evidence suggests that the dispersal of spermatia (male gametes) is extremely limited, not only in space but also in time. First, spermatia lack flagella. While water movement facilitates the dispersal of all propagules, without flagella spermatia cannot swim the final critical distance to a female reproductive cells. Second, sexual pheromones, which are instrumental in the synchronization of gamete release and/or the attraction of male gametes in many green and brown seaweeds, are unknown in red macroalgae. Consequently, spermatia depend entirely on passive transport in the water column from the time of release to the point of fusion with a female gamete. Fertilization takes place in the female plant, on a structure called the trichogyne, in Floridean rhodophytes. In most orders of this class, female gametes, once fertilized, develops into cystocarps. Previous studies emphasized the role of extrinsic factors (as the distance between parents) but also intrinsic factors (female and male genotypes and the interaction between them) on *Gracilaria gracilis* fertilization success. Fertilization success varies widely among males while the cystocarps production per centimeter of thallus is slightly more homogeneous among females. In this study, we propose to use data obtained over more than 20 years in a *Gracilaria gracilis* rook pool to study in details the interaction of several extrinsic factors (as the density and distance from males), as well as intrinsic characteristics specific to females (as age and size) on cystocarps production.

Financing: This work was supported by a doctoral fellow from the CNRS '80 prime' to Emma Lavaut

Keywords: Fertilization success, *Gracilaria gracilis*, gamete dispersal

E-Poster

CAN ENVIRONMENTAL FACTORS OR GENETIC BACKGROUND INFLUENCE GAMETOPHYTE FERTILIZATION AND EARLY SPOROPHYTIC DEVELOPMENT OF THE GIANT KELP *MACROCYSTIS PYRIFERA*?

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The giant kelp *Macrocystis pyrifera* has a high morphological plasticity which can contribute to explain its high productivity and adaptability to different environments. This trait may have a genetic component, yet the expression of sporophyte morphology and physiology goes through a 'black box' of biological processes during kelp microscopic stages (e.g. sexual reproduction). Our hypothesis is that environmental factors, independent from genetic background, can determine the developmental pattern and reproduction potential of female gametophytes that will produce sporophytes with different morphotypes (number of fronds). Sporophylls were collected from two genetically distinctive populations i.e. Valparaíso and Los Lagos (Chile). Sporulation was carried out under standardized conditions, and the spores for both populations were seeded on Petri dishes (n = 54 each). Two sets of factorial experiments were established for 50 days and constantly monitored for changes in the development up to embryonic sporophytes: i) Temperature (8°, 16°, 18°C) versus N-NO3 availability (Seawater + full-enriched, and N-limited Provasoli); ii) Temperature (8°, 16°, 18°C) versus photosynthetic photon flux (5-8 and 40-45 µmol m-2 s-1). Our results showed that female gametophytes presented complex responses to changes in environmental factors: affecting their general morphology, the number of oogonia able to produce, hence the number of embryonic sporophytes per

female gametophytes. Also, we cannot rule out the effect of genetic background as under certain stress conditions it proved to be significant. This finding may have relevant implications on population dynamics and productivity of *Macrocystis* under natural or farming conditions.

Financing: Funded by ANID-FONDECYT 1180647 and Basal CeBiB (FB-0001)

Keywords: *Macrocystis*, life cycle, morphological plasticity

E-Poster

GIANT KELP JUVENILE SPOROPHYTES IN LABORATORY CONDITIONS: IS GENETIC BACKGROUND IMPORTANT WHEN COPING WITH ENVIRONMENTAL STRESSORS?

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Different genetic clusters have been described for *Macrocystis pyrifera* along the Chilean coast: central/north and south/austral populations are different. To stablish whether *Macrocystis* juvenile sporophytes with different background show differences in tolerance to individual environmental stress, comparative experiments were designed for testing their effect on algal growth. Sporophylls were collected in Valparaíso (central population) and Los Lagos (southern population) regions. Sporulation, gametophyte, and sporophyte cultivation were carried out under standardized conditions. When sporophytes reached~2.0 cm in length (60 days), three independent experiments to test for the effect of temperature stress (12°, 15°, 18°, 21°C), active photosynthetic radiation limitation (5, 12, 25, 45 μmol m-2s-1) and N-NO3 limitation (1, 5, 10, 15, 20 μM) were set up. Experiments run for 25 days with Provasoli-enriched seawater (temperature and radiation), and 20 days in artificial seawater with Provasoli adjusted to required NO3 concentration (N-NO3 limitation). Growth as SGR (%) was measured at initial and ending points of each experiment. Results showed that algal origin have some effect when coping with temperature and N-NO3 availability but no with light stress: both populations responded similarly to dim light. Sporophyte from Valparaíso have a poorer growth at low temperatures but copes better with higher temperatures, and although both populations respond similarly to the N-NO3 availability, Valparaíso had a higher SGR. In conclusion, growth as a productive trait in giant kelp seems to have a relevant genetic background that can be used for developing strains for aquaculture depending on the site location environmental characteristic.

Financing: Funded by ANID-FONDECYT 1180647 and Basal CeBiB (FB-0001)

Keywords: Giant kelp, environmental stress, genetic

E-Poster

EXAMINING THE PHYSIOLOGY AND BIOGEOGRAPHY OF COCCOLITHOPHORE LIFE CYCLE STAGES

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Despite the significance of coccolithophores for biogeochemical cycling, much of their ecology remains poorly understood. Especially their elusive haplo-diplontic life cycle has been given little attention in the literature. Yet, it significantly impacts the extent of coccolithophore calcification, their vertical and horizontal distribution in the ocean, and potentially their global success. The aim of this project is to establish physiological differences between the life cycle stages of the ecologically important coccolithophores *Coccolithus braarudii* and *Calcidiscus leptoporus* in response to changes in nutrients and light. These differences will be assessed through a comparison of the two life stages' physiology using proteomics, biochemistry, and single cell microscopy approaches. The second major aim of this project is to analyse the phytoplankton communities of the coccolithophore-rich Great Calcite Belt in the Southern Ocean. Genetic and microscopic data collected in a time series of mesoscale eddy formation will be used to identify how coccolithophore communities change in comparison to other major phytoplankton groups. Correlating community composition to their physical drivers will further shed light on ecological preferences of haptophytes. A profound understanding of these preferences as well as the properties of coccolithophore life cycles is vital to revealing their evolutionary success and their impact on ocean biogeochemistry and ecology.

Financing: NERC INSPIRE NE/S007210/1

Keywords: Coccolithophores, life cycle, Southern Ocean phytoplankton

E-Poster

FRESHWATER RED ALGAE AS ECO-EVOLUTIONARY MODELS

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The relative frequency of sexual versus asexual reproduction governs the distribution of genetic diversity within and among populations. As a consequence, the reproductive mode affects a population's ability to track environmental change through phenotypic evolution. Most studies of the consequences of reproductive variation focus on the mating systems (i.e., outcrossing to selfing) of diploid-dominant taxa (i.e., angiosperms). Outcrossing results in greater genetic diversity, while selfing results in lower genetic diversity. Asexual reproduction has similar evolutionary consequences as selfing. Many eukaryotes are partially clonal, undergoing both sexual and asexual reproduction, but we understand less about the consequences of partial clonality. Moreover, reproductive modes should also correlate with life cycle types. Outcrossing should be associated with diploidy, while selfing and clonality should correlate with a prolonged haploid stage as deleterious mutations are exposed to selection and can be directly purged. However, these correlations have not been systematically investigated because eukaryotic reproductive mode variation is poorly described. We advocate for filling these gaps through the simultaneous investigation of life cycle and reproductive mode evolution using freshwater red macroalgae. Selfing is possible in both monoicous (hermaphroditic) and dioicous taxa (separate sexes) and asexual reproduction may result in the temporary or permanent loss of a ploidy stage. These eco-evolutionary consequences are unique for organisms with haplodiplontic life cycles, such as many freshwater reds. Understanding the evolutionary consequences of selfing and asexual reproduction will aid in our understanding of eukaryotic evolution generally and of the evolutionary ecology of freshwater red algae more specifically.

Keywords: Mating systems, reproductive mode, haplodiplontic life cycle

E-Poster

HAPLO-DIPLONTIC LIFE CYCLE EXPANDS COCCOLITHOPHORE NICHE

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Coccolithophores are most recognizable for their production of calcium carbonate platelets called 'coccoliths', which lead them to play an important role in the carbon cycle. The production of coccoliths is however not their only unique trait. As haplo-diplontic organisms, coccolithophores can reproduce asexually in two different life phases (the 'haploid' and 'diploid' phase). Which contrasts with most phytoplankton, which can reproduce asexually in only the haploid or diploid phase. Thus far, research has however focused on only one life cycle phase (the diploid phase), and the ecological role of the haploid life cycle phase is unclear. Here, using a global meta-analysis and statistics we investigate the niche of the coccolithophore life cycle. We illustrate that haploid and diploid coccolithophores inhabit contrasting niches and find that although haploid coccolithophores generally constitute a minor component of coccolithophore standing stock, by inhabiting contrasting niches the haplo-diplontic life cycle strategy allows coccolithophores to expand their niche volume. Furthermore, we show that although haploid coccolithophore abundance is generally low, haploid coccolithophores can be significant contributors to the coccolithophore standing stock in low nutrient and stratified regions. Since such conditions are predicted to increase under future climate scenarios as this may have important implications on the carbon cycle as haploid coccolithophores are less calcified than their diploid life cycle phase.

Keywords: Coccolithophores, niche space, life cycle

SYM11: Toward algal synthetic biology

Keynote lecture

PHOTOSYNTHETIC BIO-MANUFACTURING IN GREEN ALGAE – FOOD AND FUEL FOR THE 21ST CENTURY

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Eukaryotic algae offer tremendous potential for the large-scale production of bio-products, including food, feed, and a variety of specialty products. Algae are more efficient than terrestrial plants at fixing CO2 and producing biomass, and algae can be grown using non-potable water on non-arable land. If we are to meet any of our climate goals, we need a Green Revolution 2.0, and algae offer a real opportunity to achieve these as a new bio-manufacturing platform. Using "designed for purpose" photosynthetic microorganisms we have the opportunity to develop algae as a new production platforms for food, fuel, and biomaterials that have unmatched efficiencies and productivities. To achieve these goals, we need to develop the genetic tools and production processes that will enable algae to become a commercially viable bio-products platform. We are developing the genetic and synthetic biology tools to enable the production of high value products, including recombinant proteins used as nutritional supplements, as well as precursors for renewable polymers. The challenges, potential, and some early successes of engineered algae for the production of high value products will be discussed.

Keywords: synthetic biology, bio-manufacturing, microalgae

Keynote lecture

CYANOBACTERIAL CHEMICAL PRODUCTION FROM CO2

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Cyanobacteria are under investigation as a means to utilize light energy to directly recycle CO2 into renewable chemical compounds currently derived from petroleum. We have previously engineered production of the chemical feedstock 2,3-butanediol (23BD) from a cyanobacterium, *Synechococcus elongatus* PCC 7942. We subsequently explored the optimization of 23BD production by varying ribosomal binding site and promoter strength, operon organization, and gene expression at the transcriptional and translational level. Any large-scale cyanobacterial production scheme may rely on natural sunlight for energy, thereby limiting production time to only lighted hours during the day. To overcome this limitation, we engineered *S. elongatus* for production of 23BD via supplementation with sugars. Furthermore, we developed a strategy to optimize glucose and CO2 utilization and to improve 23BD production and yield. The engineered strain efficiently uses both CO2 and glucose, and produces 12.6 g/L of 23BD. This represents a significant step towards industrial viability.

Keywords: synthetic biology, *Synechococcus*, 2,3-butanediol

Oral presentation

A MOLECULAR TOOLKIT FOR THE GREEN SEAWEED *ULVA MUTABILIS*

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Green seaweeds like *Ulva* are ecologically important marine primary producers that are commercially cultivated for multiple uses. Despite their importance, several molecular tools still need to be developed to better understand seaweed biology. One such tool, the generation of stable transgenic seaweed lines expressing transgenes, is a rare feature and impedes functional genetic research necessary to unravel gene functions and interactions. Here, we report the development of a flexible and modular molecular cloning toolkit for the green seaweed *Ulva mutabilis* based on the Golden Gate cloning system. We demonstrate the importance of endogenous regulatory sequences for transgene expression. We describe two vector systems to express transgenes via two expression cassettes or a single-promoter bicistronic approach. We visualize and confirm high transgene expression in the majority (50-80%) of obtained resistant individuals. Furthermore, we created different marker lines using either transit peptides or tagged endogenous Ulva genes. Our molecular toolkit enables the study of Ulva gain-of-function lines and paves the way for gene characterization and large-scale systems biology studies in a green seaweed. Our next goal is to use these tools to study carbon concentrating mechanisms in Ulva.

Keywords: *Ulva*, molecular toolkit, CCM

Oral presentation

METABOLIC PATHWAY REGULATION OF CAROTENOIDS AND MAAS IN CYANOBACTERIA EXPOSED TO UV-B AND FAR RED LIGHT

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Carotenoids and the mycosporine-like amino acids (MAAs) are two groups of metabolites that play an important role in photosynthesis and in photoprotection. They are also widely promoted for application in health as antioxidants and sunscreens. Here I present results from transcriptomics and metabolomics studies comparing metabolic pathway regulation for the carotenoids and MAAs in the filamentous cyanobacterium species, *Chlorogleoeopsis fritshii* PCC6912. Results were obtained from two experiments using white light as a control to compare with exposure to low level UV-B and Far-Red light. The presentation will highlight the photoregulatory processes that modulate the synthesis, photoprotection and cleavage of carotenoids in cyanobacterial cells exposed to low level UV-B. The presentation will also reveal new understanding on the metabolic regulation of MAAs under far-red light supporting their role in photon dissipation and thermoregulation. Overall, the results contribute to understanding on how metabolism is regulated according to a changing environment and how metabolism can be modulated for biotechnological purposes.

Financing: BBSRC grant BB/E018998/1. Attendance at this Congress is supported by INTERREG - ATLANTIC ENHANCE project.

Keywords: Cyanobacteria, carotenoids, mycosporine-like amino acids

Oral presentation

DEVELOPMENT OF GENOME EDITING TOOLS FOR THE COCCOLITHOPHORE *CHRYSOTILA CARTERAE*

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Coccolithophores are unicellular marine algae, which decorate their cell surface with intricately shaped calcite scales known as coccoliths. Through coccolith synthesis and photosynthesis, these algae play a special role in the global carbon cycle. The extraordinary morphology of coccoliths makes them very attractive for bioinspired material science research. Currently, no genome editing methods for coccolithophores are available. Such tools would allow elucidation of the genetic basis of coccolith formation. The aim of this study is to develop the CRISPR/Cas editing technique for the model coccolithophore species *Chrysotila carterae*. In order to

achieve this goal, we are testing a DNA-free editing approach based on the delivery of CRISPR/Cas in vitro preassembled ribonucleoproteins (RNPs) via PEG-mediated transformation as well as plasmid-borne CRISPR/Cas9 genome editing. In the existing literature PEG-mediated transformation of *C. carterae* has only been shown for the plasmid delivery. In this particular study, we demonstrated that RNP delivery can be achieved through optimizing the delivery parameters and the cell growth conditions. While developing the plasmid for genome editing, we have achieved transient expression of the Cas9 protein in *C. carterae* cells and have demonstrated the functionality of the nuclear localization signal, as well as identifying a promising promoter for gRNA transcription. Using endogenous negative counter-selectable marker genes as targets allows selection of the knockout mutants without additional integration and expression of an antibiotic resistant gene. Development of CRISPR/Cas genome editing for *C. carterae* will make this species available for synthetic biology.

Keywords: Coccolithophore, CRISPR/Cas, genome editing

Oral presentation

FUNCTIONAL CHARACTERIZATION OF CELLULOSE SYNTHASES FROM THE CORALLINE RED ALGA *CALLIARTHRON TUBERCULOSUM* REVEALS OVERALL DIFFERENCES FROM CELLULOSE SYNTHESIS IN ARABIDOPSIS

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Cellulose is the most abundant biopolymer on the planet. On land, cellulose contributes to the formation of wood, helping plants grow upright; in the ocean, cellulose provides mechanical support to macroalgae helping them resist hydrodynamic stress under crashing waves. Unfortunately, our understanding of cellulose biosynthesis is primarily based on studies in bacteria and land plants, while cellulose biosynthesis in lineages such as red algae (Rhodophyta) remain poorly explored. In this study, three putative cellulose synthase (CESA) sequences were identified from the unpublished transcriptome of the calcifying red alga *Calliarthron tuberculosum* (Ct). Predicted gene domains of the red algal CESA reveals a unique CBM48 domain predicted to bind to starch. The relationships between these newly identified CtCESAs and CESAs from other species were mapped in a maximum likelihood gene tree and revealed diverging relationships between the red algal, land plant, and bacterial CESA lineages. Characterization of the purified protein CtCESA1 from *Calliarthron*, the land plant PtCESA8 from Poplar, and the bacterial BCSA/BCSB cellulose synthesis complex further emphasizes potential lineage-specific differences as seen in large variations in enzyme activity. However, the red algal CtCESA1 can partially rescue the cellulose deficiency phenotype of the Arabidopsis cesa6 mutant in heterologous expression, suggesting some aspects of cellulose synthesis are likely deeply conserved between the red alga and land plant. Overall, this analysis identifies three CESA candidates in the calcifying red algae *Calliarthron tuberculosum* and presents the first functional evidence of glucan synthase activity in a red algal CESA.

Keywords: Coralline red alga, cellulose, molecular biology

SYM12: Harmful Algal Blooms: from detection to countermeasures

Keynote lecture

GLOBALHAB (IOC-UNESCO AND SCOR): LATINAMERICA CONTRIBUTION TO THE INTERNATIONAL COORDINATION FOR SOUND KNOWLEDGE OF HABS AND MANAGEMENT OF THEIR IMPACTS

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The Global Harmful Algal Blooms (GlobalHAB, www.globalhab.info) Program is aimed at fostering international cooperative research directed toward improving the prediction of harmful algal bloom (HAB) events in aquatic ecosystems, and providing sound knowledge for policy- and decision-making to manage and mitigate HAB impacts in a changing planet. GlobalHAB is sponsored by the Intergovernmental Oceanographic Commission (IOC) of UNESCO and the Scientific Committee on Oceanic Research (SCOR). GlobalHAB was launched in 2016 and will last for 10 years. The GlobalHAB scientific objectives are focused on the research of taxonomic, ecological and toxicology knowledge gaps, on the effects of climate change on HABs and their biogeographic distribution, the implementation of HABs observing systems, and overall, to promote aquatic food and water safety and security. The GlobalHAB program has an international nature, and collaborates with international entities and programs that share objectives on HABs research, management and mitigation, as was already done by the former program GEOHAB. In particular, scientists from Latin America were active participants in GEOHAB and today Latin America is key in the implementation of GlobalHAB. Extreme HAB events affecting aquaculture sites and natural environments, *Sargassum* beachings, HABs monitoring programs, ciguatera fish poisoning, toxin transfer through the food webs, are examples of topics where scientists in Latin America are very active and thus, contribute to the implementation of GlobalHAB. Scientists are invited to participate in GlobalHAB by designing and endorsing scientific activities linked to the goals of GlobalHAB, and by participating in other international activities.

Financing: The GlobalHAB (www.globalhab.info) international program is funded by IOC UNESCO and SCOR

Keywords: GlobalHAB, GEOHAB, harmful algal blooms

Keynote lecture

FIELD APPLICATION OF A RED-TIDE ACOUSTIC SENSING SYSTEM (RASS) FOR MONITORING OF FISH KILLING HARMFUL DINOFLAGELLATE COCHLODINIUM POLYKRIKOIDES

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Globally, harmful algal blooms (HABs) caused by marine phytoplankton pose a significant threat to human health and result in enormous economic loss. HABs can suddenly appear due to rapid cell growth and the accumulation due to tidal effects. For these reasons, there have been many efforts to develop monitoring tools and techniques for the early warning of HABs. One such instrument is the Red-tide Acoustic Sensing System (RASS) which utilizes a backscattered acoustic signal to detect microalgal cells in the water column. In Korea, economic and ecological damage caused by Cochlodinium polykrikoides (=Margalefidinium polykrikoides) occurs annually, and great human and financial efforts are being made to detect and manage their impacts. Here, we introduced that *C. polykrikoides* monitoring by RASSs were conducted at fish-farms located in *C. polykrikoides* bloom areas of South Korea during the summer, and their performance examined for the HABs detection. During *C. polykrikoides* blooming periods, a standard curve between the relative received level (RRL) of acoustic intensity as measured by RASS and cell densities of *C. polykrikoides* species was constructed (R2 = 0.846) and was successfully applied to quantify the HAB cell density. To evaluate the efficacy and accuracy of the RASS, a significant correlation (R2 = 0.997) between HAB cell abundance and backscattered acoustic signals was confirmed. Our field application data strongly suggests that RASS is an accurate and efficient tool for monitoring and alerting for HABs, despite being a cheap, simple, and easy tool.

Keywords: HABs, RASS, early detection

Oral presentation

RIBOSOMAL DNA'S INTRAGENOMIC POLYMORPHISM OF *GAMBIERDISCUS* (DINOPHYCEAE) AND ITS IMPLICATIONS IN MOLECULAR SPECIES DELINEATION

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Recent molecular phylogenetic studies of the benthic harmful dinoflagellate *Gambierdiscus* flagged several new species and genotypes revitalizing its systematics. The phylogenetic analyses revealed by the preliminary sequence information of nuclear-encoded ribosomal RNA genes (rDNAs) can sometimes be equivocal, as rDNA intragenomic nucleotide heterogeneity may contribute to problematic phylogenetic reconstructions and lead to ambiguous species recognitions. We explored the extent of rDNA intragenomic variability in the regions of small and large subunits (18S and 28S) from representative species of *Gambierdiscus* and to determine if the variabilities obscure species boundaries. Gene amplification of 18S and 28S rDNA was performed on the genomic DNA extracted from clonal cultures of *Gambierdiscus*, and the nucleotide sequences were obtained via standard cloning and Sanger DNA sequencing. The results revealed high intraspecific and intragenomic polymorphisms in all *Gambierdiscus* species tested, with numerous variants discovered. Molecular dating of *Gambierdiscus* depicted its existence from 90 Ma from the Mesozoic era up to the recent 10 Ma in Cenozoic era. SplitsTree showed five splits, representing the taxonomic species of G. polynesiensis, G. carolinialus, G. scabrosus, G. balechii, and G. belizeanus. The remaining species did not show clear separation, including *G. toxicus-G. pacificus; G. carpenteri, Gambierdiscus* type 2-G. *scabrosus*; and the outgroups *F. yasumotoi-F. ruetzleri*. The SSU rDNA phylogenetic inferences the sequence-structure information generally supported species monophyly, albeit intragenomic polymorphism could give spurious results. Thus, it is crucial to examine as many strains/populations as possible and assess multiple gene markers to avoid misleading inferences for species boundaries in *Gambierdiscus*.

Keywords: Benthic harmful algal bloom, ciguatera fish poisoning, secondary structure

Oral presentation

ADVANCES IN THE DETECTION OF TOXIC ALGAE USING ELECTROCHEMICAL BIOSENSORS

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Harmful algal blooms (HABs) are becoming more frequent as climate changes, with tropical toxic species moving northward. This is especially true for the Iberian Peninsula. Monitoring programs, detecting the presence of toxic algae before they bloom, are of paramount importance to protect aquatic ecosystems, aquaculture, human health and local economies. Rapid and reliable species identification methods using molecular barcodes coupled to biosensor detection tools have received increasing attention over the past decade as an alternative to the legally required but impractical standard microscopic counting-based techniques. Our electrochemical detection system for the determination of toxic algae has been considerably improved moving from the conventional sandwich hybridization protocols using different redox mediators and signaling probes modified with different labels to a novel strategy involving the recognition of heteroduplexes by selective commercial antibodies. Each improvement has meant increased isensitivity, but the most significant (a 100-fold increase in signal) has been produced involving the use of magnetic microbeads and amperometric detection at screen-printed carbon electrodes to detect the target RNA. Although preliminary results with a 16 electrode-LOC will be discussed, our long-term goal is to apply this optimized protocol in a laboratory on a chip (LOC) with up to 200 electrodes for the simultaneous detection of all toxic species. With these improvements, our current system is able to detect as low as 4 cells per liter for some species, by using a fast, simple and cheap methodology that can be integrated in easy-to-use portable systems.

Financing: Eu emery ox

Keywords: Biosensors, electrochemical detection

Oral presentation

PHYTOPLANKTON COMPOSITION AND HARMFUL ALGAL BLOOMS DYNAMICS IN COASTAL WATERS OF CENTRAL-SOUTHERN CHILE (36° - 44°S)

Oscar Espinoza-González[1], Leonardo Guzmán[1], Emma Cascales[1], Héctor Tardón[1], Loreto López[1], Karen Correa[1]

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Harmful Algal Blooms (HABs) occur frequently in the fjords and channels of Southern Chile (55° to 44°S), causing important economic losses and social impact. The 2016 *Alexandrium catenella* bloom on the Chilean coastal waters of the Central-Southern Pacific Ocean (CSPO) constituted a radical change to the paradigm on the distribution of this microalgae (44° to 39°S). This study evaluated the phytoplankton community and the occurrence of HABs species related to coastal environments from 2018 to 2020 in CSPO. Hydrographically we identifying 3 latitudinal transition zones: Biobío (BB), La Araucanía-Los Ríos (AR) and south of the Chacao channel (LL). The diatoms dominating the phytoplankton, during spring the main species were Guinardia *delicatula, Chaetoceros curvisetus*, and *Pseudonitzschia* spp. in BB (58%), AR (33%), and LL (61%), respectively. During summer the abundance was dominated by *Skeletonema* spp. (> 30%). HABs occurred with a high abundance of dinoflagellates during the 2018 summer and 2019 spring when the favorable atmospheric – oceanographic conditions allowed the proliferation of *A. catenella* (>300 cell mL-1) in LL and *Dinophysis acuminata* (>310 cell mL-1) in BB, respectively. While, high abundances of diatoms *Pseudonitzschia cf. pseudodelicatissima* (>285.000 cell mL-1) and *P.* cf. *australis* (>260 cell mL-1) were registered during 2019 spring in AR associated with colder waters, high irradiance, and silicates. Our results indicated that hydrographic events such as upwelling, river discharges, and currents play important roles in the changes in species composition, occurrence, and abundance of HABs in CSPO Chilean coastal waters.

Financing: Red-Tide-Program MINECOM- 2020, Grant MR656137

Keywords: Phytoplankton composition, HABs, Central-Southern Chile

Oral presentation

PLANKTONIC CYANOBACTERIAL BLOOMS IN SOUTH-CENTRAL CHILE: DISTRIBUTION, FREQUENCY AND CONDITIONING FACTORS

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Following the global trend, cyanobacterial blooms in Chile are becoming more frequent, which represents a significant threat to both the use of water resources and the functioning of ecosystems. Knowledge of these events is indispensable for projecting the problems of water use in the country. We studied the phytoplankton community of 41 continental aquatic ecosystems (lotic and lentic) located between 33 - 42°S and determined blooming events when the number of cells exceeded 2,000 cells/ml (alert level 1, for drinking water according to WHO). In some cases, a molecular identification of the species and quantification of microcystins (MC-LR, MC-LA, MC-YR, MC-RR) was carried out. Trophic status and ecosystem use were analyzed in relation to the number of cyanobacterial cells and categorized by WHO alert levels. This information was compared with historical records of

blooms in the country and other countries in the region. More than 110 blooming events were registered, formed by 15 genera, mainly of *Dolichospermum* and *Microcystis*. The Nostocals were the most frequent and widely distributed, mainly *Dolichospermum* with blooms in oligotrophic and eutrophic ecosystems. The environmental conditions in which blooms of the invasive *Raphidiopsis raciborskii*, recently found in lakes in the center of the country, were described. In Chile there are no specific regulations for recreational and drinking water due to the presence of cyanobacteria and cyanotoxins. From the results, it is concluded that cyanobacterial blooms in the country's water bodies represent an emerging environmental problem and a potential health risk for both humans and animals.

Financing: CRHIAM ANID/FONDAP/15130015

Keywords: Cyanobacterial blooms, eutrophic ecosystems, South America

Oral presentation

PREDICTING THE ABUNDANCE OF *PSEUDO-NITZSCHIA CALLIANTHA* (BACILLARIOPHYCEAE) USING RANDOM FOREST TECHNIQUE

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Pseudo-nitzschia is a globally distributed genus in the oceans of our planet. Several species of this genus are associated with the production of domoic acid, a toxin responsible for amnesic shellfish poisoning. As a result, the prediction of the toxic *Pseudo-nitzschia* species abundance is crucial due to economic and ecological impacts related with harmful blooms. Machine learning techniques, which are considered to be important tools to make predictions in different scientific disciplines, have rarely been used in the prediction of harmful algae blooms. In the present study, the abundance of *Pseudo-nitzschia calliantha* species was assessed using a one-year dataset of 216 water samples collected from Kalloni Gulf, Northeast Aegean Sea in Greece, using Random Forest (RF) machine learning technique. The predictive performance of RF (r=0.86) in terms of correlation coefficient between real and predicted values of abundance was significantly higher compared to other classical algorithms, such as multiple linear regression (r=0.52), multilayer perception (r=0.39) and decision trees (r=0.68). Finally, the RF method was used to relate various meteorological, environmental and abiotic factors with the *Pseudo-nitzschia calliantha* species abundance. The analysis gave to rainfall, N to P ratio and SiO2 concentration the key roles to the species abundance. This approach may prove to be useful in predicting abundances of other harmful algae and be part of a general warning system for blooms.

Financing: The research was cofinanced by Greece and EU-ESF Fund through HRDELL 2014-2020 program (project MIS 5047187).

Keywords: Random forest, Harmful algae, *Pseudo-nitzschia calliantha*

Oral presentation

SEASONAL SUCCESSION OF *ALEXANDRIUM* SPECIES IN THE KOREA STRAIT: INSIGHT FROM THE REALIZED NICHE ANALYSIS

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Alexandrium species, the dinoflagellate responsible for producing paralytic shellfish poisoning toxins, are distributed around the world. To assess the impacts of multiple environmental factors and their contribution to niche formation and breadth within species, we investigate their ecological niche dynamics using the Outlying Mean Index analysis (OMI) and additional calculation of Within Outlying Mean Index analysis (WitOMI). Ecologically niche is defined as the total of the adaptation of an organismic unit, meaning the place or environmental conditions where it lives. The dynamics of niche, such as shift and conservatism, depend mainly on the change of environmental conditions. The abundance of A. affine, *A. catenella* and *A. pacificum* was quantified using digital-droplet PCR. In addition, many of environmental variables that affect plankton dynamics or distribution were obtained from KNIFS database and GOA-ON Portal. The stability and velocity of currents at 38 stations in the Korea Strait were analyzed over a period from 2017-2018. Three species have different niches and ecological requirements in the Korea Strait. *A. catenella, A. pacificum and A. affine* occurred sequentially from spring to summer. This result indicates that a high PSP concentration during spring in the southern coastal waters of Korea, which is caused by populations of *A. catenella* and/or *A. pacificum. Furthermore*, we can better understand which factors can cause harmful algal bloom, and where and when it happened.

Keywords: *Alexandrium*, seasonal succession, realized niche

Oral presentation

MODELLING HARMFUL ALGAL BLOOMS IN EASTERN AUSTRALIAN ESTUARIES USING QUANTITATIVE PCR AND MOLECULAR BARCODING

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In south-eastern Australia, marine harmful algal blooms (HABs) leading to the uptake of toxins in shellfish above the regulatory limits are occurring with increasing regularity. To investigate and model factors impacting HAB development in southern Australian estuaries, and separately, to

provide an early warning system that can be used on site by shellfish farmers, we have developed quantitative PCR assays for functional and barcoding gene regions of paralytic shellfish toxin-producing species of *Alexandrium* and the saxitoxin related gene sxtA, *Prorocentrum minimum*, a common estuarine dinoflagellate associated with eutrophication, and the diatom *Pseudo-nitzschia cuspidata*, the source of amnesic shellfish toxins in farmed oysters in New South Wales, Australia. We have collected weekly, long term datasets of estuarine water using environmental DNA methods in oyster-producing estuaries and a mussel farm, and applied assays to investigate the abundance of certain HAB species over time and in relation to environmental variables. We compared results of qPCR quantification assays to information collected from other sources: light microscopy-based counting, toxin detection using LC-MS/MS and molecular barcoding, based on the detection of the V4 region of the 18S rRNA gene.

Financing: We thank the Food Agility CRC, the Australian Research Council, and the University of Technology Sydney

Keywords: *Alexandrium pacificum*, *Pseudo-nitzschia* spp

Oral presentation

INFLUENCE OF NITROGEN ON BLOOM-FORMING CYANOBACTERIA SPECIES COMPOSITION AND NUTRIENT STOICHIOMETRY IN A MESOTROPHIC LAKE

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Harmful algal blooms (HABs) are a global water quality concern in freshwater lakes associated with ecosystem degradation and toxicity events. Water quality monitoring of lakes in the New York City metropolitan area suggests that nitrogen supply may have a critical role in cyanobacteria bloom formation and species composition. We conducted large-scale outdoor mesocosms at Fordham University - Louis Calder Center's Experimental Lake Facility testing forms and concentrations of nitrogen in 24, (5400 L) tanks containing mesotrophic lake water. Replicated mesocosms were supplied with surplus phosphorus and amended with different forms (nitrate, ammonium nitrate, urea) and concentrations (+15 uM, +50 uM N) of nitrogen in a factorial design. We collected samples weekly for dissolved nutrients, particulate C:N:P, pigments (chl-a, phycocyanin), and taxonomic diversity. Cyanobacteria blooms dominated by *Aphanizomenon flos-aquae* were observed in all +N treatments. Chl-a concentrations in +P-only treatments did not differ significantly from controls, suggesting that productivity was not limited by P alone. Particulate N:P ratios in +urea and +NH4NO3 experiments increased significantly, but decreased in the nitrate-treatments, suggesting a strong preference for incorporation of urea and ammonium. Nitrate uptake was significantly reduced in experiments replete with ammonium. Our results highlight the importance of N in the development of cyanobacteria blooms, and that management strategies to mitigate HABs should include efforts to reduce N loading concurrently with reduction of P loads.

Keywords: Nitrogen, Cyanobacteria, eutrophication

Oral presentation

GENETIC DIVERSITY AND TOXIN PRODUCTION OF *PSEUDO-NITZSCHIA* ISOLATES FROM AOTEAROA/ NEW ZEALAND COASTAL WATERS

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Almost half of the species belonging to the planktonic diatom genus *Pseudo-nitzschia* are known to produce neurotoxins, domoic acid (DA) and its isomers. DA causes amnesic shellfish poisoning (ASP) and it is therefore important to investigate the species diversity and toxin production of those species for ASP risk assessments. Between 2018 and 2020, seawater samples were collected at 21 sites in Aotearoa/New Zealand (subtropical and temperate zones, 0–15 m depths), and 99 clonal isolates of Pseudo-nitzschia were established. Molecular phylogenetic analysis of the large-subunit rDNA D1–D3 and/or internal transcribed spacer 1-5.8S rDNA-ITS 2 regions revealed that the isolates were separated into 14 species (*P. americana, P. arenysensis, P. australis, P. calliantha, P. cuspidata, P. delicatissima, P. fraudulenta, P. galaxiae, P. hasleana, P. heimii/P. subpacifica, P. multiseries, P. multistriata, P. plurisecta, and P. pungens*). Furthermore, the strains of *P. delicatissima* were separated into two subclades (subclades I and II). Domoic acid (and isomer) production was assessed by liquid chromatography-tandem mass spectrometry analysis for a representative 38 strains of the 14 species isolated. The analyses revealed that two of the 14 species (*P. australis* and *P. multiseries*) produced DA and isodomoic acids A, B, C/c5'-epidomoic acid, D, and/or E. The DA contents of *P. multiseries* strains (1.65–7.20 pg/cell) tended to be higher than those of P. australis strains (0.04–0.73 pg/cell). This study is the first distribution record of *P. arenysensis, P. delicatissima subclade II, P. galaxiae, P. hasleana*, and *P. plurisecta* in New Zealand.

Keywords: Domoic acid, New Zealand, *Pseudo-nitzschia*

Oral presentation

AN UNUSUAL RED TIDE AND TOXIC EPISODE DUE TO *ALEXANDRIUM MINUTUM* IN RÍA DE VIGO AND PONTEVEDRA IN 2018

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In 2018 an unusually intense red tide of the common dinoflagellate *Alexandrium minutum*, cyst-forming producer of paralyzing toxins, provoked social alarm and closure of bivalve production in the Rias of Vigo and Pontevedra because saxitoxin exceeded the legal limit. INTECMAR monitors marine environmental quality and enforces sanitary standards of marine products in Galicia (NW Spain). Since 1992, weekly analysis of bivalve and infaunal molluscs are carried out. When the concentrations of PSP toxins in the molluscs exceed 800 μg equiv. STX/kg, mollusk extraction in the affected zone is prohibited. INTECMAR also monitors weekly salinity and temperature data and phytoplankton at 42 marine and 16 coastal sites. The seawater is analyzed directly and fixed with formaldehyde for species identification. Quantification is done by the Utermöhl method on 25 mL samples fixed with lugol. The taxonomy of *Alexandrium minutum* were confirmed by plate staining with calcofluor, scanning electron microscope and microarrays. The cells, with the posterior sulcal plate wider than long and its pore characteristic of 1', and temporal cysts were observed. In the 2018 outbreak, maximum cellular concentrations reached 1.5 and 0.8 .106 cells L-1 in July at two sites near urban wastewater treatment plants. The maximum coincided with surface temperatures >20ºC, low tide, and upwelling relaxation (upwelling Index < 500). Oceanographic analysis, including satellite observation, revealed the red tides originated in the bay of Baiona and later extended throughout the Ria de Vigo and into the Ria de Pontevedra. Maximum saxitoxin levels found were 5000 μgSTXKg-1 in mussels from Baiona.

Financing: Consellería do Mar. Xunta de Galicia

Keywords: *Alexandrium minutum*, Paralytic Shellfish Poison, red tide

Oral presentation

ALEXANDRIUM OSTENFELDII IN A SHALLOW BAY IN THE SOUTHERN COAST OF PERU: BLOOMS AND PARALYTIC SHELLFISH TOXINS IN SCALLOPS

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Abundances of *Alexandrium ostenfeldii* and *Alexandrium* spp. were followed in Paracas Bay, in which the *Argopecten purpuratus* commercial culture traditionally developed. In the present work, we report blooms of these species, paralytic shellfish toxin (PST) concentrations and some environmental variables. Data from 2003-2018 were obtained from monitoring programs developed by Organismo Nacional de Sanidad Pesquera (SANIPES) and by Instituto del Mar del Peru (IMARPE). A divisible hose sampler and a bucket (10L) were used for seawater sample collection. *Alexandrium* species counting was performed according Utermöhl method or using a Sedgwick-Rafter Cell. PSTs were analyzed using mouse bioassay method. Environmental variables analyzed were: sea surface temperature (SST), wind-driven upwelling index, and river flows. Between 2003 and 2018, a total of twelve algal blooms were associated to *Alexandrium* species with abundances of 1.1x105 –3.1x107 cells l-1. Most events were caused by *A. ostenfeldii*. PSTs exceed the maximum permissible level (800 μg STX eq kg-1) in 2017 and 2018 samples. In 2017, PSTs and *A. ostenfeldii* abundances were significantly correlated. In 2018, the highest levels of PST were detected after abundances of ~20x103 cells l-1. Blooms were recorded during summer and fall months, at periods with the highest SST and river flows and the lowest upwelling index values. The results demonstrate that phytoplankton monitoring is an adequate measure for the early detection of harmful algal blooms in Paracas Bay. SANIPES plans to implement PST analysis through liquid chromatography with fluorescence detection and experimental studies with *Alexandrium* cultures will be conducted in future studies.

Financing: Proyecto Concytec - Banco Mundial, a través de su unidad ejecutora el Fondecyt

Keywords: Harmful algal blooms (HABs), aquaculture, food safety.

Oral presentation

SPATIAL AND TEMPORAL PATTERNS OF HARMFUL SPECIES OF *ALEXANDRIUM, DINOPHYSIS* AND *PROTOCERATIUM* THROUGHOUT CHILEAN FJORDS IN A 12-YEARS PERIOD

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Chilean fjords are a heterogenous geographic area ranging from 41° to 55° S.L. where small scale fisheries and salmon and mussel aquaculture are developed. The area is affected by a variety of species causing harmful algal blooms, being *Alexandrium catenella, A. ostenfeldii, Dinophysis acuminata, D. acuta* and *Protoceratium reticulatum* five dinoflagellate species associated to different hydrophilic and lipophylic toxins, causing varying and intense effects to social and economic sectors. A time series on the abundances and environmental data such as sea water temperature and salinity from October 2007 to February 2019, obtained monthly from 147 sampling sites distributed along the Chilean fjords are analyzed. The distribution and abundance patterns through time and space of these species in association with environmental variables are shown. Excluding *A. ostenfeldii*, the other species showed the same tendencies in their abundances, reflecting similarities during seasonal periods and specific geographical sectors, independently that environmental factors can generate declinations in abundance with latitude, specific variations in localized sectors and differential use of the habitat by these species. The relative abundances of the five taxa of *Alexandrium, Dinophysis* and *Protoceratium* showed a clear environmental change of great geographical coverage, splitting a period with lower abundance of these microalga between 2007 and 2011, of other, of greater abundance, defined between 2012 and 2018, with a transitional period defined by the Autumn and Winter of 2012. Results are analyzed considering sea water temperature and salinity along the studied area.

Financing: Ministerio de Economía, Fomento y Turismo MINECON 656-129

Keywords: Harmful-species, Chile, fjords

E-Poster

CIGUATERA FISH POISONING RISK FOR AOTEAROA/NEW ZEALAND: EFFECTS OF TEMPERATURE AND MACROALGAL HABITAT ON GAMBIERDISCUS SUCCESS

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The risk of ciguatera fish poisoning occurring in Aotearoa/New Zealand is increasing as the temperature of coastal waters continues to rise. The causative organism is the epiphytic dinoflagellate *Gambierdiscus* and recent research has highlighted that temperature is more critical for proliferation than a specific macroalgae substrate. For example, in Japanese temperate waters, a significant correlation has been found between *Gambierdiscus* cell densities and seawater temperatures, with no macroalgae preference evident. Some *Gambierdiscus* species are also becoming acclimated to temperate waters, further compounding the risk to New Zealand. *Gambierdiscus* has now been isolated from many different macroalgal species across the Pacific region, including rhodophytes, chlorophytes and phaeophytes. It has been recorded, although only once, in New Zealand's northern waters, attached to *Sargassum* sp. and several *Gambierdiscus* species have been isolated from macroalgae in Rangitāhua/Kermadec Islands, a New Zealand territory 1000 km to the northeast. Comparisons of macroalgal habitat are made between Japan, the Federated States of Micronesia, the Cook Islands, New Zealand, and Rangitāhua/Kermadec Islands and are presented here.

Financing: MBIE

Keywords: Harmful algal blooms, dinoflagellate

E-Poster

PROROCENTRUM LIMA FROM SOUTHERN TUNISIA: MORPHOLOGICAL, MOLECULAR AND TOXICOLOGICAL CHARACTERIZATION

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Prorocentrum lima was isolated from the Gulf of Gabès coasts, Tunisia, Southeastern Mediterranean and seventeen clonal cultures were established. Morphological and molecular characterization as well as toxicity analyses were carried out. Morphological descriptions of P. lima strains (Pl.1-Pl.17) using light, epifluorescence and scanning electron microscopy revealed that cells were oblong-to-ovate in shape, broad in the middle region, and narrow at the anterior end. The periflagellar area was triangular, set into a V-shaped depression and was composed of eight periflagellar platelets of different sizes. The morphology fits well the characterization of the species isolated from elsewhere. Sequence analysis of the internal transcribed spacer region (ITS- 5.8S rDNA) and the D1/D3 region of the large subunit (LSU rDNA) confirmed the morphological identification of P. lima strains. The results regarding the mouse bioassay revealed that P. lima strains Pl.1 and Pl.16 were toxic to mice after i.p. injection. Characteristic symptoms of DSP were observed in all the mice tested and kept 24 h under observation. Extracts of Pl.1 and Pl.16 strains with respective amounts of injected cells of 2.3 × 107and 3.4 × 107 resulted in the death of all the three mice tested after 14 to 20 min and 10 to 15 min, respectively. Toxin analysis of the culture extract, using liquid chromatography mass spectrometry showed that the toxic profile was dominated by OA. The estimated amount of OA was 29.03 and 21.65 pg cell-1 for strains Pl.1 and Pl.16, respectively.

Keywords: Toxic benthic dinoflagellate; morphology; ITS; LSU rDNA; Mouse bioassay; LC-MS; Mediterranean Sea.

E-Poster

GROWTH OF BLOOM-FORMING CYANOBACTERIA UNDER DIFFERENT FORMS OF NITROGEN IN SUMMER AND AUTUMN

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Cyanobacteria Harmful Algal blooms (cHABs) are not novel phenomena, however cHABs continue to threaten the stability of freshwater habitats with increasing frequency. Our project aimed to understand how the growth of bloom-forming cyanobacteria species (*Aphanizomenon flos-aquae, Microcystis* sp., *Planktothrix agardhii)* respond to different N compounds in P-rich conditions in summer and autumn. We manipulated phytoplankton communities in 4L microcosms using whole lake water collected in mid-summer (July) and autumn (November). We tested the effects of added nitrate, ammonium, and urea as specific N-sources on ambient and supplemented algal species. Growth of the summer assemblage, which was amended with *Microcystis* sp., was enhanced by ammonium addition to a greater degree than by added nitrate. An ambient population of *Aphanizomenon flos-aquae* proliferated with and without supplemental N. We also present evidence based on short-term changes in nutrient concentration and particulate C:N:P, that N and P uptake differ largely in response to N treatments alone. The autumn assemblage supplemented with *Planktothrix agardhii* exhibited lesser growth, and was more sensitive to P addition, which may be attributed to autumn turnover in the lake. Overall, N was the key trigger for algal growth during summer, in which different N affinities influenced the growth and composition of the summer assemblage, dominated by cyanobacteria. Our results suggest that different N compounds may influence the magnitude of eutrophication, particularly under P-surplus conditions. Results of our study also suggest that management of cHABs requires mitigation of both P and N inputs year round.

Keywords: Cyanobacteria, Harmful Algal Blooms, nitrogen

E-Poster

FIRST RECORD OF *GLOCHIDINIUM PENARDIFORME* FOR THE NORTHEAST COAST OF BRAZIL

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Glochidinium penardiforme is a species of dinoflagellate with an occurrence previously recorded only for the northern, southeastern and southern of Brazil. We aimed to report the first occurrence of *G. penardiforme* to the northeast coast of Brazil and the environmental conditions where this species was registered, from bi-monthly collections (March 2018 to March 2019) in 12 sampling points, where *in-situ* measurements, salinity and water transparency, in addition to water samples collected for analysis of dissolved inorganic nutrients. Water samples collected using plankton net (20 µm) for analysis of species composition. *G. penadirforme* was recorded in two zones of the Paraguaçu River estuary, in two months: in the Lower River Course (LRC) in July/2018 with values of salinity 1.2, water transparency of 0.4m, nitrite 1.5mM, nitrate 11.4mM, phosphate 1.8mM, ammonia 3.3mM and silicate 31.3mM, in January/2019 in the same zone with means of salinity 17.7, water transparency of 1.4m, nitrite 0.1mM, phosphate 0.3mM, ammonia 2.2mM and silicate 8.6mM, and yet for the Iguape Bay (IB), with values of salinity 28.6, water transparency of 1.7m, nitrite 0.3mM, phosphate 0.1mM, ammonia 2.5mM and silicate 7.0mM. Although it is cited as a typically freshwater species, we recorded *G. penadirforme* in brackish environments, showing that the species can withstand wide salinity variations. This species had been registered only for the states of Amazonas, Rio de Janeiro and Rio Grande do Sul, so this is the first record of *G. penadirforme* on the northeast coast of Brazil, state of Bahia, in the Paraguaçu River Estuary.

Financing: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES), finance code 001

Keywords: Dinoflagellate, distribution, estuary

E-Poster

ON TWO POPULATIONS OF *STYLODINIUM LITTORALE* (DINOPHYCEAE) FROM WIDELY DIFFERENT AREAS IN EUROPE

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The predominantly coccoid dinoflagellate *Stylodinium littorale* was described in 1983 from sandy bottom in the seashores of Japan and the Phillipines. Cells of this species attach to sand grains through a stalk produced by the apical complex of a briefly motile stage. The coccoid stage is surrounded by a wall that underlies the amphiesma. Plates are visible in the amphiesma of both motile and attached cells. The species was recorded also from Southern Australia, Canada and South Africa, but had not been reported from Europe. We found one population in the sandy intertidal sediment near Vista Alegre, in the Aveiro Coastal Lagoon (Ria de Aveiro), Portugal, in February 2016, at a salinity of 17 psu. A second population was found in Nivå bay, Sealand, Denmark, in August 2016, where it was collected from sandy bottom in knee-deep water with about 20 psu. The tabulation of both populations matched the one described from the Japanese strains. Coccoid cells of the European strains released motile cells through an opening that involved the antapical plate and precingulars 3 and 4; SEM observations of these open thecae did not show traces of an underlying wall. Detailed observations of the sulcus revealed a flap-like right sulcal plate. Comparisons of ribosomal operon DNA sequences suggest that the two European populations are not the result of a recent introduction.

Keywords: Coccoid dinoflagellates, DNA sequence comparisons, tabulation

E-Poster

LATITUDINAL VARIATION IN TOXICITY AND SEXUAL COMPATIBILITY OF *ALEXANDRIUM CATENELLA* STRAINS FROM SOUTHERN CHILE

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Harmful algal blooms of the toxic dinoflagellate *Alexandrium catenella* are the main episodes responsible for Paralytic Shellfish Poisoning (PSP) in Southern Chile (39.5-55°S). This large geographical area has been affected by intense PSP outbreaks (world record in toxicity levels) since their first detection 50 years ago. Considering, *Alexandrium* complex life history that involves the formation of benthic resting cysts, we selected nine strains of *A. catenella* isolated from the three southernmost regions of Chile (Los Lagos, Aysén, Magallanes). Thus, we conducted self and out-crosses in all possible combinations (n=45) and we assessed the effect of geographical distances in: i) toxin profiles of parental strains; ii) reproductive success indexes, and iii) resting cysts production. The toxin profiles were similar for all strains and characterized by C1, C2, GTX4, GTX1, GTX3, and NeoSTX. Nonetheless, both the analogs proportion (%) and the toxins (pg cell-1) presented variation according to strain geographical origin being more toxic strains located at the north (Bahía Mansa ~40.6°S). The highest reproductive success was found in Aysén strains (~45.5°S) followed by Magallanes (~54.9°S) and Bahía Mansa (40.6°S). Neither self-crossed were compatible indicating no evidence of homothallic behavior. Compatible pairings distanced between 1000-1650 km displayed the highest median of resting cysts abundance indicating a strong geographical distance effect. Our results contribute to the understanding of the intensity of PSP outbreaks in the austral region and enhance the importance of the resting cysts to fuel new HAB events.

Keywords: Saxitoxins, mating systems, resting cysts

E-Poster

SMALL-SCALE DISTRIBUTION OF LIPOPHILIC TOXIN-PRODUCERS *DINOPHYSIS ACUMINATA* AND *D. ACUTA* IN TWO STRATIFIED FJORD SYSTEMS

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Dinophysis acuminata and *D. acuta* are the main lipophilic toxin-producers in the highly stratified Chilean fjords system. During late Austral summer 2020, blooms of Dinophysis with a strong dominance of *D. acuminata* provided a unique opportunity to identify the optimal environmental conditions selecting this species versus *D. acuta*. High-resolution measurement of physical properties was carried out at a fixed station during two intensives 24h cruises to monitor: i) cell-cycle stages and estimate *in situ* growth of *D. acuminata*; ii) circadian distribution of its potential ciliate Mesodinium prey. These cruises were carried out in two neighbouring fjords, Puyuhuapi and Pitipalena, with distinct hydrodynamic conditions, during mid- (February 18-19) and late-summer (March 18-19), respectively. The comparative approach illustrated important differences in water column structure and *D. acuminata* distribution between the two fjords. High *D. acuminata* cell densities (>3 x 103 cells L-1, from 4 to 6 m) were found in Puyuhuapi Fjord associated with a warmer (14.5-15ºC) sub-surface (2-6 m) water layer. In contrast, cell densities in Pitipalena Fjord didn't exceed 1.5 x 103 cells L-1, and the cell maxima was associated with colder (13.4–14.0°C) surface (0-4 m) waters. *Dinophysis acuminata in situ* division rates were higher in Puyuhuapi (μ= 0.34 d-1) than in Pitipalena (μ= 0.22 d-1). Mesodinium prey was present in the two fjords, suggesting *D. acuminata* was not food-limited. This study highlights the importance of high spatio-temporal resolution measurements of physical properties and in situ division rates to gain knowledge on the species response to changing environmental conditions.

Keywords: Physical-biological interactions, lipophilic toxins, Chilean fjords

E-Poster

TOWARDS SATELLITE IDENTIFICATION OF ALGAL BLOOMS AND PHYTOPLANKTON GROUPS IN THE NORTHERN HUMBOLDT CURRENT ECOSYSTEM

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The Northern Humboldt Current Ecosystem (NHCE) hosts one of the most important coastal upwelling areas in the world, sustaining a high rate of primary productivity. The PHYSAT algorithm, developed for major phytoplankton groups detection, has not been yet specifically tested for the NHCE. For this purpose, it is essential to identify and analyze the spectral signatures of the main phytoplankton groups and their Spatio-temporal variability. First, an exploration of the algal blooms occurrence was carried out using chlorophyll-a satellite data from 2002 to the present, based on the MODIS sensor Level-4 data set. We simultaneously used the in-situ database of the Instituto del Mar del Perú (IMARPE) that extensively determines phytoplanktonic taxa in the region from repeated oceanographic cruises. Spectral signatures, from MODIS sensor Level-3 reflectance data, were then analyzed at concomitant *in-situ* determinations and generally dominated by a single phytoplankton group. The most intense blooms occurred from Chicama (5°S) to Pisco (15°S) within 5 km off the coast, with the highest frequencies recorded near upwelling areas. Diatom was the dominant phytoplankton group in the NHCE, and its spectral signature is significantly modified by the presence of other phytoplankton groups during contrasted environmental conditions (e.g. El Niño and La Niña). These results will contribute to the adaptation of a regional PHYSAT algorithm for the automatic identification of phytoplanktonic groups in the NHCE, and ultimately to contribute to an early warning system for Harmful Algal Blooms (HAB) occurrence.

Keywords: Algal blooms, remote sensing, upwelling

E-Poster

CYANOBACTERIA COMMUNITY COMPOSITION AND DIVERSITY AMONG LAKES FROM FORESTED WATERSHEDS UTILIZED AS DRINKING WATER SOURCES IN TWO MARITIME ECOZONES

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Forested watersheds naturally provide high quality drinking water to communities but are threatened by climate change induced disturbances such as wildfires and hurricanes, leading to anthropogenic input of nutrients and increase in water temperatures. This can result in the proliferation of cyanobacteria which may threaten water quality through the production of toxins plus taste and odour (T&O) compounds. Hence, it is important to detect the presence of harmful cyanobacteria before an event that could impact water quality arises. In this study, water samples from 2019 were collected once a month in May and September from the Comox Lake watershed (British Columbia, Canada), July and August from the Leech River and Sooke Lake watersheds (British Columbia, Canada), and in June, August, September and October from the Pockwock Lake watershed (Nova Scotia, Canada) to observe the composition and relative abundance of cyanobacteria. To achieve this, microbial DNA was extracted from water samples for 16S rRNA gene sequencing and assigned taxonomy in QIIME2 using a SILVA classifier and resulting cyanobacteria ASVs were analyzed using the R package *mirlyn*. Lakes within the same watershed typically contained similar communities, however monthly variations in diversity were observed for some lakes while others were more consistent. Despite this, community composition was relatively unique among watersheds. Collectively, most cyanobacteria ASVs resolved to the genus/species-level were assigned to *Cyanobium* (51%) or *Rhabdogloea smithii* (42%). Due to the high occurrence of these sequences, the potential for toxin and T&O production by these genera should be the focus of future studies.

Keywords: Cyanobacteria, diversity, drinking water

SYM13: Ocean Global Change: acclimation and adaptation to multiple environmental drivers

Keynote lecture

FUTURE PROOFING KELP FORESTS

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

Keywords: Kelp, genomics, climate change

Keynote lecture

UNDERSTANDING THE CAUSES AND CONSEQUENCES OF THE SHAPE OF DRIVER INTERACTIONS

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The response of organisms and populations to environmental drivers - such as temperature, nutrients and light - is highly nonlinear. We have a moderately good understanding of these responses for single drivers. However, the state of our knowledge of how drivers interact to influence biological processes (such as growth) remains rudimentary at best. Without equations that characterise the effects of driver interactions accurately, and sufficient mechanistic understanding or data to develop these equations, our ability to predict performance in natural environments will remain weak. I will discuss recent empirical and theoretical efforts to understand how temperature, nutrients and light interact to influence algal population growth. Models of these interactions raise several novel, testable hypotheses, including that the optimum temperature for growth declines strongly at low nutrient conditions as well as at low and high light levels – all of which are supported by experimental and observational data. Having empirically-validated models of driver interactions can help us link physiology with population and community dynamics, and identify trade-offs that constrain performance and shape competitive outcomes. This will improve our ability to accurately model growth and competition in dynamic natural environments and to predict the ecological and evolutionary consequences of environmental change.

Keywords: Interactions, modelling, growth rate

Keynote lecture

ENVIRONMENTAL GRADIENTS INFLUENCE ECO-EVOLUTIONARY DYNAMICS OF SEAWEEDS AND THEIR RESILIENCE TO CLIMATE CHANGE

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Seaweeds are characterized by a global pattern of latitudinal diversity in which species richness increases from the tropics to the poles. Across this latitudinal gradient, the abundance, growth, and reproduction of many species are highly variable in time, with strong seasonal changes that are influenced by water temperature, nutrient availability and day length, particularly in temperate regions. The different regimes of environmental conditions experienced from the tropics to poles, influence local adaptation and differential capacities of species and populations to cope with environmental stress and climate change. These factors are of paramount importance as anthropogenic pressures, increasing ocean temperatures and extreme events, have threatened the ecological integrity of several seaweed species, contributing to significant range shifts and local extinctions of their natural populations. Tropical and polar seaweeds are predicted to be particularly sensitive to the effects of climate change because they are considered more narrowly endemic in both geographic and climatic space. Additionally, their thermal limits are near to the current maximum temperature they experience, posing some important constraints in the face of warming oceans. In contrast, temperate seaweeds are expected to be more resilient/tolerant to these changes due to their greater physiological plasticity that results from the broader range of seasonal temperatures that they experience compared to tropical or polar species. In this presentation, through the integration of comparative physiology, transcriptomics and metagenomics, I will provide evidences regarding the role of latitudinal gradients shaping different ecological and evolutionary responses of seaweeds around the globe.

Financing: JDGE was supported by the Research Grants Council (ECS 27124318) of Hong Kong.

Keywords: Local adaptation, phenotypic plasticity, climate change

Oral presentation

EFFECTS OF PH/CO2, TEMPERATURE AND LIGHT ON THE EARLY DEVELOPMENT, GROWTH AND CARBON METABOLISM ON GAMETOPHYTES OF *MACROCYSTIS PYRIFERA*

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The absorption of CO2 by the oceans is causing a reduction in pH in 0.3-0.4 units is expected by the year 2100, process known as ocean acidification (OA). This impacts the marine ecosystem in a complex way. There is a growing interest in knowing the functioning of Ci uptake mechanisms (CCMs) in species such as *Macrocystis pyrifera* who play a fundamental role as a primary producer. The CCMs in macroscopic stages might vary from the mechanisms present in microscopic stages such as gametophytes. Studies predict that early stages of macroalgae are vulnerable to OA and are critical for population survival. This study evaluated the effect of pH, light and temperature on the *M. pyrifera* gametophytes. The methodology included: analysis of physiological variables (growth, photosynthesis, pigments concentration) and activity of the carbonic anhydrase (CA). Our results show that pH, light and temperature have a significant effect on *M. pyrifera* gametophytes. A decrease in pH was beneficial because growth, pigments and (Fv/Fm) increased. However, the reproductive success decreased at reduced pH. Sex ratio and photosynthesis were not affected. Also, *M. pyrifera* gametophytes use a different CCM (external dehydration of HCO3-

to CO2 by CA) than that described for sporophytes. A second CCM was detected at low pH and high temperature (direct uptake of HCO3- by AE). This study confirmed the importance of studying different environmental drivers and including different stages of the life cycle of this species. This may provide important clues to how this species might cope with adverse environmental conditions.

Keywords: Acidification, *Macrocystis*, carbonic anhydrase

Oral presentation

INORGANIC NITROGEN SOURCES INFLUENCE THE THERMAL PHYSIOLOGY OF EARLY LIFE STAGES IN THE GIANT KELP *MACROCYSTIS PYRIFERA*

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Abrupt changes in environmental temperatures can trigger physiological and biochemical modifications in seaweeds. However, these responses are individually determined by the thermal sensitivities and tolerances (i.e. thermal plasticity) of each organism. Moreover, in some seaweeds, for example habitat-forming kelp, these responses are also influenced by the interaction with other environmental drivers (nitrogen) and can vary across life stages. This study examined whether alternative inorganic N sources can differentially affect the thermal tolerance of early life stages in the giant kelp *Macrocystis pyrifera*. To do this, microscopic life stages (spores to gametophytes) of *Macrocystis* from Tasmania (45°47'S, 170°43'E), were incubated under two inorganic N sources (nitrate - NO3- and ammonium - NH4+) under a range of 12 temperatures (6-27°C) for 15 days. The influence of temperature on physiological performance of *Macrocystis* early life stages was assessed through non-linear thermal performance curves (TPCs), whereas changes in the curves were proxies of the influence of N on thermal plasticity. We found that NO3-, rather than NH4+, enhanced growth in gametophytes of *Macrocystis* at temperatures of 14.5-21.0°C, and their thermal tolerance. Meiospore germination had a narrower temperature window compared to other early developmental stages and physiological traits, suggesting that meiospore might be more susceptible to abrupt changes in temperatures than other life stages (gametophytes, sporophytes and adults). Our results suggest that although NO3- can modulate the thermal plasticity of early life stages in *Macrocystis*, the transition from meiospore to gametophytes can be negatively impacted by ocean warming, which might lead to mortality and cause severe population declines.

Financing: REDES 180023

Keywords: Kelp, ocean warming, thermal plasticity

Oral presentation

EXPLORING THE PLASTIC AND EVOLUTIONARY POTENTIAL OF MARINE DIATOMS IN TRAIT SPACE

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Phytoplankton are typically characterized by a range of functional traits. Taken together these traits form the multidimensional phytoplankton trait space. Evolutionary experiments indicate that correlations between those traits beyond well-established trade-offs strongly limit evolution in trait space. Here, we explore how constrained plastic and evolutionary movement in trait space for marine diatoms is using experimental evolution. For this purpose, we first dampened the action of natural selection through a series of bottlenecks, leading populations into fitness valleys in trait space. Secondly, we let selection act again allowing populations to recover from bottlenecking and reach higher fitness again. This back-selection was performed in a control and a high temperature regime. Both high and low fitness phenotypes, as well as plastic responses to high temperature were determined including multiple functional traits such as cell size, growth rate and carbon content. To evaluate the plastic and evolutionary potential of marine diatoms including multiple functional traits, the trait space was collapsed to its main axes of trait change using principal component analysis. Our study reveals similarities and differences between plastic and evolutionary responses and provides the base for integrating multi-trait plasticity and evolution into modelling frameworks.

Financing: The research project was funded by the Gordon and Betty Moore foundation, grant GBMF#7397.

Keywords: Trait space, plasticity, evolution

Oral presentation

IMPACTS OF COMBINED TEMPERATURE AND SALINITY STRESS ON THE ENDEMIC ARCTIC BROWN SEAWEED *LAMINARIA SOLIDUNGULA*

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Polar regions are facing rapid temperature increase. Consequent glacier and sea ice melting, and enhanced terrestrial run-off can result in hyposaline conditions in stratified fjord systems. Combined, these factors might have a strong impact on primary producers. The endemic kelp *Laminaria solidungula* is one important foundation species in Arctic ecosystems. It might be particularly imperiled by temperature increase and become locally extinct from Arctic fjord systems in the future. We conducted a multiple-stressor experiment at four temperatures (0, 5, 10, 15°C) and two salinities (SA 25, 35) to investigate the combined effects of increasing temperatures and decreasing salinities on the physiological and biochemical status of young *L. solidungula* sporophytes. Therefore, the maximum quantum yield (Fv/Fm), mannitol, and C:N ratio were analyzed. Both stressors had significant and interacting impacts, either in an additive or antagonistic way, dependent on the respective response variable. Fv/Fm significantly declined with temperature increase and low salinity. The storage product mannitol acts as a compatible solute and decreased at SA 25. Whereas its concentration at SA 35 was steady between 0 and 10°C, the 15°C treatment resulted in a significant decrease. The C:N ratio was strongly affected by temperature increase, mainly due to reduced nitrogen uptake, while SA 25 supported the nitrogen uptake, resulting in an attenuation of the effect. Our results showed *L. solidungula* to be very susceptible to both factors of climate change and their ecological consequences, especially when drivers are combined.

Keywords: Kelp, physiology, biochemistry

Oral presentation

DISTRIBUTIONS OF CORALLINE ALGAE ALONG A SALINITY AND DEPTH GRADIENT IN A PATAGONIAN FJORD

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Crustose coralline algae (CCA) are susceptible to global change and ocean acidification through changes in seawater carbonate chemistry due to their calcium carbonate cellular structure. In southern Chilean fjords, rainwater and ice melt create a freshwater lens overtop of a marine layer and due to a lack of vertical mixing, these areas remain stratified much of the year. Stratification creates different salinity and carbonate chemistry regimes in the surface and deeper waters. Observations of CCA absence at shallower depths (0-5 m) on the walls of the Comau Fjord and presence at deeper depths (~ 33% cover) lead to questions using field and laboratory analyses to ascertain the effects of freshwater input on CCA distributions within the fjord. Cobbles with *Lithothamnion glaciale* and other CCA crusts were transplanted from 20 m to 5 m for 9 months to compare pigmentation and physiology of control and transplanted specimens. Transplant experiments revealed tolerance to the surface water conditions in *L. glaciale*, but near mortality of other CCA species (22% vs. 65% of pigmented areas lost respectively). Water samples taken from 0-20 m in austral autumn and summer and calculated Ωarag levels highlighted stratification within the fjord. While autumn Ωarag levels did not fall below equilibrium at any depth, summer samples were below equilibrium in the surface waters (0.20) creating conditions that negatively affect CCA physiology and their distribution within the Comau Fjord. These results inform us how distributions may vary with global climate change and reduced ocean Ωarag levels.

Keywords: Coralline algae, physiology, salinity

Oral presentation

DIFFERENTIAL CARBON ACQUISITION, PARTITIONING AND RELEASE BETWEEN CORALLINE ALGAE THAT EVOLVED TO OCCUPY DISTINCT LIGHT ENVIRONMENTS: STRATEGIES IN THE ANTHROPOCENE

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Crustose coralline algae (CCA) are active participants in the carbon cycle of reefs worldwide. However, mechanisms underpinning the flux of carbon into (acquisition), within (partitioning via photosynthesis and calcification) and out (DOC release) of the thalli of reef-building CCA is largely unknown. With the carbonate chemistry and temperature of seawater changing at rapid rates, the quantification of these patterns would provide an essential tool for understanding the underlying physiological strategies and responses to environmental change in CCA. We quantified carbon acquisition, partitioning, and release in two high-light (*Porolithon* cf. *onkodes* and *Lithophyllum* cf. *insipidum*) and low-light (*Lithothamnion proliferum* and *Sporolithon* cf. *durum*) species of CCA under ambient and elevated (IPCC RCP 8.5) levels of pCO2 and temperature. We found distinct ambient acquisition, partitioning, and release strategies between high- and low-light reef-builders. When faced with global stressors, there was an association in high-light CCA between decreased surficial carbon retention, increased DOC release, and failure to increase bicarbonate uptake for photosynthesis. In low-light CCA, there was an association between maintained or even increased carbon retention, reversal of DOC release (i.e. uptake, likely involving surface microbes), and increased bicarbonate uptake. Our results suggest that the surficial carbon metabolism of CCA occupying low-light reef environments is more robust than that of high-light reef-builders amidst OA and warming.

Financing: Australian Research Council Discovery: DP160103071, School of Environment and Science, Griffith

University: postgraduate support, and Australian Rivers Institute

Keywords: Carbon partitioning, DOC release, crustose coralline algae

Oral presentation

SEASONALITY AFFECTS SPORE CHARACTERISTICS AND THERMAL PERFORMANCE IN THE BROWN SEAWEED *DICTYOTA DICHOTOMA*

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The importance of seasonality in affecting algal fertility, growth, and chemical composition has been demonstrated in a wide range of seaweeds. While most studies focus on the direct effects of such seasonal patterns, it has become clear that the seasonal origin of fertile tissue and, hence, spores, may also affect the performance of the resulting offspring. The aim of this study was to investigate to which extent seasonal variation affects spore characteristics and juvenile thermal performance in the brown macroalga *Dictyota dichotoma*, a key component of European coastal ecosystems. To this end, fertile sporophytes were sampled in Wimereux (France) and Goes (the Netherlands) at three time points during the growing season. At every time point, sporophyte length, spore size and fatty acid content were measured and the thermal response of growth was examined in 3-week old germlings by constructing thermal performance curves. Our results indicate a clear effect of seasonality on spore size as well as on the thermal response of growth. These patterns seem to be largely consistent across populations.

Keywords: Seasonality, *Dictyota dichotoma*, temperature

Oral presentation

ECOLOGICAL IMPORTANCE OF VIRAL LYSIS OF PHYTOPLANKTON IN THE SOUTHERN OCEAN

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Viruses are obligatory parasites with typically high host-specificity and as such may be considered to structure not only host population dynamics but also host community composition. Lytic viruses have been shown to infect all taxonomic groups of phytoplankton in the ocean. Still, their ecological importance in polar oceans is highly understudied. Upon the release of the newly produced progeny viruses from the host, also the cellular matter is released which is subsequently shunted away from the traditional food web towards the microbial loop. Viral activity thus impacts the flux of organic matter differently than grazing does, resulting in a reduced trophic transfer efficiency. It is timely to quantify viral lysis rates of phytoplankton in the (warming) polar oceans. We will present results on viral lysis rates of the different phytoplankton from both the Amundsen Sea and Weddell Sea, that were obtained using the modified dilution assay in combination with flow cytometry, and compare these rates to simultaneously obtained grazing rates. Our results demonstrate that viral lysis occurred for all phytoplankton groups discriminated and that viral lysis is substantial in these cold waters. Viral lysis clearly affects host abundances and we advise to include viral lysis of Antarctic phytoplankton into ecosystem models to improve our understanding of the carbon flow through the Antarctic pelagic ecosystem, and to allow better predictions in times of global climate change.

Keywords: Phytoplankton, viruses, biogeochemical cycling

Oral presentation

UNDARIA PINNATIFIDA IN BREAKSEA SOUND, FIORDLAND, NEW ZEALAND: AN MBACI EXPERIMENTAL DESIGN TO ASSESS REMOVAL IMPACTS OF THE INVASIVE KELP

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The rate of introduced species has reached its highest level in recent years, particularly with respect to algae species, thus intensifying the pressure on marine systems to adapt quickly to change. Because aquatic species are some of the more difficult introductions to manage, the majority form dense colonies that increase biomass pools quickly and substantially, ecological research of invaded ecosystems is increasingly valuable to environmental management. This study was conducted from 2019-2020 in the Fiordland Marine Area, a region of natural and cultural significance to New Zealand. This area is valued as being mostly untouched wilderness, but the invasive kelp *Undaria pinnatifida* was first recorded here at Sunday Cove in 2010 and has since spread into the surrounding area. To evaluate the impact of removing the invader, we ran a study using a multiple before-after control-impact (MBACI) design at sites within Breaksea Sound. All work was completed in the subtidal between the 0.5-8m depth. Prior to removal, density surveys of all brown macroalgae were completed at 18 sites. In 2019, we removed 629.42 kg of *Undaria* from approximately 9173.5m2. We will be returning to these sites in early December 2020 to resurvey all sites and conduct a second invasive removal at the 'impact' sites in order to assess any changes to the native and invasive densities.

Financing: University of Otago, Environment Southland

Keywords: Invasive species, *Undaria pinnatifida*, kelp forest ecology

Oral presentation

TURF AND CANOPY MACROALGAE DISPLAY SPECIES-SPECIFIC FUNCTIONAL RESPONSES UNDER A CLIMATE CHANGE SCENARIO

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Warming and other human-mediated stressors are globally promoting the decline of canopy-forming algae that are replaced by turf-forming species. In the north-western Iberian Peninsula, the intertidal canopy-forming *Fucus serratus* is reducing its abundance while the warm-water turf-forming *Vertebrata hypnoides* and *V. reptabunda* are becoming more abundant. Ecophysiological performance of seaweeds is constrained by temperature and the species responses under thermal gradients can be used to predict their vulnerability to water warming. In this study, we analysed the variation in primary productivity and respiration rate in response to warming of a declining canopy and two expanding turf-forming species. Samples of the three species were exposed under controlled laboratory conditions to a resolved temperature gradient (from 7 to 31°C). As expected, optimum temperature for photosynthetic yield was higher in the two Vertebrata spp. than in F. serratus and turfs were significantly more productive at Topt. However, photosynthesis responsiveness to temperature was species-specific for turfs and consistent differences with the canopy were only observed in *V. hypnoides*, while responsiveness of *V. reptabunda* was more similar to that of *F. serratus*. Respiration in *F. serratus* was more sensible to warming than in *V. reptabunda*, while *V. hypnoides* showed an intermediate sensitivity but these differences were not significant. Results for F. serratus agree with previous studies on canopy species. For the first time, functional responses of turf-forming species to thermal gradients were studied evidencing that they are species-specific. Therefore, this study highlights the importance of taking into account the composition of turfs in future studies.

Financing: This work was supported by the European Cooperation in Science and Technology (COST) and Xunta de Galicia

Keywords: Ecophysiological functional traits, *Fucus*, Vertebrata

Oral presentation

WILL CO2 ENRICHMENT ENHANCE THE TOLERANCE OF MARINE MACROALGAE TO OCEAN WARMING?

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Ocean acidification and ocean warming are occurring simultaneously, and our goal is to discover if rising levels of CO2, often considered a limiting resource, will enhance the thermal tolerance of seaweeds. For terrestrial plants, rising CO2 levels can enhance productivity and increase temperature tolerance of growth rate. Seaweeds, however, have two sources of dissolved inorganic carbon for photosynthesis: CO2 taken up by passive diffusion, and bicarbonate (HCO3-) which is abundant but taken up by processes that that require energy i.e. carbon dioxide concentrating mechanisms (CCMs). Therefore, the responses of seaweeds to ocean acidification depend on their carbon acquisition strategy and/or temperature tolerance. Seaweeds have at least five mechanisms of acquiring dissolved inorganic carbon: For species using only CO2 (non-CCM species): 1. Low- and 2. high-affinity uptake systems. For CCM species: 3. a low-affinity CCM, 4. a high-affinity CCM with down regulation of the CCM when additional CO2 is supplied and 5. a high-affinity CCM with no downregulation of the CCM when CO2 is supplied. Additionally, some species are sensitive to increased levels of H+ ions under ocean acidification which may negatively affect photosynthesis and growth. In laboratory experiments, we demonstrate that for the brown seaweed *Phyllospora comosa*, which operates a high-affinity CCM, increased CO2 enhances thermal tolerance for growth via adjustments to the lipid composition of cellular membranes. Our results indicate that knowledge of seaweeds' carbon uptake strategy and whether CO2 limits productivity are critical in determining their responses in a future warmer and more acidic ocean.

Financing: Supported to ARC DP 200101467 to CLH, JB, JAR, AB, J-DGE

Keywords: Multiple drivers, acclimation, macroalgae

Oral presentation

RESISTANCE OF CORALLINE ALGAE TO OCEAN WARMING AND MARINE HEATWAVES

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Anthropogenic greenhouse gas forcing is heating up the world's oceans. Accompanied by this long- term rise of average sea surface temperatures (ocean warming) is the increase in frequency and intensity of extreme short-term temperature events (marine heatwave). Heatwaves and ocean warming have both been identified as a main threat to marine ecosystems. However, research on the impacts of ocean warming and marine heatwaves on foundational species in temperate oceans is lacking. To this end, a manipulative laboratory experiment was conducted exploring the physiological, geochemical, and transcriptional responses of four temperate coralline algal species to ocean warming and marine heatwaves. Thus, all coralline specimens were exposed to either present day (16°C) or future summer temperatures (18.8°C) for fourteen days. A two-week long marine heatwave was simulated for half of the specimens of both mean temperatures after this temperature acclimation. Temperatures increased during the first week of the heatwave until peak temperatures were reached (16+2.8°C and 18.8 +2.8°C). During the second week temperatures were gradually decreased to pre-heatwave conditions. A two-week recovery period followed. Unexpectedly, none of the species showed signs of detrimental impacts caused by either long- or short-term exposure to higher water temperatures across a large range of response metrics measured. This indicates either the lack of thermal sensitivity of examined parameters or the ability to buffer detectable phenotypic changes at the molecular level. The results suggest that temperate coralline algae may be more robust to marine heatwaves than other important foundations species, such as kelps and corals.

Financing: This project is supported by the Rutherford Discovery Fellowship awarded to C. E. Cornwall.

Keywords: Ocean warming, marine heatwave, coralline algae

Oral presentation

CONTRASTING RESPONSES OF TWO KEYSTONE SEAWEEDS TO OCEAN GLOBAL CHANGE IN SOUTHEASTERN AUSTRALIA

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Seaweeds are likely to have varied responses to ocean global change, which will be driven by their relative responses to each driver. For example, some fleshy species may respond positively to ocean acidification as they are able to benefit from the elevated CO2 but may be negatively impacted by ocean warming, whereas calcified species are likely to be negatively impacted by acidification but may respond to positively to small temperature increases. Therefore, the overall response will depend on whether the positive (or negative) effect of acidification outweighs the negative (or positive) effects of warming. In shallow subtidal wave-exposed reefs in Tasmania, Australia, the fucoid *Phyllospora comosa* is the dominant canopy-forming species, while crustose coralline algae (CCA) dominate the rock surface. Both *P. comosa* and the CCA are keystone species in this system with *P. comosa* providing habitat and a food source for commercially and ecological valuable invertebrates and CCA providing settlement cues for invertebrate larvae. In two manipulative laboratory experiments, we show differential responses of these keystone species to ocean global change: *P. comosa* was tolerant to ocean warming and marine heatwaves as it utilised additional CO2 to provide energy for adjustment of fatty acid composition, which counteracted negative effects of warming. In contrast, the CCA were negatively affected by near future (2030) levels of warming and acidification. These responses highlight that changes in seaweed assemblages in eastern Tasmania to ocean global change will be complex and driven by the differential effects of individual drivers.

Keywords: Marine heatwaves, fatty acids, ocean acidification

Oral presentation

THE EVOLUTION OF MORPHOLOGY IN DIATOMS: ASSESSMENT OF SELECTIVE PRESSURES THAT HAVE SHAPED THEIR LONG-TERM SPECIATION

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Diatoms are important oceans' primary producers, which affect global food webs. Their silica cell walls are suited for the study of the interaction among physiology, biomechanics and environmental change that have shaped their morphological evolution. Key aspects of the general principles ruling silica accumulation in frustules will be clarified considering the synergic action of multiple selective pressures. First diatoms had spherical and high silicified cells, only in a second step they evolved elongated and thinner frustules with low Si content. The decrease in Si availability observed in oceans through the Mesozoic Era, was investigated as a potential factor implicated in diatom radiation. Species differing in size and shape were adapted to reconstructed paleoenvironments: when exposed to Mesozoic Si concentration (500 µM Si), silica accumulated in frustules and measured by Total reflection X-ray fluorescence was higher than at intermediate and present Si concentrations (205 and 25 µM Si), growth and photosynthetic performance were lower. The role of frustule in the prey-predator interaction was investigated in grazing experiments where diatoms differing in size and shape were exposed to copepods in monospecific and mixed cultures. Imaging Flow Cytometer analysis was newly applied to study phytoplankton interaction in presence or absence of grazer, providing multiple high-quality cellular features. Smaller species were the most affected by grazers in terms of growth, Si fluctuation and morphological modification in monospecific cultures. On the other hand, in mixed cultures the small size was crucial to minimize grazing pressure, suggesting that interspecific competition is often underestimated in prey-predator relation.

Keywords: Frustule, morphology, selective pressure

Oral presentation

FINE-SCALE ASSESSMENT OF SOUTHERN DISTRIBUTION LIMIT OF COLD-WATER SPECIES IN NORTHWESTERN IBERIA

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Rocky intertidal systems display some of the most thermally complex environments on Earth. Species distribution limits are expected to shift due to changes in temperature associated with global warming. Populations at the limits of their distribution are often more vulnerable than those at the distribution center since they experience suboptimal conditions. Water temperatures off NW Iberia are seasonally colder than in adjacent areas due to summer upwelling, making this an interesting biogeographic transition zone, harboring both the rear-edge populations of polar/temperate species extending from the North of Europe (i.e. cold-water species) and the front-edge of several warm-water species common in north Africa and the Mediterranean Sea. Anecdotal field data suggests that the last biogeographic studies in NW Iberia are already outdated. This, combined with the fact that range shifts of cold-water species in the region have not always followed predictions based on warming trends, prompts for a comprehensive reassessment of their current distribution. In this study we surveyed over 40 rocky shores in NW Iberia and assessed abundance of 34 species with known distributional limits in the region. Changes in distribution were compared with historical biodiversity data, and related with temperatures obtained by autonomous loggers deployed at sun-exposed and shaded microhabitats, providing a detailed picture of the local thermal variability. This work contributes to the identification and characterization of climate refugia that may allow for species to persist and/or extend their distributional ranges to otherwise unfavorable areas, counteracting global and regional trends.

Financing: This study was funded by FEDER through COMPETE (POCI-01-0145-FEDER-031088), through POR Norte (NORTE-01-0145-FEDER-031053), and through FCT (PTDC/BIA-BMA/31088/2017 and PTDC/BIA-BMA/31053/2017).

Keywords: Biodiversity, microhabitat, biogeography

Oral presentation

REMEMBRANCE OF THE PAST: EVOLUTIONARY HISTORY OF COMMUNITY-WISE STRATEGIES AND ACCLIMATION POTENTIAL OF NATURAL PICO-PHYTOPLANKTON ASSEMBLAGES

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Marine microbes, with short generation times and large populations, are ideal model organisms to investigate how evolution acts when population size is not a limiting factor. To date, experimental evolution still has a long way to go to incorporate organisms´ particular biology and ecology. Moreover, acclimation dynamics acting on communities with complex biotic interactions, are still poorly investigated, often relying on upscaling of single species´ responses. Here we examine how ecology (here, community composition) and evolutionary history (ultimately determined here by biogeography) shape the predictability of adaptive potential of pico-phytoplankton (0.2 – ca. 2 μm). Natural assemblages were isolated from the southern Baltic Sea along a gradient of salinity, temperature and predictability. We measured the short-term responses (i.e. on the scale of a few generations) of the assemblages. Growth rates and metabolism were analysed over a gradient of temperatures. We show that plasticity and community buffering are influenced by overarching evolutionary histories and conditions at sampling time: thermal reaction norms of assemblages from more unpredictable environments, do change within seasons, mainly because communities are rearranged at the functional groups level in a short period of time (i.e. ca. two weeks). We also mechanistically investigated the relations between reaction norms and shift in communities´ composition. Moreover, we also present a comparison with immediate (i.e. within one generation) metabolic responses, taken during several surveys, to analyse how time scale influences the choice of coping mechanisms and strategies.

Keywords: Phytoplankton, community, temperature

Oral presentation

FROM FOOD TO FUNCTION: CLIMATE CHANGE IMPACTS ON FATTY ACIDS IN SEAWEEDS

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Marine food webs, which include many economically and ecologically important species, ultimately depend on energy generated by primary producers such as seaweeds. Seaweeds are unique as they metabolize omega-3 and omega-6 polyunsaturated fatty acids (PUFA), in particular the long-chain (≥C20) PUFA (LC-PUFA), which play essential physiological roles both in the algae themselves and the animals that consume them. Environmental conditions strongly impact the content and composition of fatty acids in seaweeds. The expected climatic changes including increased temperature and levels of dissolved CO2in the future ocean is projected to lead to a decline in essential LC-PUFA in seaweeds with flow-on effects to higher trophic levels. To investigate the effects of climate change on biochemical composition of seaweeds, we exposed various species (e.g. *Macrocystis pyrifera, Cystophora torulosa, Xiphophora gladiata, Sargassum fallax, Carpoglossum confluens, Phacelocarpus peperocarpos, Grateloupia subpectinata, Hymenena affinis* and *Plocamium dilatatum*) to future ocean conditions in a laboratory setting. Results demonstrate how ocean warming and ocean acidification will affect production of key LC-PUFA in seaweeds, and the implications this will have for the functioning of coastal ecosystems. Key findings indicate that ecosystem effects will be driven by biochemical changes on a species level in combination with changes in species composition driven by changing environmental parameters. Results also highlight how seaweeds respond to environmental drivers (e.g. rapid warming events driven by heatwaves), and how adjustments in fatty acids provide a mechanism to quickly respond to changes in their environment.

Financing: The project was supported by funding through the Deutsche Forschungsgemeinschaft (DFG, grant ID: SCHM 3335/1)

Keywords: Climate change, fatty acids, food web

Oral presentation

TRENDS WITH BENEFITS? PHYTOPLANKTON DYNAMICS UNDER CLIMATE CHANGE AT A LONG TERM PACIFIC OCEAN STATION

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Understanding the impacts of global warming on phytoplankton is critical to predicting changes in future biodiversity, ocean productivity, and ultimately fisheries production. Examining phytoplankton community abundance and environmental data from 1931 to 2019, we investigated the response of phytoplankton to ocean warming at a long-term Pacific Ocean coastal station off Sydney, Australia. With warming of ~1.8°C since 1931, we found a significant increase in the Community Temperature Index (CTI) of the phytoplankton, suggesting that the relative proportion of warm-water to cold-water species has increased since this time. The shift in CTI was a consequence of, amongst others, the substantial increase in the warm-affinity (21.5°C) chain-forming diatom *Leptocylindrus danicus* (20% in 1931–1932 to 57% in 2009 onward). By examining 35 clonal cultures of this ubiquitous marine microbe, which we isolated from six locations spanning 2000km of the eastern Australian coastline, we found *that L. danicus* reproduces rapidly, forms resting spores under nutrient depletion, and displays a wide thermal range. Moreover, significant morphological and metabolic trait variability for 8 of 9 traits examined (growth rate, biovolume, C:N, silica deposition, silica incorporation rate, chl-a, and photosynthetic efficiency under dark adapted, growth irradiance, and high-light adaptation), were greater within a species than between species, suggesting high standing variability which would allow for rapid evolution. We conclude that species such as *L. danicus* may provide a glimpse of the functional traits necessary to be a “winner” under climate change.

Keywords: Phytoplankton, climate change, diatom

Oral presentation

TIMIMG OF DISTURBANCE, TOP-DOWN, AND BOTTOM-UP DRIVING EARLY ALGAL SUCCESSION PATTERNS IN A TROPICAL INTERTIDAL COMMUNITY

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Herbivory and nutrient enrichment are major drivers of the dynamics of algal communities. However, their effects on algal abundance are under the influence of seasons. This study investigated the effects of herbivory and nutrient enrichment on early algal succession patterns using cages (uncaged and fully caged treatments) and two nutrient levels (ambient and enriched concentrations). To determine seasonal influences, experimental plots on dead coral patches were cleared during both dry and rainy seasons. Of the 17 algal species recruited in the experiment plots, three were dominant: *Ulva paradoxa C. Agardh, Padina* in the *Vaughaniella* stage, and *Polysiphonia sphaerocarpa Børgesen*. In this succession process, *U. paradoxa* was the earliest colonizer and occupied the cleared plots within the first month after clearing with the highest percentage of 83.33 ± 1.67% to 88.33 ±

9.28%. Then, it was replaced by the late successional algae, Padina in the *Vaughaniella* stage, and *P. sphaerocarpa*. The effects of herbivory and nutrient enrichment on algal abundance varied across algal functional groups and seasons. During the dry season, neither herbivory nor nutrient enrichment affected Ulva cover but during the rainy season, *Ulva* cover was influenced by nutrient enrichment. However, the abundance of algae in this early stage was not apparently affected by either herbivory or nutrient enrichment. Our results indicated that the timing of disturbance strongly influenced the algal abundance and successional patterns in this tropical intertidal community.

Keywords: Algal recruitment, eutrophication, herbivory

Oral presentation

DOES OCEAN WARMING POSE A SIGNIFICANT THREAT TO THE SURVIVAL OF MARINE FORESTS? THE POSSIBLE FATE OF *CYSTOSEIRA HYBLAEA* (FUCALES)

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Canopy-forming brown algae support highly productive ecosystems, whose decline was ascribed to the interplay of several anthropogenic impacts. Climate change may disrupt the biology of these species, nonetheless the role of temperature in early-life stages development is poorly known. This study aimed to evaluate the response of *Cystoseira hyblaea* Giaccone, a winter-reproducing Southern-Mediterranean endemic species, to thermal stress by testing five temperatures (12, 15, 18, 24, 28 °C) on early stages and adults. To assess egg release, zygote settlement, and embryo growth rate, ca. 1200 receptacles were cultivated on 6 Petri dishes per temperature treatment. At 0, 20, 44, 92 h after fertilization, 10 random subareas of 2x2 mm were examined in 3 Petri. Adults' chlorophyll a fluorescence was measured at 0, 24, 72, 120 h on 9 fronds in each of the 3 aquaria per treatment. The embryo developmental rate was highest at 12 and 15 °C, whereas it was delayed at 18 and 24 °C. Mortality rates increased at 18 and 24 °C and no zygotes survived at 28 °C. Adults showed a more plastic physiological response and thermal stress did not significantly affect PSII efficiency. In a scenario of ongoing rising temperatures, the warming effects could be a threat for recruitment of *C. hyblaea* and increase its vulnerability to further stressors, with possible cascading effects on the ecosystem. Knowledge of factors that impair the survival of early stages should be integrated into conservation and restoration management to preserve canopy-forming macroalgal populations and their associated biodiversity and ecosystem services.

Financing: This study was supported by the LIFE financial instrument of the European Community, project ROC-POP-LIFE (LIFE16 NAT/IT/000816).

Keywords: Canopy-forming macroalgae, thermal stress, early-life stages

Oral presentation

IS SEAWEED ADAPTATION TO ENVIRONMENTAL STRESSES DEPENDENT ON ITS MICROBIOME INFOCHEMICALS?

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The underlying infochemical-mediated strategies causing changes in algal–bacterial interaction are not still completely known but given that bacteria release algal growth- and morphogenesis-promoting factors (AGMPFs) required for (green)macroalgae growth and development, adaptive responses to environmental stressors must be considered within the community structure too. To investigate and assess the complex interactions underlying macroalgae and its microbiome responses to various stress factors particularly temperature, we propose a reductionist analysis of a tripartite model system consisting of the axenic green alga *Ulva* (Chlorophyta) re-infected with two essential bacteria. This analysis will allow us to decipher the stress response of each symbiont within this cross-kingdom interaction and will help to understand the enormous ecological success of *Ulva*. This research includes the effect of recently isolated bacteria from the Potter Cove, King George Island (Isla 25 de Mayo) in Antarctica, on the model system *Ulva mutabilis* Føyn purified gametes. The results indicate that cold-adapted bacteria release AGMPFs, inducing cell differentiation, and cell division in purified cultures. Integrating the chemical ecology to aquatic-microbiome investigations will allow us to shed light on underlying adaptation and acclimation mechanisms in macroalgae to stress situations with implications, e.g., for the sustainable management of aquacultures.

Financing: This work was supported by the Deutsche Forschungsgemeinschaft (DFG) in the framework of the priority program (SPP 1158).

Keywords: Cross-kingdom interactions, adaptation, *Ulva mutabilis*

Oral presentation

MODELLING THE SEASONAL GROWTH AND COMPOSITION OF *FUCUS VESICULOSUS* IN ITS BENTHIC COMMUNITY UNDER DIFFERENT GLOBAL CHANGE SCENARIOS

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Environmental change increasingly threatens coastal marine ecosystems. The individual and combined impact of elevated seawater temperature and pCO2 on the brown macroalga *Fucus vesiculosus* and its associated community was studied in mesocosm experiments between April 2013 and March 2014. A numerical box model simulating the seasonal growth of Fucus in mesocosms was developed, based on parameters and process rates measured in the Kiel Outdoor Benthocosm (KOB) and laboratory experiments. Nitrogen (N) and carbon (C) cycling in the KOBs was included and relevant physiological and ecological processes were implemented, including (1) storage of C and N assimilates by Fucus, (2) shading effects of epiphytes and (3) grazing by different herbivores on both Fucus and epiphytes, but with species-specific rates and preferences. To validate the model, we compared simulation results with observations in the KOB experiment that lasted from April 2013 until March 2014 under ambient and global-change scenarios, that is, increased atmospheric temperature and partial pressure of carbon dioxide. The model reproduced the magnitude and seasonal cycles of Fucus growth and other processes in the KOBs over 1 yr under different scenarios. Ongoing global change requires a synthesis of existing knowledge of habitat-forming species and their sensitivities to changing environmental conditions. Thus, understanding of the ecological role of Fucus as a primary producer and carbon sink in the coastal ecosystem of the Baltic Sea may allow more reliable predictions in the future.

Financing: This research was funded by BMBF (FKZ 03F0728K) and DFG (GR5088/2-1).

Keywords: Ecological modeling, carbon and nitrogen storage, bladder wrack

Oral presentation

HOW CAN SEASONALITY MODULATE THERMAL SENSITIVITY IN EARLY STAGES OF FUCOIDS?: THE COLDER, THE BETTER

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In the face of ocean global change, determining critical thermal thresholds for marine organisms is a key aspect to predict the survival and persistence of populations, particularly those from rear-edge areas. Seasonal variability implies acclimation of adult individuals, which might result in shifting thermal sensitivities of their recruits. In this work, we aimed to investigate the influence of natural seasonal parental acclimation on the warming response of single- and few-celled stages of *Fucus guiryi*, a monoecious fucoid from the east Atlantic coast and Strait of Gibraltar, whose populations are iteroparous. To address this, we obtained embryos from fertile thalli collected in early summer, late summer, and winter. In the three replicate experiments under laboratory-controlled conditions, we followed growth, development, survival, and photosynthetic responses of embryos exposed to control (15ºC) and warming conditions (25ºC) for 3 weeks, and initial elemental composition was characterized. Our findings revealed that breeding from winter parents possessed broader thermal sensitivity and thrived better under warming conditions than those from summer specimens, where only 50% survived and experience 75% reductions in photosynthetic rates. Nevertheless, there was a significant gain in thermal resilience from early to late summer regarding survival at 25º C. This research highlighted that warmer winters would not potentially harm new recruits, while extreme temperature events in early summer might compromise the survival of the most sensitive early summer recruits, considering the RCP8.5 predictions for 2050. The influence of parental and provisioning effects and how this might be applied to ecological restoration is discussed.

Financing: European project BiodivERsA3- MARFOR funded by Ministerio de Economía y Competitividad (PCIN-2016-090).

Keywords: Ocean warming, thermal resilience, fucoids

Oral presentation

IDENTIFICATION AND EVOLUTIONARY ANALYSIS OF THE LOW AFFINITY NITRATE TRANSPORTERS IN DIATOMS, DINPFS, REVEAL AN INTRIGUING EVOLUTIONARY HISTORY

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Nitrogen (N) is an essential nutrient for all living organism. Diatoms, the dominant component of phytoplankton in the ocean, continuously subjected to fluctuating environmental conditions and nutrient concentrations, have a complex evolutionary history with a combination of animal, plant and bacteria-like traits. As other organisms, diatoms rely on a range of transmembrane transporters for N uptake. Here we report a
comprehensive characterization of the Nitrate Transporter 1/ Peptide Transporter Family (NPF)
in diatoms. NPFs are well characterized in many organisms where they recognize a remarkably
broad range of diverse natural substrates, ranging from di- and tri-peptides in bacteria, fungi and mammals to nitrate and phytohormones in plants

Sequence alignment and phylogenetic analysis revealed that diNPFs cluster in two clades, one of which lost in plants. With structural data available for both plant and bacterial NPFs/POTs, we obtained structural models for the two NPFs from the model species *Phaeodactylum tricornutum*, one each belonging to the two different clades. Our structural analysis reveals that Clade I diNPFs have structural features that are found in bacterial POTs, but not in plants, while Clade II diNPFs are structurally closer to plant NPFs. This subdivision is supported by a different subcellular predicted localization which are most likely reflected affinity to different substrates and different role in cell metabolism. Moreover, transcription analysis of diNPFs genes under different laboratory and environmental growth conditions suggests an unexpected complexity of these transporters, revealing once again the chimeric nature and the complex physiology of these unique successful microalgae.

Keywords: Diatoms, nitrogen transporters, metagenomics and gene phylogeny.

Oral presentation

PHYSIOLOGY OF MAERL ALGAE: COMPARISON OF INTER- AND INTRASPECIES VARIATIONS

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Free-living red coralline algae play an important role in the carbon and carbonate cycles of coastal environments. In this study, we examined the physiology of free-living coralline algae forming maerl beds in the Bay of Brest (Brittany, France), where *Lithothamnion corallioides* is the dominant maerl (i.e. rhodolith) species. *Phymatolithon calcareum* and *Lithophyllum incrustans* are also present (in lower abundances) at a specific site in the bay. We aimed to assess how maerl physiology is affected by seasonality and/or local environmental variations at the inter- and intraspecific levels. Physiological measurements (respiration, photosynthetic and calcification rates) were performed using incubation chambers in winter and summer to compare (1) the dominant maerl species at three sites and (2) three co-existing maerl species at one site. Comparison of the three co-existing maerl species suggests that *L. corallioides* is the best adapted to the current environmental conditions in the Bay of Brest, because this species is the most robust to dissolution in the dark in winter and has the highest calcification efficiency in the light. Comparisons of *L. corallioides* metabolic rates between stations showed that morphological variations within this species are the main factor affecting its photosynthetic and calcification rates. Environmental factors such as freshwater inputs also affect its calcification rates in the dark. In addition to interspecies variation in maerl physiology, there were intraspecific variations associated with direct (water physico-chemistry) or indirect (morphology) local environmental conditions. This study demonstrates the plasticity of maerl physiology in response to environmental changes, which is fundamental for maerl persistence

Financing: This work benefited from the French investment expenditure program IDEALG ANR-10-BTBR and the project EC2CO MAERLCHANGE.

Keywords: Coralline algae, physiology

Oral presentation

IS THE OXYCLINE A BARRIER TO PHYTOPLANKTON IN THE OXYGEN MINIMUM ZONES? THE RESPONSE OF IMANTONIA TO LOW O2/PH CONDITIONS

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Oxygen minimum zones (OMZs) are environments that present naturally low O2 as well as high CO2 concentrations (and thus low pH) and are currently believed to be in expansion due to climate change. In many OMZs, the oxycline is sufficiently shallow for phytoplankton to be exposed to these low O2 and high CO2/low pH conditions. In the present study, we evaluated the effect of low pH/low O2 conditions on a phytoplankton strain isolated from the Eastern Tropical South Pacific OMZ, *Imantonia* sp. (Strain SEPA721), using a 6-day experiment. Under control conditions (pH = 8.1; dissolved O2 = saturation), *Imantonia* sp. in vivo fluorescence increased over fifty times, generating supersaturated O2 levels and an increase in pH due to photosynthesis. Under OMZ conditions (pH = 7.5; dissolved O2 = 55.6 uM, light = 169.6 µEm-2s-1), both pH and O2 values remained constant and in vivo fluorescence declined, indicating that *Imantonia* sp. did not survive. Future experiments with other *Imantonia* sp. strains could help to better evaluate the behavior of different important phytoplankton functional groups in the ocean, explaining their vertical niches in the water column of OMZ zones.

Financing: Funded by Fondecyt 1170065 and Millennium Institute of Oceanography (IMO)

Keywords: Ocean acidification, phytoplankton, OMZ

Oral presentation

PHOTOSYNTHETIC ACTION SPECTRA IN THREE MARINE MACROALGAE

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Action spectra are useful tools for determining how algae can deal with variable radiation in the environment and also considering biotechnological perspectives. In this way, our study aimed to obtain the photosynthetic action spectra of three different algal species: the phaeophyceans *Laminaria ochroleuca* and *Rugulopteryx okamurae*, and the red alga *Chondracanthus acicularis*, considering some variable experimental conditions. Algae were sampled in the field and transferred to laboratory, where they were acclimated for one week. Different experimental conditions were prepared for each alga, during another week: *L. ochroleuca* was cultivated in seawater enriched with 0.5 mM Nitrate and without any enrichment; *R. okamurae* was grown under two different temperatures (15 and 25°C) and *C. acicularis* was treated with two salinities, 30 and 45. After the experimental period, in vivo chlorophyll fluorescence was measured i.e. Photosynthetic action spectra were assessed using the chlorophyll a fluorescence (PAM). Maximal quantum yield (Fv/Fm) and maximal photosynthetic capacity (ETRmax) were determined and photosynthetic pigments were quantified. Algal thalli were exposed to five different intensities of light for 6 minutes (sequentially from the lowest to the highest, or separately). Seven different light quality ranges covering the visible were used, peaking in 400, 450, 500, 550, 600, 650 and 700 nm. The strategy of exposure for each light intensity influenced in the action spectra obtained, with influence of previous light received by each sample. Yellow to orange light resulted in lower photosynthetic responses of the algae evaluated.

Financing: CAPES, CNPq

Keywords: Light quality, photosynthesis, marine macroalgae

Oral presentation

HERITABLE PHENOTYPIC DIVERGENCE ALONG A LATITUDINAL GRADIENT IN THE GIANT KELP *MACROCYSTIS PYRIFERA*: OCEANOGRAPHY, PHYSIOLOGY AND TRANSCRIPTIONAL PROFILES

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Intraspecific phenotypic variation and the capacity of species to respond to environmental drivers is an outstanding question in biology, while current threats to kelp ecosystems from extreme climate events (such as marine heatwaves) lends urgency. We used physiological indicators and transcriptome profiling to investigate variation in thermal responses in *Macrocystis pyrifera* at a regional scale over 1,200 km at 4 sites between central California and the southern limit in the northern hemisphere, central Baja (hereafter NO, NC, SC and SO, respectively). Analysis of oceanographic data indicated that maximum marine heat wave temperatures vary by > 6°C across this range. We report the results of 1) a short-term common garden experiment on field-collected sporophyte blades, 2) an experiment with F1 sporophytes raised in common garden culture, and 3) growth and survival of isolated gametophyte cultures. Physiological indicators (rETRmax) suggested that SO (adult blades) or both SO and SC (F1 sporophytes) outperformed the more northern regions at high temperatures (24 and 23°C, respectively). Female gametophytes from SO clearly outgrew those from NO over 15-27°C. However, male gametophytes from the two regions were equally resilient at intermediate temperatures (25-26°C). Transcriptional profiles indicated a strong regional component of variation, particularly for SO. Importantly, this variation carried over into F1 sporophytes, demonstrating a heritable component rarely established with common garden approaches in non-model systems. Annotation and functional analysis revealed a suite of differentially expressed mitochondrial-targeted genes in SO, particularly involved in fatty acid beta-oxidation that may provide a fruitful avenue for future investigation.

Financing: Portuguese Science Foundation (FCT) programs UID/Multi/04326/2019 and GENEKELP-PTDC/MAR-EST/6053/2014

Keywords: Kelp, molecular phenotype, intraspecific variation

Oral presentation

ELEVATED TEMPERATURE AFFECTS PHENOTYPIC PLASTICITY IN THE BULL KELP *NEREOCYSTIS LUETKEANA*

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The sensitivity of kelps to elevated temperatures has been linked to declines in some kelp populations. However, it remains unclear how thermal stress affects the ability of kelps to respond to other environmental factors, which could influence their vulnerability to climate change. We investigated the effect of thermal stress on the ability of the bull kelp *Nereocystis luetkeana* to acclimate to its surrounding hydrodynamic environment through tension-regulated plasticity in blade morphology. We first determined optimal and stressful temperatures for *N. luetkeana* by measuring growth over nine temperatures from 5 to 22 °C. We then exposed *N. luetkeana* blades to factorial combinations of temperature (13°C and 20°C) and tension (0.5N and 2.0N) simulating different flow conditions, and measured changes in blade length and width after seven days. The temperature at which *N. luetkeana* exhibited maximum growth was estimated to be ~12°C, though growth was high over a relatively wide temperature range. When thermally stressed, *N. luetkeana* blades maintained morphological responses to simulated high flow, but were inhibited from acclimating to low flow. Our results suggest that *N. luetkeana* in sheltered habitats may be particularly vulnerable to climate warming, where an inability to adjust blade morphology to local hydrodynamic conditions could drive declines at sublethal increases in temperature. As ecologically important foundation species, declines in sheltered kelp populations could result in biodiversity loss and disrupt ecosystem function.

Financing: NSERC Discovery grant and Canada Foundation for Innovation (#27431) funds awarded to PTM

Keywords: Kelp, plasticity, temperature

E-Poster

CLIMATE-DRIVEN RANGE SHIFTS OF BROWN SEAWEED *SARGASSUM HORNERI* IN THE NORTHWEST PACIFIC

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Climate-driven shifts of coastal species' ranges constitute a key factor shaping both the vegetation composition and biodiversity of coastal ecosystems. *Sargassum horneri* is a warm-temperate and habitat-forming species found in the coastal ecosystem of the NW-Pacific, where it provides substrate for epiphytic communities and habitat for fish and invertebrates. Here, we used a combination of species distribution models (SDMs) and genetic data to explain the causes of population persistence and genetic differentiation and their consequences for the brown seaweed *Sargassum horneri* in the NW-Pacific. Population genetic structure and SDMs based on paleoclimatic data consistently revealed that southern coasts of the Sea of Japan, North-Pacific-Japan, and the northern part of Okinawa Trough might have served as potential refugia for *S. horneri* during the Last Glacial Maximum (LGM). Furthermore, we projected the distribution dynamics of *S. horneri* under future climate scenarios. The range of *S. horneri* was predicted to move northward, with a significant loss of suitable habitat, under the high emissions scenario (RCP 8.5). By contrast, projected range shifts were minimal under the low emissions scenario (RCP 2.6). Furthermore, North-Pacific-Japan was projected to be long-term persistence habitat for *S. horneri* under future climatic conditions, thus including this area in conservation planning could help mitigate for climate change implications. Our results enable a better understanding of the impacts of climate change on the spatio-temporal distribution of macroalgae and how this can inform coastal management and marine conservation planning.

Keywords: *Sargassum horneri*, climate change, suitable habitat

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E-Poster

ECOLOGICAL PLASTICITY OF PHYTOPLANKTON AND CARBON CYCLES IN A TEMPERATE ESTUARY

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Phytoplankton build the basis of the aquatic food web and contribute about 50 % to global primary production. Due to their short generation times and high standing genetic variation, they can react quickly to changes, potentially determining a climate feedback of the aquatic ecosystems. As they depend on nutrients and light, phytoplankton appear in high numbers at specific locations such as estuaries. While the high primary production here mechanistically drives an air-to-water flux of CO2, studies so far state that these areas are CO2 sources. This classification however depends on several factors and the underlying biotic processes – which might also be affected by climate change - are poorly understood. In the overall project (consisting of 15 PhD positions in the first 3 years), these factors will be studied with respect to the Elbe estuary (Germany), including different trophic levels, seasons and locations as well as marsh-channel interactions. The sub-project presented here deals with the role of phytoplankton in this estuary. Freshwater phytoplankton communities supplied with the river infeed are faced with drastic ongoing changes when entering the estuary and travelling downstream (e.g. salinity gradients). These conditions give manifold opportunities to investigate how communities and single groups of phytoplankton deal with a fast-changing environment and how this affects their role in the estuarine carbon cycles.

Keywords: Estuary, carbon cycling

E-Poster

SEASONAL ECOPHYSIOLOGICAL RESPONSES OF *LESSONIA SPICATA* A HABITAT-FORMING SPECIES MODULATED BY CLIMATE CHANGE SCENARIOS IN CENTRAL CHILE

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The variations of the solar radiation, nutrient contents, temperature, among other ambient parameters, are detrimental for many species. Indeed, they can be modulating their ecophysiological responses under these stressors' conditions. The study of ecophysiological responses along to the daily cycles in seasonal time, in *Lessonia spicata* (Ochrophyta) - in the Costal of the Pacific Ocean, can permit the use of it as a model to explain futures responses in front of the global climate change, as a model. In this context, different physiological variables were measured, such as photoinhibition and photosynthetic capacity, photosynthetic pigments, and photoprotective substances related to their antioxidant capacity. The biological responses presented seasonal and Dayle cycle patterns, with an increase in the photosynthetic capacity in spring and summertime, and the non-photochemical quenching or photoprotection capacity was lower at the same time. In addition, the increase of the photoprotective compounds under high solar radiation conditions and had a positive correlation with the antioxidant activity. The concentration of the photosynthetic pigments as Chla and Chlc, were higher under high solar irradiance. All physiological and biochemical responses in *L. spicata* were related to high photoacclimation in the seasonal period, with high solar radiation conditions, overall producing less vulnerability for this macroalga and high photoacclimation related to seasonal environmental parameters.

Financing: FONDECYT project 11180197 granted to Paula S. M. Celis Plá.

Keywords: Brown algae, seasonal responses, climate change

E-Poster

ADAPTIVE POTENTIAL AND THERMAL PLASTICITY OF MICROSCOPIC LIFE STAGES OF *LAMINARIA DIGITATA*

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Thermal characteristics of kelp species have been studied in many ways, but potentially persistent effects of temperature across generations are yet poorly understood. In this context, the effect of thermal history on fertility and growth of the N-Atlantic kelp species *Laminaria digitata* was investigated within and across life cycle generations in a common garden experiment. Using vegetative gametophytes from cold (5 °C) and warm (15 °C) long-term cultivation (3 years), we quantified gametogenesis and recruitment over two weeks at a common temperature of 10 °C. Then, recruited sporophytes were transferred to a temperature gradient spanning the tolerance of the species from 0 °C to 20 °C. We hypothesized that a warm gametophyte temperature history promotes performance of sporophytes at warm temperatures and vice versa. Interestingly, gametogenesis speed and sporophyte recruitment were higher in gametophytes with a cold temperature history compared to the warm temperature history. Moreover, a cold temperature history of gametophytes enhanced the performance of juvenile *Laminaria digitata* sporophytes at the extreme low and high temperatures of 0 °C and 20 °C, which is evidence for a cross-generational effect between gametophytes and young sporophytes. As a consequence, the cold season might be especially crucial in the field to increase sporophyte recruitment, and to produce sporophytes with a wider thermal performance range, especially in regions where populations are close to their physiological thermal limit.

Keywords: Life cycle, gametogenesis, cross-generational plasticity

E-Poster

MARINE MICROALGAE OF DIFFERENT PHYLOGENY DISPLAY A DIVERSIFIED ABILITY TO FACE SULFUR LIMITATION

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Sulfur (S) is an essential macronutrient in algae, acquired by cells as sulfate and assimilated as sulfide in an energy demanding reductive process. Despite the central role of S in multiple cellular processes, our knowledge on the regulation of *S assimilation* in algal taxa is presently still limited. Although in today's oceans sulfate concentration is rarely limiting for the growth of marine phytoplankton, algae of different phylogeny evolved in the presence of diversified sulfate concentration (lower in the Paleozoic oceans than today). Further, algae live in an extremely variable environment, and changes in the availability of other resources, as other nutrients or light energy, may impact *S assimilation*. We are characterizing the growth of marine microalgae cultured in a wide range of sulfate concentration and light regimes. S limiting concentrations appear to be markedly different in microalgae belonging to the green and red lineage. *In vivo* chlorophyll fluorescence analysis reveals the effects of diversified S availability on microalgae photosynthesis, an essential process dependent on S on multiple levels. Elemental analyses by CHN Analyzer and Total reflection X-ray fluorescence allow to determine elemental composition in cells, and Fourier Transformed Infrared Spectroscopy allows to investigate how microalgae allocate available energy and resources into the main macromolecular pools. This study will allow a deeper understanding of microalgae general and species-specific features of photosynthetic and metabolic responses to changes in S availability. Further, it will help to comprehend the role S availability played in the evolutionary transition in phytoplankton communities.

Keywords: Sulfur, nutrient metabolism, photosynthesis

E-Poster

CLIMATE CHANGE RESPONSES OF NE ATLANTIC KELPS: *SACCORHIZA POLYSCHIDES* AS AN OCEAN WARMING "WINNER" IN THE UK?

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Large macroalgae, such as kelp species and kelp-like brown algae, are dominant foundation organisms along temperate coastlines. They provide complex biogenic habitat for a high diversity of associated flora and fauna and support a range of ecosystem services. *Saccorhiza polyschides* (Lightfoot) Batters 1902 ('Furbelows') is a warm-temperate kelp-like species found in the Northeast Atlantic, ranging from the Mediterranean and Morocco polewards to Norway. In the warmer, southern, part of its range, *S. polyschides* is often the dominant habitat former with high population densities. In cooler, northern regions *S. polyschides* tends to be outcompeted by Laminaria species and is generally found in mixed kelp beds. Recent range expansions and population growth have been observed and are predicted to increase under continued ocean warming in northern regions. Here, we present preliminary data of density and biomass of *S. polyschides* sporophytes and their assemblages at three sites within Plymouth Sound (UK) throughout the annual cycle. We also present some results of an experimental temperature tolerance study. With predicted increases in sea temperature, *S. polyschides* is expected to continue to proliferate along southern coastlines of the UK. Should it displace cold-adapted northern species (e.g. several Laminaria spp.), changes in kelp forest habitats, associated communities and provision of their ecosystem services could ensue, due to the short lifespan of *S. polyschides* (12-18 months) in comparison with dominant kelp species (>10 years).

Financing: NS was supported by the UKRI INSPIRE DTP (NERC NE/SO07210/1). DS was funded by a UKRI Future Leader Fellowship (MR/S032827/1).

Keywords: Kelp, ocean warming, distribution shifts

E-Poster

THERMAL PLASTICITY IS MODULATED BY LIGHT INTENSITY IN MARINE PHYTOPLANKTON

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Marine phytoplankton are highly diverse and widely distributed throughout the oceans, playing important roles in biochemical cycles and primary productivity. These organisms are exposed to continuous changes in environmental conditions that influence their physiology and eco-evolutionary dynamics. Their capacity to cope with these environmental changes is the result of a combination of plastic phenotypic responses and adaptive evolution. Among the bottom-up controllers of phytoplankton dynamics, temperature and light are considered the two major drivers. These factors change marked temporal and spatial changes across latitudinal gradients. Their interacting effects influence the overall metabolic rate and energy flux of phytoplankton organisms. Our research aims to understand the modulating role of light and temperature variation in determining the physiological and phenotypic plasticity of two key microalgae groups (diatom and coccolithophore). Our results show that the modulation of light intensity on thermal plasticity constrains both 1) the maximum performance and 2) the breadth due to the interaction between light and temperature. The shifted patterns of thermal reaction norm support our generalist-specialist assumption and indicate that the ecological niche of phytoplankton is determined by the interaction of multiple environmental factors. In addition, the environmental regulation of phenotypic performance is also constrained by the past trait evolution, while how the evolutionary process shapes the genetic variation is not well known. Our intention of future work will focus on exploring how adaptive evolution would improve the responses of phytoplankton to complex environmental heterogeneity, which will contribute to the blueprint of the eco-evolutionary dynamics of phytoplankton.

Keywords: Thermal plasticity, light, phytoplankton

E-Poster

PHOTOPHYSIOLOGICAL AND BIOCHEMICAL RESPONSES OF *LESSONIA SPICATA* (OCHROPHYTA) UNDER SOLAR RADIANCE ECLIPSE IN CHILE

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Solar radiation is one of the main environmental factors that allow life on Earth, allowing the performance of different biological processes, such as photosynthesis in algae. An abrupt event in the variation of the incident solar irradiance from the earth is solar eclipses, phenomena in which the Moon casts a shadow on the earth's surface. In this study, *Lessonia spicata* (Ochrophyta) collected in Viña de Mar, Chile was exposed to an eclipse of the sun that occurred in July (2019) in two treatments (exposure - E and recovery - R). Ecophysiological responses were measurements through photosynthesis as in vivo fluorescence of chlorophyll a of PSII, and biochemical analyzes. The results indicated that the effective yield (Yield II) was higher in recovery treatments whereas, in exposure, this indicator was lower. The phenolic compounds were higher in the midday and the antioxidant activity was higher at the end of the experiment, with the same trend showed oxidative stress measurements through the H2O2. The above suggests, that the intense changes in the reduction of the total solar radiation can affect their metabolic and physiological processes seeing a small recovery when these changes are isolated or dimmed.

Financing: FONDECYT project 11180197 granted to Paula S. M. Celis Plá

Keywords: Brown algae, *Lessonia spicata*, solar radiation

SYM14: Algae at the extremes

Keynote lecture

ZYGENEMATOPHYCEAE IN STRESSFUL ENVIRONMENTS: HOW THEY DEAL WITH IT AND HOW IT SHAPED THEIR TRANSITION TO LAND

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

Financing: This study was supported by Austrian Science Fund FWF project P 34181.

Keywords: abiotic stress, Zygnema, metabolite profiling

Keynote lecture

KELPS IN THE ARCTIC: THEIR ABILITY TO COPE WITH CLIMATE CHANGE

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The Arctic phytogeographic region stretches between the 9-10 and 0°C mean August and February oceanic sea-surface isotherms. Macroalgal biodiversity in the Arctic is rather poor with ~200 species recorded for Svalbard and Greenland, including subarctic regions. A minor fraction of species is endemic. Ecological and physiological data are mostly missing and *in situ* community data are fractionated. Although kelps (Laminariales, Phaeophyceae) only constitute a minor fraction of Arctic macroalgal biodiversity their ability to cope with climate change is crucial for the resilience of future Arctic kelp ecosystems. In this keynote talk I will present in situ biomass data and developmental, eco-physiological and transcriptomic data from several kelp species of Kongsfjorden (western Spitsbergen) and will elaborate on the ability of microscopic stages (spores, gametophytes, juvenile sporophytes) to cope with changes in abiotic factors (temperature, sedimentation, salinity). Although the upper temperature survival limit of Arctic material is quite similar to populations from southern sites in *Laminaria digitata*, slight local adaptation is evident in their sub-lethal temperature response and at low temperatures. Local adaptation is also evident for salinity stress in *Sacharina latissima*. A rise in temperature has the ability to shape the dominance pattern of co-occurring kelp species during recruitment and early growth. In addition, increased temperatures during winter (darkness) may negatively affect survival of juvenile sporophytes but with different rates in kelp species with contrasting temperature affinities. The responses of Arctic endemic and Arctic to temperate kelp species will be contrasted and a conceptual model of driving forces presented.

Financing: Funding of the 2015-2016 BiodivERsA COFUND call (program MARFOR), national funder German Research Foundation (DFG-grant-no. VA105/25-1) is acknowledged

Keywords: Arctic, kelp, adaptation

Oral presentation

RED SNOW, WRONG NAMES AND PSYCHROPHILIC SPECIES

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When the first samples of Red Snow were collected in 1818 at Crimson Cliffs in Greenland and brought back to Europe, a long debate on the causing organism began. Many well-known scientists of that time were engaged in the discussions that lasted almost for one hundred years. The confusion over its identity was not without reason as its microscopic morphology - red and whitish globules with little stalks - did not reveal much. First a fungus, then a lichen was suspected. Finally, culture observations prompted the suspicion that it must be a green alga, as green flagellates were observed when snow samples were let standing. In 1903 Wille finally described the organism as *Chlamydomonas nivalis*. Today, another 100 years later, we know even that was wrong. Red Snow still cannot be subcultured, no “green” strains exist, we know nothing about its life cycle. Yet, with molecular analyses we deciphered parts of this enigma. Samples from 42 localities collected between 1999 and 2018 from alpine and polar regions were analysed and revealed that it is neither a *Chlamydomonas* nor a Chloromonas, but in fact two species of a new genus - *Sanguina nivaloides* and *S. aurantia*. Moreover, for studying these extremophiles, special care has to be given to strains from algal collections to make sure their correct identity is given. In a number of studies putative strains of *Chlamydomonas nivalis* had been used, but actually these were neither the alga causing Red Snow nor other algae obligatorily adapted to cold environments.

Keywords: Snow algae, *Chlamydomonas nivalis*, cryophilic

Oral presentation

TRANSCRIPTIONAL RESPONSE OF THE MARINE DIATOM *SKELETONEMA MARINOI* DURING ACCLIMATION ALONG A SALINITY GRADIENT

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The salinity gradient separating marine and freshwater environments represents one of the major ecological divides for diatoms, and is thought to be an important driver for diversification. Yet, the mechanisms by which marine diatoms adapt to, and ultimately diversify in, freshwater environments are poorly understood. Here, we investigate the transcriptional response of the ancestrally marine diatom *Skeletonema marinoi* during long-term exposure to low salinities, mimicking the Baltic Sea salinity cline along which *S. marinoi* naturally occurs. We found that *S. marinoi* substantially alters its metabolism in low salinities: cell division rates decreased, cells had higher energy demands, and they produced more storage compounds and fewer osmolytes. Inclusion of eight different culture strains revealed that different genotypes differ significantly in their response, both in the direction and magnitude of gene expression. These differences include fundamental cellular processes such as nuclear division, regulation of transcription and translation, and aerobic respiration. Of the 7,905 differentially expressed genes, only 27 were differentially expressed in each genotype, representing genes involved in oxidative stress management, potassium transmembrane transport, and carbohydrate, lipid and amino acid biosynthesis. Altogether, our results reveal substantial variation in the response of different genotypes, highlighting an important but often overlooked source of biological variation associated with how diatoms respond and adapt to environmental change.

Financing: Belgian American Education Foundation; Fulbright Belgium; Simons Foundation

Keywords: Transcriptomics, diatoms, low salinity stress

Oral presentation

BLOOMING GLACIERS IN THE EUROPEAN ALPS: PHYLOGENY AND ECOPHYSIOLOGICAL COMPARISON OF *ANCYLONEMA NORDENSKIÖLDII* VS. *MESOTAENIUM BERGGRENII* (STREPTOPHYTA)

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Glacial ice surfaces are inhabited by extremophilic microalgae, which cause darkening leading to significant albedo reduction. These blooms have been long-term accelerating melting processes in Alpine and Polar regions. The most common species are the unicellular *Mesotaenium berggrenii* and the filamentous *Ancylonema nordenskiöldii*. They are members of the Mesotaeniaceae, a family in which semi-terrestrial or aerophytic habitats dominate. The aim of this study was to infer the phylogenetic position, elucidate the taxonomic relation and explore ecophysiological differences between *M. berggrenii* and *A. nordenskiöldii*, sampled in the European Alps. Since lab strains are not available to our knowledge, field populations dominated by either one or another alga were investigated. Photosynthetic performance (using PAM), the profile of the fatty acids (GC-MS) and phenolic pigments (HPLC) have been compared. In the 18S rDNA phylogeny of conjugating algae, the two glacial species form an independent, well-supported clade, together with samples from a glacier in Alaska. The closest non-psychrophilic relative is *Mesotaenium* sp. AG-2009-1. The fluorometric measurements showed that *A. nordenskiöldii* was adapted to very high light levels while *M. berggrenii* got earlier light saturated. The glacial algae produced a high level of polyunsaturated fatty acids (~50% in total fatty acids). Abundant, water-soluble polyphenolic pigments were present, and these putative ferrous organic complexes represent a powerful, broad sunscreen in both the UV and VIS region to protect cell against excessive ambient irradiation.

Financing: This research was funded by the Czech Science Foundation (GACR) projects 18-02634S and the Austrian Science Fund (FWF) project P29959.

Keywords: Photosynthesis, polyunsaturated fatty acids, polyphenols

Oral presentation

MULTI-OMICS REVEALS MECHANISMS OF TOTAL RESISTANCE TO EXTREME ILLUMINATION OF A DESERT ALGA

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The unparalleled performance of Chlorella ohadii (Treves *et al.*, 2016), clearly indicated that we lack essential information on the photosynthetic machinery and what sets the upper growth limits. Unlike other photosynthetic organisms, *C. ohadii* productivity is unaffected by irradiances of twice full sun light; Rather than succumbing to photodamage *C. ohadii* undergoes major structural and compositional changes emphasizing the unique PSII functioning as well as highly efficient reductant metabolic utilization downstream of the photosynthetic reaction centers. When grown under optimal laboratory or controlled outdoor conditions, this alga, recently isolated from one of the harshest environments (desert sand crusts), exhibits the fastest growth rates ever reported for an alga, division times shorter than 2 h were recorded. Growth of batch cultures under continuous high light (3000 μmol photons m-2 s-1) combined with metabolome analyses revealed a highly coordinated metabolic switch, supporting growth to higher densities than those achieved if abolished, and regulated by specific signaling molecules of the Polyamines group (Treves *et al.*, 2017). We applied an array of systems biology tools to reveal regulation of gene networks at the metabolic, redox and expression levels, for the first time under extreme illumination (Treves *et al.*, 2020). Combined multi-omics analyses identified key response regulators and provided novel insights into the mechanism underlying its exceptional photodamage resistance, including growth vs. stress signaling, morphological response and starch excess effects. These, together with a transformation system developed these days for *C. ohadii* will allow to dissect what distinguishes this alga from its more sensitive counterparts.

Keywords: Systems biology, abiotic stress, photosynthesis

Oral presentation

CHARACTERIZATION OF ZYGOSPORE FORMATION IN THE CONJUGATING GREEN ALGA *MOUGEOTIA* (ZYGNEMATOPHYCEAE)

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Zygnematophyceae are a class of streptophyte green algae, sister to Embryophytes. They are characterized by a special form of sexual reproduction, termed conjugation, which results in the formation of zygospores. Zygospores possess a thick, resistant cell wall, enabling them to endure unfavorable conditions like desiccation or freezing events for a prolonged period. This study presents investigations of the conjugation morphology of *Mougeotia parvula* and *Mougeotia disjuncta*, collected from field samples from the Austrian Alps. Both species performed an isogamous extra-gametangial scalariform conjugation. During the conjugation process pectins (mainly homogalacturonan), xyloglucans, xylans, arabino-galactan proteins and extensins, were detected by glycan microarray analysis. In the course of a 4-months maturation process, the zygospores developed a multi-layered cell wall and accumulated storage compounds in their cell lumen, while the surface was covered by a loose polysaccharide layer. The zygospore wall encompassed four layers, an inner polysaccharide rich endospore, a thin layer with a lipid-like appearance, a massive electron dense mesospore and an outer very thin exospore, composed of polysaccharides. In situ localization by fluorescently labelled oligogalacturonides in young zygospore walls as wells as in vegetative filaments, but most prominent in cross walls and conjugation tubes. Raman imaging allowed to detect carbohydrates and lipids in the cell lumen as well as an enrichment of lipids and an aromate-rich layer in the wall, the latter possibly containing sporopollenin-like components. The results of this multi-technical approach indicate that the zygospore resistance is caused by the formation of an entirely new zygospore wall during their maturation.

Financing: This study was supported by the Austrian Science Fund FWF project P 34181

Keywords: Conjugation, Zygnematophyceae, *Mougeotia*

Oral presentation

CYANIDIOPHYCEAE AS A MODEL FOR UNDERSTANDING HORIZONTAL GENE TRANSFER AS A DRIVER OF CELL ADAPTATION IN EXTREME ENVIRONMENTS

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The Cyanidiophyceae are a group of unicellular red algae such as *Galdieria*, *Cyanidium*, and *Cyanidioschyzon* that occupy a variety of hot springs and acid mining sites characterized by variable light levels, high temperature, low pH, with high salt and toxic heavy metal concentrations. Recent collaborative work in our lab shows that the HGT candidates bioinformatically identified within the Cyanidiophyceae encode proteins that function in pathways related to polyextremophily, including metal and xenobiotic resistance/detoxification, cellular oxidant reduction, carbon metabolism, amino acid metabolism, osmotic resistance, and salt tolerance. This presentation will highlight my ongoing work to confirm the existence of these HGTs functionally and model their role within metabolic networks to better understand how these organisms evolved to inhabit such extreme environments and how HGT can act as a driver of evolution in eukaryotes, underpinning major lifestyle transitions.

Financing: NASA FINESST grant: 80NSSC19K1542, JGI CSP FY21

Keywords: HGT, red algae, extremophiles

Oral presentation

METABOLIC COMPARISON OF SIX CHLOROMONAS STRAINS (CHLOROPHYTA) ISOLATED FROM MELTING ALPINE SNOW, GROWN AT 1 AND 15°C

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Psychrophilic microalgae living in melting snow cause green, yellow or red blooms during spring and summer. Such Polar and Alpine habitats are characterized by low temperatures and diurnal freeze-thaw-cycles. Life-cycle traits like the formation of robust cysts stages and abundant cytosolic, protective pigments are well-known measures of adaptations. In this study, GC-MS based metabolite profiling was applied to investigate metabolite accumulation in six strains of *Chloromonas* (Chlorophyta). The strains, isolated from mountainous snow, were grown at 1 and 15°C to evaluate temperature-dependent or individual differences on a species level. This method allowed the identification and quantification of more than 120 primary and secondary compounds. On the one hand, we found metabolites such as glycerol and carbohydrates, which showed a significant accumulation at the lower temperature, whereas others such as pipecolic acid, involved in plant-pathogen defence, were more abundant at the higher temperature, likely as a response to co-present bacteria which subsequently became more dominant at 15°C. A third group of metabolites including the antioxidant α-tocopherol showed no uniform trend for all six species, pointing to individual responses to temperature change. With this protocol, it was possible to distinguish "true", psychrophilic snow algae, from rather psychrotolerant species. The latter were present in the harvested snow as well but had not the capability of causing macroscopic blooms.

Financing: This work was supported by the Austrian Science Fund (FWF): P29959 and P34073 to D.R.

Keywords: Snow algae, metabolomics, temperature

Oral presentation

MICROALGAE ASSOCIATIONS ON THE SURFACE OF MARINE DEBRIS FROM THE BLACK SEA REGION

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Marine debris, which mainly consists of different types of polymer synthetic materials, is colonized by marine organisms that could use it as a substrate, participate in their decomposition and form unusual biological communities. The character of microalgae formation on the surface of marine debris (PP, PE, PET, PVC, LDPE, HDPE) was analyzed from different locations in the Black Sea region in 2016-2020. We revealed limited number of species that dwell on the surface of the debris: on the sea-floor this is mainly *Cocconeis* and *Amphora*, on the surface – *Mastogloia* and *Neosynedra*. The main patterns for different genera were revealed. Most of the mobile species lose their mobility and attach to the plastics. Assemblages of microalgae on plastic surface form complicated multilayer structure, that is often structured with a matrix of diatoms and cyanobacteria, which protects their cells from the aggressive environment (insolation, temperature extremes and wide ranges of salinity in the surface water layer). On the surface of marine debris benthic forms of diatoms and cyanobacteria predominated. Most of the species are typical for the region, however the diversity on the polymers is significantly lower. The phytofouling on the debris demonstrates the complex of adaptations that was not registered on the natural substrates. The assemblages that colonize various types of plastics in the same environment were slightly different by the species composition but possess another structure and spatial organization.

Keywords: Diatoms, plastic substrate, Black Sea

Oral presentation

COMPREHENSIVE PROTEOMIC AND PHOSPHOPROTEOMIC ANALYSIS OF *PYROPIA YEZOENSIS* RESPONDING TO DESICCATION/ REHYDRATION STRESS

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Daily changes of tides in the intertidal zone is a severe stress factor for the organisms living in that environment. *Pyropia yezoensis*, a representative seaweed inhabiting the intertidal zone, can tolerate dissication-rehydration stress effectively. However, the mechanisms underlying the response of *P. yezoensis to* dessication stress remain tittle understood. Here, we elucidate the proteomic and post-translational changes in P. yezoensis following desiccation and rehydration stress. Tandem mass tags (TMT) technology was used to characterise the proteome and phosphoproteomic profiles. To study the molecular mechanisms underlying water stress response further, the proteome differences between control and desiccation (DE)/rehydration (RE) treatments were compared pairwise with a control treatment (DEH30, DEH50, DEH70 and REH30). In total, 20 differentially expressed proteins (DEPs) were up-regulated and 28 were down-regulated in the DEH30 versus control comparison; 229 DEPs were up-regulated, and 149 were down-regulated in the ‘DEH50 versus Control’ comparison; 469 DEPs were up-regulated, and 248 were down-regulated in the DEH70 versus control comparison; 107 DEPs were up-regulated, and 52 were down-regulated in the REH30 versus control comparison. The functions of these DEPs were classified according to their pathways by KEGG analysis. The top five pathways included “Ribosome”, Oxidative phosphorylation”, Aminoacyl-tRNA biosynthesis”, RNA transport” and Thermogenesis”. Further phosphoproteomic analysis showed the phosphorylation levels of 412 peptides were up-regulated and 509 were down-regulated. Among the KEGG pathways of the proteins involved in these peptides, the top five included “RNA transport”, “RNA degradion”, Pi3K-Akt signaling pathway”, “spliceosome” and “AMPK signaling pathway”. These information provide understanding the mechanisms of *P. yezoensis* response to water stress.

Keywords: Proteome, phosphoproteomics, water stress

Oral presentation

CARBON ASSIMILATION IN THE COMMUNITY INHABITING THE SECONDARY CHLOROPHYLL MAXIMUM OF ANOXIC MARINE ZONES OF THE EASTERN TROPICAL PACIFIC OCEAN

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The anoxic marine zones (AMZs) are pelagic systems characterized by the complete absence of detectable oxygen, a low pH values but plenty of nutrients. In some cases, the anoxic layer overlaps with very low levels of light (<1% of incident light) allowing the development of a secondary chlorophyll maximum (SCM), composed mainly by not yet cultivated ecotypes of Prochlorococcus. The success of Prochlorococcus in the SCM has been explained in part by the presence of divinyl chlorophyll-a as the main photosynthetic pigment, very efficient capturing solar energy at such depths. However, some genomic studies suggest a possible complementary heterotrophy, that would be very important due that they experience long periods with insufficient solar radiation to perform photosynthesis. Here, we compared measurements of δ13C for particulate organic carbon (POC) from the primary and secondary chlorophyll maximum (PCM and SCM respectively) and also at the top of the anoxic layer when no SCM was developed, and complemented these measurements with community C uptake rates experiments. Our results showed significant differences in δ13CPOC values among stations with and without SCMs, being 3.0‰ heavier when a SCM is developed in the top of the AMZ. Depleted δ13CPOC values were found when no SCM was present indicating stronger chemoautotrophic activity, probably by anammox and sulfur-oxidizing bacteria. Uptake rates showed that in the majority of the stations both glucose and acetate exceeded inorganic C fixation rates, being performed probably by members of SAR11 clade and Prochlorococcus, supporting that often the SCM is still a net heterotrophic system.
Financing: Supported by the Millennium Science Initiative (grant ICN_019), Agencia Nacional de Investigación y Desarrollo (Fondecyt 1161483 and Conicyt-USA 20120014).

Keywords: Carbon, anoxic marine zones, *Prochorococcus*

Oral presentation

NOVEL CYANOBACTERIAL DIVERSITY FROM LAKE HURON SINKHOLE COMMUNITIES: DESCRIPTIONS OF *GEITLERINEMA VISII, PHORMIDESMIS*

TABULATUM, JAAGINEMA SULFUREA, AND *MICROCOLEUS COMMUNIS*

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Cyanobacteria are a diverse assemblage of organisms present in nearly every known ecosystem. While superficially similar in morphology, the cyanobacteria as a whole likely contain vast amounts of cryptic diversity. Recent investigations around the world have recovered vast amounts of novel biodiversity in seldom sampled extreme habitats. Submerged sinkholes with oxygen-poor, sulfur-rich groundwater in Lake Huron (U.S.A.) contain microbial mats dominated by both oxygenic and anoxygenic cyanobacteria. We sought to document some of this unique cyanobacterial diversity in diver-collected sediment cores with intact overlying microbial mats from a depth of 23m. Filamentous cyanobacteria formed elaborate, entwined benthic mat communities that undertake diel vertical migrations. Using culture-based investigations, we recovered 20 unique strains. The strains were analyzed using a total evidence approach employing 16S-23S rDNA sequences, ITS folding patterns, ecology, and morphology. Using this approach, we erected four new taxa according to the International Code of Nomenclature for Algae, Fungi, and Plants: *Geitlerinema visii, Phormidesmis tabulatum, Jaaginema sulfurea*, and *Microcoleus communis.*

Financing: National Aeronautics and Space Administration (NASA) grant.

Keywords: ITS, systematics, benthic mats

Oral presentation

COMPARATIVE METAGENOMICS OF SNOW ALGAL BLOOMS

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Snowy and glaciated alpine environments are among the most threatened on our warming planet. The organisms that live in and on glaciers are experiencing dramatic changes in their physical environment and rapid loss of habitat. Glacial environments are host to complex microbial eukaryotic communities largely driven by algal primary production that produce pink or red blooms on snow. Blooms of snow algae are intricately tied to this process of melting — they need liquid water to reproduce while colored blooms increase melt that in turn reduces available habitat. Despite the impact of snow algae on glacial melt, there are outstanding questions about the life cycle of these algae, their dispersal, and community biodiversity across mountain ranges that are critical to our understanding of how and why blooms emerge in these dynamic habitats. Recent DNA surveys from snow algae sampled from snowy and glaciated environments globally suggest few taxa have the ability to create large blooms that could have a quantitative impact on snowmelt. In this study, we compare metagenomes from three, spatially and temporally distinct bloom samples from the Cascade Mountains, a low elevation highly glaciated mountain range with comparatively high snow algal diversity. Our early season sample hosts a new *Clainomonas* species, which reliably blooms each year. Two later season samples host *Sangunia* species that are morphologically distinct. We discuss the implications of these results in the context of algal life cycles and dynamic snow habitats.

Keywords: Snow algae, metagenomomics, snow

Oral presentation

PHYTOPLANKTON DIVERSITY ACROSS THE MARGINAL ICE ZONE IN BAFFIN BAY, ARCTIC

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The importance of under-ice blooms in the Arctic Ocean has been increasingly acknowledged, representing a paradigm shift in our understanding of phytoplankton phenology and biogeochemical cycling in the region. Baffin Bay is a seasonally ice-covered sea within the Canadian Arctic, with a complex interplay of Atlantic and Arctic-originated water masses. In order to investigate the plankton communities across the marginal ice zone in Baffin Bay, we sampled the water column on 16 stations at 6 depths each from June to July 2016, filtered seawater through three different size fractions (20µm, 3µm, and 0.22µm), and used high-throughput sequencing (Illumina) to sequence the V4 region of the 18S rRNA gene. Stations were grouped into “Open Water” (OW), “Marginal Ice Zone” (MIZ), and “Under Ice” (UI) based on its sea-ice cover. The plankton community structure was markedly different between ice-associated and open-water stations, as well as between size fractions. The >20µm size fraction was dominated by Bacillariophyta, with *Melosira, Porosira*, and *Fragilariopsis* particularly present at MIZ and UI stations. The 3-20µm size fraction was the most diverse, especially at UI stations, being dominated by *Fragilariopsis, Chaetoceros*, and *Phaeocystis*, followed by the cryptophytes *Falcomonas* and *Teleaulax*, along with MOCH-2 (Marine OCHrophyta). The 0.2-3µm size fraction was dominated by *Phaeocystis* at OW stations, while the Mamiellophyceae *Micromonas polaris* dominated UI stations along with

a much more diverse community. The Arctic is undergoing drastic changes directly linked to sea-ice decline, and the present study provides insights on the impact of sea-ice loss on ice-associated pelagic plankton.

Financing: FONDECYT project (3190827); Green Edge project (ANR-14-CE01-0017, Fondation Total); ANR PhytoPol (ANR-15-CE02-0007); TaxMArc (Research Council of Norway, 268286/E40).

Keywords: Polar phytoplankton, Arctic, 18S rRNA

Oral presentation

METABOLITE CHANGES DURING DESICCATION-REHYDRATION CYCLE IN DESERT AND AQUATIC GREEN ALGAE FROM *TETRADESMUS*

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Desert algae in the phylum Chlorophyta are not monophyletic and diverse taxa possess the ability to recover from extreme desiccation without forming specialized resting structures. The green algal genus *Tetradesmus* (Sphaeropleales, Chlorophyceae) contains temperate terrestrial, desert, and aquatic species, and recent analysis indicates multiple habitat switches in the genus. Habitat of origin was shown to be predictive of a desiccation tolerance phenotype, with terrestrial, but not aquatic species, recovered their photosynthetic activity upon rehydration after desiccation. Close phylogenetic relationships of these algae and their distinct responses to desiccation provide a unique opportunity to pinpoint specific physiological adaptations of terrestrial algae to their habitat. We used liquid chromatography tandem mass spectrometry (LC-MS/MS) methodology to study changes in composition of small water-soluble molecules in aquatic and terrestrial *Tetradesmus* under desiccation followed by rehydration. Our questions focused on assessing if there are constitutive protective compounds in the terrestrial algae, determining their composition, and how these might compare from other desiccation tolerant green algae. We also examined how the metabolomic profiles change over the course of a dehydration and rehydration cycle. Our analysis shows that each of the cell hydration state (dehydrated, desiccated, rehydrated for 15 min, and rehydrated for 24 h) are characterized by a distinct metabolite profile.

Financing: 2018 UConn EEB Research Award; 2020 North-Eastern Algal Society Graduate Research Award; 2020 Uconn Doctoral Dissertation Fellowship

Keywords: Desiccation-tolerance, metabolomics, *Tetradesmus*

E-Poster

THE GENETIC DIVERSITY OF BIOFILM COMMUNITIES COLONISING A CENTRAL MEDITERRANEAN SHORELINE

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Phototrophic biofilms and microbial mats colonise coastal rocky shores around the Maltese islands. Such communities are under-investigated, both locally in Malta and regionally in the Mediterranean area. This study aims to increase the knowledge of the genetic diversity of phototrophic communities forming biofilms and microbial mats along a central Mediterranean shoreline, that are adapted to survive stressors of temperature, salinity and UV radiation. Representative samples were obtained using techniques that were non-invasive to the underlying substratum. These were studied by direct observation using light and electron microscopy, as well as by molecular and phylogenetic analyses based on the sequencing of the SSU rRNA genes and the ITS. Microscopic analysis showed that the biofilms and microbial mats were highly diverse communities made up of both phototrophic and heterotrophic organisms. The predominant microorganisms were filamentous cyanobacteria belonging to species of the Leptolyngbyaceae, including *Leptolyngbya, Phormidesmis* and *Nodosilinea* spp. strains, together with *Toxifilum* sp. strains of the Pseudanabaenaceae, the non- heterocytous Phormidium and Lyngbya, as well as heterocytous *Calothrix* and *Nunduva* spp. representatives. The coccal cyanobacteria included species of *Aphanocapsa and Chroococcus*, while coccal microalgae belonged to *Chlorella, Chlamydomonas* and *Coelastrella* spp., diatoms of *Navicula* spp., as well as germlings of the filamentous macroalga Cladophora. Ciliated protozoans and microcrustaceans were also observed interacting within the community. The isolation of new cyanobacterial and microalgal strains from these phototrophic communities highlights the importance of a combined polyphasic approach to supplement current knowledge about the biodiversity of phototrophic biofilms and microbial mats colonising rocky shores.

Keywords: Biofilm, cyanobacteria, microalgae

E-Poster

THE ROLE OF CYANOPROKARYOTA IN THE RHIZOSPHERES OF GYPSOPHYTES AND EFFECTS OF DROUGHT AND WATER PULSES ON MICROBIAL FUNCTIONALITY

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In a Mediterranean environment plants are subject to water stress and lack of nutrients, among others. The adaptations

that they can present are very varied and depend on the type of soil and the climate itself. In gypsiferous soils the adaptations of gypsophytes are numerous and unclear. Cyanoprokaryota had a relevant role in the rhizospheres of gypsophytes in drought conditions. We detect the responses to the availability of water in the rhizospheres of three gypsophytes and in non-rhizospheric soil during a summer drought and during spring. Water retention and water loss were studied. We were obtained the highest values in drought conditions due to the association of Cyanoprokaryota with the rhizospheres. The results are also explained by two water pulses that occurred before the samplings. Several parameters, whose values changed markedly due to the microbiological activation just after the drought and water pulses, are proposed as indicators of this activation: microbial biomass carbon and basal respiration rate, together with urease and protease. However, it was the dehydrogenase activity in spring that best reflected the microbiology associated with the carbon cycle, together with β-glucosidase. The interrelationships between carbon and nitrogen were shown through the indices: water soluble nitrogen and water soluble carbon. We propose three functional adaptation mechanisms of these plants associated with the Cyanoprokaryota in their rhizospheres and related to the water availability as determined by drought and water pulse effects.

Financing: This study was funded by the Spanish National Government (CICYTCGL2009-12582-C02-02) and by the Valencian Autonomous Government (AICO/2019/258)

Keywords: cyanobacteria, rhizospheres of gypsophytes, water availability

E-Poster

OSTREOBIUM: LIVING IN A DARK PLACE

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Ostreobium is an endolithic green alga that lives inside the coral's skeleton, which is a very dimly lit environment with strong fluctuations of pH and O_2. When the coral is healthy, the light availability inside the coral skeleton consists mostly of the far-red wavelengths that are not used by the coral dinoflagellate endosymbionts. During coral bleaching events, when the coral expelled its endosymbionts, the *Ostreobium* blooms and can provide photosynthate to the corals. We present the *Ostreobium* nuclear genome, which provides insights about *Ostreobium's* adaptations to its extreme environment. This alga is adapted to a low-light environment because it presents a rich repertoire of light-harvesting complex proteins associated with both photosystems (PSI and PSII). It shows duplications of the Lhca1 and Lhca6 genes associated with PSI and both *Lhcp* and *Lhcb* genes in PSII. The Lhca1 protein in *Ostreobium* seems to be adapted to absorb red-shifted light. The Lhca1 typically uses histidine in the A5 site as the chlorophyll-binding residue, and these proteins in *Ostreobium* have asparagine instead. Lhca1 mutants with asparagine absorb red-shifted light in Arabidopsis thaliana. *Ostreobium* has a large arsenal of genes for combat reactive oxygen species (ROS), which is essential to protect itself in an environment with a high variation of pH and O_2. It presents tandem copied of catalase, and high copy numbers of enzymes belong to the glutathione-ascorbate cycle, both are important to neutralise hydrogen peroxide. Our work provides a comprehensive understanding of the adaptations of *Ostreobium* to its extreme environment.

Keywords: Coral holobiont, green algae, low-light adaptation

E-Poster

DIATOMS FROM EUTROPHIC HYPERSALINE LAGOONS IN BIOREMEDIATION AND FATTY ACID PRODUCTION

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Microphytobenthos contributes in a high proportion to total primary production in hypersaline coastal lagoons. However, microalgal benthic communities have been scarcely studied. Flora and species dynamics are poorly known as is their potential biotechnological applications. The Mar Menor coastal lagoon (Murcia, SE Spain) is one of the biggest lagoons in the Mediterranean region and has historically suffered various environmental impacts. The most important at present is the high level of eutrophication derived from agriculture practices and the high concentrations of heavy metals from run off of temporary streams draining old mines. The aims of this study were to know the potential of diatoms in bioremediation and as a source of fatty acids. Strains of *Halamphora, Nitzschia, Cylindrotheca* and *Rhoicosphenia* (Bacillariophyta) were isolated from the lagoon and maintained in culture under 80 mM m-2s-1 of PAR and a photoperiod of 16L:8D, in f2 medium with aeration. The oligoelements and fatty acid methyl esters (FAMEs) were identified and quantified with ICP-MSD and GC/MSD spectrometry, respectively. All strains accumulated fairly high concentrations of P and heavy metals, especially Cu and Zn but a great variability was found between strains. The saturated fatty acids were the predominant but a high proportion of the omega-3 eicosapentaenoic acid (EPA) was also found. The results show the interest of diatoms in bioremediation and also as feedstock of fatty acids and likely several other valuable compounds.

Financing: This work was partially supported by the Fundación Seneca (CARM, Murcia, Spain) Project 20961/PI/18; and University of Murcia Project UMU15452.

Keywords: Diatoms, fatty acids, hypersaline lagoons

E-Poster

WATER-SOLUBLE ASTAXANTHIN-BINDING PROTEINS FOR PHOTOOXIDATIVE STRESS TOLERANCE FOUND IN EUKARYOTIC MICROALGAE

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Astaxanthin, a known potent antioxidant carotenoid, accumulates as lipid droplets under stressful environments in eukaryotic microalgae. Until recently a water-soluble form of astaxanthin was unknown. In our study, a novel water-soluble astaxanthin-binding protein named AstaP has been found in *Coelastrella astaxanthina* Ki-4 (Scenedesmaceae) isolated from an asphalt surface in mid-summer1-3. AstaP was identified as a photooxidative stress-inducible protein. The protein is a secreted fasciclin-like glycoprotein with potent O2 quenching activity in aqueous solutions. Recently, we also identified three novel AstaP orthologs in a eukaryotic microalga, *Scenedesmus* sp. Oki-4N4. The characteristics of purified proteins, named AstaP-orange2, AstaP-pink1, and AstaP-pink2, were similar to those of Ki-4 AstaP including photooxidative stress-inducible expressions. However, proteins differed significantly concerning the absence of glycosylation in the AstaP-pinks, and the presence of a glycosylphosphatidylinositol (GPI) anchor motif in AstaP-orange2. These had highly acidic isoelectric points (pI = 3.6–4.7), whereas pI of Ki-4 AstaP is basic 10.5. We concluded that these algae produced AstaPs as bifunctional proteins that provide shade effect and exert antioxidant activity under photooxidative stress conditions. To our knowledge, other related proteins have not yet been reported. In this presentation, we report the results of further analyses concerning the function of AstaPs in photooxidative stress protection as well as the distribution of this protein in microalgae including Scenedesmaceae. References: 1. Kawasaki et al. Plant Cell Physiology 54:1027-1040 (2013)//2. Kawasaki et al. Phycological Research 68:107-114 (2020)//3. Toyoshima et al. Algal Research 50:101988 (2020)//4. Kawasaki et al. Communications Biology 3:490 (2020)

Financing: Japan Society for Promotion of Science (No. 26440155); Institute for Fermentation, Osaka (IFO, No. G-2014-2-072); Cosmetology Research Foundation (J-15-2).

Keywords: Astaxanthin, photooxidative stress, extreme environments

E-Poster

MICROBIAL DIVERSITY OF PINNACLE AND CONICAL MICROBIAL MATS IN THE PERENNIALLY ICE-COVERED LAKE UNTERSEE, EAST ANTARCTICA

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Cyanobacteria are particularly successful at surviving in extreme environments and Antarctic perennially ice-covered lakes provide a stable low-disturbance environment where complex microbially mediated structures can grow. Lake Untersee, an ultra-oligotrophic lake in East Antarctica, is characterised by extreme conditions including low temperatures, alkaline pH and seasonal low light availability. The lake floor is covered in benthic microbial mat communities, where laminated organo-sedimentary structures form with three distinct, sympatric morphologies: small, elongated cuspate pinnacles, large complex cones and flat mats. We examined the diversity of prokaryotes and eukaryotes in pinnacles, cones and flat microbial mats using high-throughput sequencing of 16S and 18S rRNA genes and assessed how microbial composition may underpin the formation of these distinct macroscopic mat morphologies under the same environmental conditions. The prokaryotic communities were dominated by Cyanobacteria, Proteobacteria, Verrucomicrobia, Planctomycetes, and Actinobacteria. The cyanobacterial taxa were composed largely of *Tychonema*, but also included *Leptolynbya* and *Pseudanabaena* in all samples. These genera have been found in other Antarctic lakes, such as Lake Vanda, suggesting that these genera are ideal candidates for further research on the adaptation of cyanobacteria to cold environments. Our study provides the first report of the eukaryotic community structure of Lake Untersee benthic mats, which was dominated by Ciliophora, Chlorophyta, Fungi, Cercozoa and Discicristata. These findings revealed that the macroscopic microbial mats of Lake Untersee harbour diverse cyanobacteria, bacteria and eukaryote communities which play a role in structure morphogenesis, allowing distinct structures to form across a small spatial scale.

Financing: TAWANI Foundation, the Trottier Family Foundation, NASA's Exobiology Program (80NSSC18K1094) and the Russian Antarctic Expedition. NERC GW4+ DTP [NE/L002434/1].

Keywords: Cyanobacteria, microbial mats, Antarctica

E-Poster

MESOPHOTIC MACROALGAE OF CUBA: THE 2017 JOINT CUBA-U.S. EXPEDITION

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The 2017 Cuba-U.S. Expedition, on the R/V Walton Smith, employing ROV surveys and collections, provided the first significant sampling of the mesophotic macroalgal community in Cuban waters. 102 macroalgal taxa have been observed in images and samples collected with the ROV. Rhodophytes had the highest richness (47 taxa, 46.1%), followed by chlorophytes (35 taxa, 34.3%), and phaeophyceans (20 taxa, 19.6%). Macroalgal taxa common to all regions of these mesophotic reefs included coralline red algae (Subclass Corallinophycidae) and the family Peyssonneliaceae in the Rhodophyta; some green unidentified crustose forms, the genera *Halimeda* (particularly *H. copiosa, H. goreaui, H. tuna), Avrainvillea, Penicillus*, and *Udotea* (particularly *U. cyathiformis*) in the Chlorophyta; and the genera Dictyota and Lobophora in the Phaeophyceae (Ochrophyta). Macroalgal diversity and coverage of algae were low on the deep island slope (125–150 m); only crustose coralline algae (CCA) and thin encrusting green algae occurred. Between 50–100 m, macroalgal diversity and cover increased, with *H. copiosa* and CCA dominating. In the upper mesophotic zone (30–50 m), species richness increased, with phaeophyceans (*Lobophora* spp., other Dictyotales) dominating. The presence of macroalgae appeared highest in the western zone of the Cuban shelf. This abundance may be caused by distribution by oceanic currents and higher levels of nutrients that might be related with upwelling at San Antonio Bank. In addition to their important role as primary producers, mesophotic macroalgae are no doubt important to structuring MEs and merit more study to better elucidate and quantify their multiple roles at these depths.

Keywords: Mesophotic, macroalgae, Cuba

SYM15: Applied Phycology – Research and Innovation

Keynote lecture

TROPICAL SEAWEEDS: ‘BLUE’ STEPS TOWARDS THEIR POTENTIAL UTILIZATION

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The concept of ecological integrated aquaculture to obtain algal biomass, coupled with the use of environmentally friendly extraction techniques as well as the biorefinery concept are novel research strategies focus into the ‘blue economy’ which highlights the sustainable use of marine resources by providing economic and ecological benefits. Among the current important carragenophytes, one of the most abundant genus belongs to the Solieriaceae family. Among them, the tropical species *Solieria filiformis* (Kützing) P.W. Gabrielson has been reported as an important source of iota-carrageenan. Previous biochemical studies have revealed that this species also contains other valuable compounds with bioactive capacity. Moreover, *S. filiformis* has been successfully integrated into a sustainable aquaculture system (IMTA) obtaining high productivity and growth rates that have allowed us to obtain a clean and healthy biomass. In addition, this species has shown a potential capacity to mitigate the environmental impacts of aquaculture by improving water quality due to its biofiltration capacity. In this context, and with the need of a sustainable and an ecofriendly use of this species in mind, results on some of its valuable products of pharmacological and nutraceutical importance obtained through of cascading approach using ecofriendly extraction technologies will be exposed and discussed.

Financing: PN-CONACYT 2015-01-118 project; ECOS-Nord CONACYT collaboration project M14A03

Keywords: *Solieria filiformis*, ecofriendly technologies

Keynote lecture

POTENTIAL OF MICROALGAE-BASED BIOREFINERIES UTILIZING WASTEWATER AND AQUATIC PLANTS

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Microalgae-based biorefineries offer several advantages compared to first and second generation biorefineries, especially because they do not compete with food production land and may offer simultaneously a variety of biofuels and high added products. However, there are still several challenges and limitations to overcome such as the cost of production, high biomass yields and integration of appropriate unit operations, especially downstream. Thus, one of the alternatives that can be envisaged is the use of wastewater in mixotrophic cultures. This research line has already grown substantially in the recent years, demonstrating the advantage of using certain type of wastewater to lower the cost of production. Furthermore, our research group has integrated the use of a “phytofiltration lagoon” with aquatic plants (*Pistia stratiotes*), as a first module of a microalgae-based biorefinery, to treat the water of a polluted river and to avoid the use of water for agriculture. An additional advantage is that the harvested biomass of P. stratiotes is processed in a second module to produce biogas or hydrogen. Microalgae biomass of different species has been cultivated in a third module utilizing digestates of agricultural wastes, either for accumulation of lipids in the case of *N. oleoabundans* or accumulation of carbohydrates in the case of *Chlorococcum* sp. with the purpose of producing biodiesel or bioethanol, respectively. Finally, the production of phycocyanin in a novel two-phase process from *Arthrospira* maxima using membranes for harvesting, extraction and purification has also been integrated in the biorefinery at pilot plant level.

Keywords: High-added value products, cyanobacteria, biofuels

Oral presentation

VALIDATING THE CIRCULAR ECONOMY CONCEPT IN MICROALGAE BIOTECHNOLOGY

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Circular economy is a concept that has been implemented in several industries in recent years. Microalgae biotechnology is gaining attention as a method for industrial bioremediation and for biomass production that could have several commercial applications. In this work, we report a successful validation of a circular economy concept for the first time by using microalgae biotechnology at a relevant industrial scale (> 5m3) using a new two-step process. During the first phase biomass was grown autotrophically, biomass was then concentrated using membrane technology (0.1 µm) for the second phase where mixotrophic conditions (glucose, acetate and dextrose used as a carbon source) were applied to boost growth further. *Chlorella vulgaris* microalgae cultures were able to produce over 5.5 g/L of dry biomass in mixotrophic conditions, uptake over 104 mg/L/day of ammonium and bioremediate nutrients from an anaerobic digestion side-stream (digestate), obtaining high quality microalgae biomass (> 40% in protein content) suitable for use as animal feed. Better results (> 12 g/L and > 134 mg/L/day of ammonium uptake) were obtained when Scenedesmus obliquus was the target species, producing microalgae biomass in a sustainable way and closing the circular economy loop for industrial applications.

Financing: This work was funded by the Interreg North West European Regional development fund, project ALG-AD.

Keywords: Circular-economy, microalgae, anaerobic-digestion

Oral presentation

HIGHLY EFFICIENT WATER-BASED EXTRACTION OF R-PHYCOERYTHRIN FROM MACROALGAE *GIGARTINA SCOTTSBERGII* (RHODOPHYTA): OPTIMIZATION OF CONDITIONS BY ULTRASOUND AND HIGH-PRESSURE HOMOGENIZATION METHODS

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Gigartina skottsbergii is a phycoerythrin-producing specie, endemic to the southern region of South America, which produces near of twenty thousand tons of dry alga to be commercialized in Europe and Asia. The valuation of phycoerythrin in a model of biorefinery is still incipient in algal biotechnology and thus has great prospects in the food, pharmaceutical, cosmeceutical, and nutraceutical industry. The aim of this work was to evaluate the extraction and separation processes variables of two green technologies (ultrasound and high-pressure homogenization) from *G. skottsbergii* to obtain a phycoerythrin enriched extract. Based on a two-level three-factor central composite design (CCD) and response surface methodology (RSM) was carried out to optimize the extraction conditions, including the variables for ultrasound (time, amplitude and solvent of extraction) and high-pressure homogenization (Pression, number of passes and solvent of extraction). Additionally, a second-order polynomial fit was performed to fit the experimental data by the green method. The optimal conditions were obtained for the HPP including, pressure power (300-400MPa), number of passes (2-3) and solvent of extraction (distillated water). Furthermore, the experimental extraction yields ranging from 5.1-5.5 mg/g of phycoerythrin by dry biomass under the optimal extraction conditions, which was in good agreement with the predictive yield of 4.8-5.4mg/g of phycoerythrin by dry biomass. The ultrafiltration membrane exhibited at total rejection of phycoerythrin (100% was recovered) without denaturation. Interestingly, the cost for extraction of phycoerythrin can be lower with water than buffer phosphate, visualizing a possible cost-effective biorefinery from this macroalgae for food ingredients industry.

Financing: We are thankful to Gelymar S.A.for providing algal biomass and the ANID for PhD scholarship to Mr. Pablo Castro-Varela.

Keywords: R-Phycoerythrin, *Gigartina skottsbergii*, food ingredients.

Oral presentation

SUSTAINED POWER OUTPUT FROM ALGAL BIOPHOTOVOLTAIC (BPV) PLATFORMS USING SELECTED MARINE AND FRESHWATER MICROALGAE

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The rise in fossil fuel consumption to meet the demands of rapidly growing economic and social sectors, has exacted a toll on the environment. Accelerated melting of icecaps, pollution, and rising sea levels are among the detrimental effects of excessive burning of fossil fuels. The global community has addressed these warning signs of environmental degradation by scaling up the use of renewable energy to minimize our dependency on fossil fuels. The current renewable energy market trend revolves around conversion of biomass including microalgae into energy through biofuel and bioelectricity generation. Algae are amongst the most efficient photosynthetic organisms, amenable to growth on a wide range of substrates, and have high tolerance for fluctuating abiotic factors. The integration of microalgae and photovoltaics is an innovative concept for provision of energy for small-scale applications. Our algal BPV platforms have evolved from ITO-based anode with biofilm grown on its surface to an integrated, multi-functional device that generates bioelectricity, removes carbon dioxide and bioremediates wastewater. This present work explores the sustainability of power output from our algal BPV platforms as well as their performance recovery after they were refreshed with fresh media. Our BPV platforms generated up to 0.10 mWm-3 from the freshwater cyanobacterium *Synechococcus elongatus* UMACC 105. An external resistance of 62K W was applied to the BPV devices for 50 days to determine the durability of our algal BPV platforms in bioelectricity generation. Correlation between the physiological state of the microalgae, biomass and stability of the power output will be discussed.

Keywords: Bioelectricity, microalgae, biophotovoltaics

Oral presentation

CO-CULTURE UNDER OCEAN ACIDIFICATION CONDITIONS: MACROALGAE CREATE FAVOURABLE CONDITIONS FOR MUSSEL CALCIFICATION ONLY DURING DAY-TIME IN A CLOSED ENVIRONMENT

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Changes in the seawater carbonate system due to ocean acidification (OA) such as reduced seawater pH and aragonite saturation state (Ωarg) can negatively affect the production and maintenance of bivalves ´shells (calcification). Thus, OA have the potential to adversely affect mussel aquaculture worldwide. Physiological process such as mussel respiration releases CO2 to the environment, decreasing seawater pH to levels similar to those predicted under OA. However, incorporating macroalgae into mussel farms may buffer OA impacts on mussels because they can reduce excess of CO2 through photosynthesis that increases pH and Ωarg. To test this hypothesis, we monitored changes in seawater carbonate chemistry (pH, O2, CO2, Ωarg) produced by a mussel (*Mytilus chilensis*) and three macroalgae (*Agarophyton chilensis, Macrocystis pyrifera* and *Ulva* sp.) in mono-cultures and co-cultures conditions under two initial pH (pHinitial) treatments (7.20 and 8.20), for 28h. In mono-cultures at both pHinitial treatments, mussel respiration reduced pH to <7.00 (Ωarg <1 and O2 <25%) while the three macroalgae increased pH to >8.20 (Ωarg >1 and O2 >200%) during day and decreased pH to 8.00 during night. In co-cultures at both pH initial treatments, pH was increased to >8.20 during day-time but pH dropped to ~7.00 for ~3 h during night-time. Our results indicate that, in a closed system, macroalgae may mitigate OA impacts on mussel calcification by raising seawater pH and providing refuge from acidification stress but only during day-time. These results will be discussed in order to understand how macroalgae can protect mussels from OA in actual aquaculture farms.

Financing: ANID - FONDECYT iniciación 11190297

Keywords: Aquaculture, climate change, mitigation

Oral presentation

EXPERIMENTAL EVIDENCE OF ANTIMICROBIAL ACTIVITY IN ANTARCTIC SEAWEEDS: ECOLOGICAL CONTEXT AND POTENTIAL APPLICATIONS

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Seaweeds, as sessile marine organisms, are exposed to a great variety of microorganisms that along evolution have led the seaweeds to exhibit a wide range of secondary metabolites to interact with them. Aside from the ecological role that these chemical compounds play in their habitats, they have potential interest for humans due to their diverse bioactivities, often including antibiotic properties. Aiming to broaden the knowledge of these functions and potentiality in Antarctic seaweeds, we carried out an antibiotic screening of crude extracts from 22 Antarctic species (14 Rhodophyta and 8 Phaeophyceae). Samples were extracted using organic solvents and fractionated into lipophilic and hydrophilic fractions. Antimicrobial assays of the crude extracts were performed at natural concentrations on seven sympatric bacteria and common human pathogens (six bacteria and one fungus). The antibiotic activity of the extracts was assessed by measuring the growth inhibition halos in each case, if any. Our results showed as a general trend that hydrophilic compounds were less active than lipophilic ones. Also, rhodophytes samples inhibited a higher number of microorganisms compared to phaeophycean ones (10 active Rhodophyta, versus the 4 Phaeophyceae that showed positive inhibition). From those groups of seaweeds, the strongest inhibitions were displayed by *Delisea pulchra* (Greville) Montagne and *Desmarestia antarctica* R.L.Moe & P.C.Silva. Both Gram-negative and Gram-positive

bacteria were inhibited, suggesting a general trend of non-specific chemical defense from the tested seaweeds. However, Gram-negative bacteria (especially *Escherichia coli* and *Pseudomonas aeruginosa*) along with the pathogenic fungus *Candida albicans* showed greater resistance.
Financing: This work was developed within the frames of the ACTIQUIM and DISTANTCOM (CTM2010-17415, CTM2013-42667/ANT) research projects.

Keywords: Antarctica, seaweeds, antimicrobial activity

Oral presentation

SCREENING ANTIBACTERIAL PROPERTIES OF *EUCHEUMA DENTICULATUM* EXTRACTS AGAINST *VIBRIO HARVEYI*

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Antimicrobial activity of seaweeds against fish pathogens has been reported in different studies in an effort towards finding natural solutions to fish diseases which cause massive losses in aquaculture installations globally. Finding sustainable solutions is meant to replace the use of antibiotics that are associated with the cases of antibacterial resistance which has occasioned the ban of such drugs in food production for some countries. The present study aimed at using locally farmed seaweed, *Eucheuma denticulatum*, as a fish disease control mechanism against *Vibrio harveyi*. This was to find an alternative to use of antibiotics in controlling luminous bioluminescence and explore alternative use of the seaweed species geared towards product diversification for enhanced seaweed economy. Activity against *V. harveyi* was not evident following in vitro screening. Validation of these results using immersion and Artemia as the model organisms and challenge test using *V. harveyi* revealed significantly higher final survival values, after a 4-day culture period, ($p<0.05$) of 80.0 ±5.0%, 43.33±7.64%, 50.0±7.07% and 56.67±5.77% for animals cultured in the presence of extracts from seaweeds sampled in September 2018, October 2018, November 2018 and March 2019 respectively compared to those cultured without inclusion of extracts, 31.67±2.99%, and challenged with the bacterial strain. The efficacy of extracts also varied with sampling period indicating differentiated activity with season which influences prevailing physico-chemical properties of sea water. The results indicate that *E. denticulatum* can be used to regulate luminous bioluminescence in fish as its extracts exhibited quorum quenching properties.
Financing: Research funding received from Western Indian Ocean Marine Science Association under the Marine Research Grant (MARG-I) programme (2018-2019)

Keywords: *Eucheuma denticulatum*, antibacterial, quorum quenching

Oral presentation

COSMETIC PROPERTIES OF RED MACROALGAE AND CYANOBACTERIA

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In the last years, research on natural products has gained considerable attention, particularly in the cosmetic industry, which is looking for new bio-active and biodegradable molecules. In this study, cosmetic properties in cyanobacteria and red macroalgae species were analyzed, focusing on antioxidant and photoprotective capacities. The main molecules with these properties, mycosporine like aminoacids (MAAs), scytonemin and phenolic compounds, were quantified. The antioxidant activity was determined in vitro through the ABTS assay. The photoprotective capacity was also measured in vitro using a novel technique, that can be made quickly, easily and without using animal or human volunteers. In this research, a high content of scytonemin was observed in *Scytonema* sp. and *Lyngbya* sp., and the highest content of MAAs was obtained in *Porphyra umbilicalis* (max. absorption at 334nm). *Scytonema* sp. was the unique species that presented a MAA with maximum absorption in the UV-B band (310nm). The highest content of polyphenols was also observed in *Scytonema* sp. and *P. umbilicalis*. In general, cyanobacteria presented a higher antioxidant activity than red macroalgae. Extracts of some species incorporated in creams showed an increase in the photoprotection capacity in comparison with the base cream. Extracts of these organisms can be used as natural photoprotectors, improving the photoprotection of sunscreens. The combination of different extracts enriched in scytonemin and MAAs could be useful to design broad-band natural UV screen cosmeceutical products.

Keywords: mycosporine like aminoacids, *Porphyra, Scytonema*

Oral presentation

COSMECEUTICS AND BLUE BIOTECHNOLOGY WITH MARINE ALGAE

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Integrated multitrophic aquaculture (IMTA) of fishes and seaweeds is included in the blue biotechnology approach since the fish effluents are used as fertilizers for algal growth and the biofiltration of ammonium by the seaweeds reduces eutrophication risk associated to the aquaculture i.e. ecosystem services. In addition, the algal biomass produced can be used as feed, food, cosmeceutics, biostimulants in agriculture or bioenergy, among others. The use of different red algae of the genus *Gracilaria* and *Hydropuntia (Crassa)* grown in IMTA systems as biofilters and as source of UV-photoprotectors, mycosporine –like aminoacids (MAAs) is presented. The MAA productivity ranged from 10 to 240 mg MAAs m-2 d-1 and the antioxidant activity for 20 to 80 mmol Trolox equivalent g-1 DW determined by ABTS method. On the other hand, a screening of red marine seaweeds as source of MAAs and antioxidants was conducted in algae grown in high solar radiation habitats as Southern Spain. *Porphyra umbilicalis* and *Osmundea pinnatifida* presented the highest level of MAAs and antioxidant capacity. In order to quantify the photoprotection capacity of the extracts against different biological effects of UV-Vis radiation (Vitamin D3 synthesis, erythema, Immunosupression, lipid peroxidation, Elastosis, Photoaging and Persistent pigment darkening), two new indexes are used, i.e., effective solar absorpted radiation (%ESAR) and extract photoprotection index (EPI), considering the extract absorbed and transmitted radiation, respectively. Photoprotection creams were design by using the best algal extracts and other bioactive compounds against damage provoked by UVR. The strategy for the development of biological photoprotectors is discussed.
Financing: Project UMA 18 FEDER JA 162

Keywords: UV photoprotectors, antioxidants, ammonium

Oral presentation

CELL BANKING OF MARINE RED MICROALGAE

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In biotechnological processes, the establishment of a standardized master and working cell bank (MCB and WCB) guarantees an upstream process with high reproducibility and quality. However, critical steps during cryopreservation are cooling and thawing, where ice crystal formation prevents cell death due to osmotic stress and injury to the cellular structures. Therefore, cryoprotective agents are used which either reduce the osmotic potential of the cells or induce the vitrification of water. Several studies have shown the importance of empirical tests relating to strain-specific cryoprotective agents and their concentration (e.g. 1-3). A strain-specific optimization of the cryopreservation process, including the cultivation conditions prior to freezing as well as the thawing process, is therefore absolutely necessary. Especially, cell density and physiological activity have an influence on the success of cryopreservation. The objective of the present study was to establish a method for cell banking of marine red microalgae strains allowing for a high post-thaw viability. (1) Gwo et al., 2005 doi: 10.1016/j.cryobiol.2005.02.001 (2) Day et al., 2005 doi: 10.1515/micbi-2015-0001 (3) Kapoore et al., 2019 doi: 10.1038/s41598-019-38588-6.
Financing: Internal Funding University of Applied Sciences Bremerhaven and European Union's Horizon 2020 no.730984 (ASSEMBLE Plus).

Keywords: Cryopreservation, post-thaw viability, flow cytometry

Oral presentation

THE CULTURE COLLECTION OF ALGAE AND PROTOZOA (CCAP): PIONEERING NEW DEVELOPMENTS

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The Culture Collection of Algae and Protozoa (CCAP) is the most diverse biological resource center in the world, with nearly 3000 strains available for users in the scientific, biotechnological, and industrial communities. CCAP also provides a variety of services ranging from cryopreservation, taxonomic and genomic studies, to training workshops. In 2021, CCAP is expanding the services it offers with two new developments. First, to address the expanding interest in algal biotechnology, CCAP is launching the Algal Research, Innovation and Environmental Science Centre (ARIES). This facility will allow the cultivation and harvesting of hundreds of liters of algal culture, coupled with a contemporary nucleotide extraction service and trait analysis using metabolomics. Second, to facilitate protist research and continue the taxonomic curation of the collection, CCAP has collated all nucleotide sequence data for CCAP strains generated by CCAP staff, collaborators and other researchers. These data are accessible from the CCAP Bioinformatics Gateway and the CCAP's main website (www.ccap.ac.uk), where users can browse and access sequence data associated with the CCAP strains. A key future development aims to provide a comparative functional analysis of protistan genomes. With these research and developments, CCAP will continue to build upon its world-class research facility, with which to investigate the unique and underexplored diversity of protistan organisms for the understanding of the natural world and the development of new biotechnological applications.

Keywords: Protists, biotechnology, algae

Oral presentation

SEAWEED BEACH-CAST EXTRACTS AS INHIBITORS OF DIFFERENT VIRAL INFECTION STAGES FROM HERPES SIMPLEX VIRUS

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Seaweed beach-cast biomass is more than a nuisance matter on the beach, they have proven to be exceptionally rich sources of bioactive compounds for the development of new and effective therapeutic applications. In this research, Sulfated Polysaccharides (SPs) and fractions rich in GlycoProteins (GPs) isolated by enzyme-assisted extraction or hot-water extracts, from eight species of seaweeds collected from the beach-cast biomass in France and Mexico, were evaluated in vitro against Herpes simplex virus type-1. After three days, all extracts showed at MOI 0.001 ID50/cells antiviral activity without cytotoxicity, the strongest activities were found in SPs from *Sargassum filipendula* and *Halymenia floresii*, and GPs from *Solieria chordalis* (EC50 5.6, 0.9 and 6.3 μg/mL). The mechanism of action of these extracts suggested that virus inhibition occurs at different stages of infection. The virucidal assay and the viral adsorption showed activity as high as the control zovirax (EC50 0.53 μg/mL) when SPs from *H. floresii* were added during and after the viral infection (EC50 0.40 μg/mL). During the post-infection stage, this SP showed an EC50 of 2.0 μg/mL when was added 2h after infection. SPs from *H. floresii* was composed of high amounts of sulfates (27% dw), and neutral sugars (30% dw). The main monosaccharides were galactose, glucose, arabinose, and glucuronic acid. The apparent molecular weight determined by HPSEC was higher than 1000 KDa, FTIR showed characteristics bands of λ-carrageenan. Preliminary characterization of GPs from *S. chordalis* was done by HPSEC, SDS-PAGE, FTIR, MALDI-TOF. SPs and GPs appear as potent natural antiviral agents.

Financing: Postdoctoral fellowship funded by SECTEI-Ciudad de Mexico (SECTEII/130/2019) and LBCM-UBS, France.

Keywords: Antiviral polysaccharides, *Herpes simplex* virus type 1, seaweed glycoproteins

Oral presentation

MYCOPROTEIN AND HYDROPHOBIN LIKE PROTEINS PRODUCED FROM MARINE FUNGI *PARADENDRYPHIELLA SALINA* IN SUBMERGED FERMENTATION WITH GREEN SEAWEED *ULVA* SPP

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The production of new sources of protein with low environmental impact will guarantee the future of food security. Seaweed-derived bioactive substances like polysaccharides are known to have nutritional and health benefits. Marine fungi are included in screens for new metabolites and their ability to assimilate complex polymers from seaweed and even increase their digestibility and bio-functional properties. Fungi are gaining importance as a promising source of food protein (mycoprotein) and also have the ability to produce surface-active proteins. This is the first time that the growth of *Paradendryphiella salina* (a marine fungus) on Ulva spp. (a green algae) through the submerged liquid fermentation for the production of mycoprotein (from mycelium) and hydrophobin like proteins (from culture broth) is reported. The biomass was analyzed before, and after fermentation, complex carbohydrates, and chemical composition with FT-IR (Fourier-transform infrared spectroscopy) were determined. Also, the nutritional composition (protein, amino acids, total fibre, caloric energy, fat), and surface-active proteins were investigated The results of nutritional composition of mycoprotein were a yield of 561.3 g of mycoprotein from 1 kg of dry algae, a good concentration of total protein (48.2 g/100 g), and a considerable concentration of total amino acids (21 g/100 g). The characterization of surface-active protein displays consistent behaviors with the Class II hydrophobin. This study proves that sustainable production of mycoproteins and surface-active proteins can be developed growing a marine fungal strain, contributing to shed light on the potentiality of an integrated method that promotes the circular economy.

Financing: This research was supported by the Chilean National Research and Development Agency of Chile ANID, and the Centre for Biotechnology and Bioengineering, CeBiB

Keywords: Mycoproteins, *Ulva* spp., hydrophobin

Oral presentation

PHENOL TOLERANT ALGAE AND RESOURCE REVALORIZATION

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Olive oil extraction is a process that requires large amounts of water (about 1L per kg of processed olives). The water introduced into the process is later discarded as olive oil mill wastewater (OMW), a waste product rich in sugars, fatty acids, nutrients and phenols. The amount of OMW generated by the olive-oil industry represents a key environmental

problem in Europe, particularly in Mediterranean countries: good water management and new added value to agricultural wastes are crucial. With this purpose, marine, freshwater and halotolerant microalgae were cultured in the presence of the most common and abundant phenols in the OMW studying cytotoxic effects on growth and cell composition. Scenedesmus sp. showed high tolerance towards phenols and growth rate in the OMW was comparable to or higher than the rate of control cells grown in BG11. Moreover, the work presents an integrated approach involving a physicochemical and a biological treatment for OMW. Primary treatment of OMW consisted in NaOCl oxidation and/or flocculation and/or microfiltration. Secondary treatment consisted in culturing Scenedesmus sp. in diluted OMW (33%) water as culture media. Experiments were performed at 20°C under constant illumination (80 μmol m−2s−1) and in 12: 12-h light: dark cycles. High global removal levels of the main OMW constituents were achieved after the two-step treatment. Concentration of phenolic compounds was less than 1 mg L-1 in the effluent. Best growth parameters are discussed in order to achieve high added value algal biomass. Although on a lab scale, results prove effective phytoremediation and waste revalorization.

Keywords: Cell composition, olive oil mill wastewaters, phenolic compounds

Oral presentation

EXPLORATION AND POSSIBLE ENHANCEMENT OF SEAWEEDS FROM ITALIAN COASTS

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Seaweeds are extremely versatile and the products obtained can be consumed directly or used in many fields. Apart from contributing greatly to the nutritional status of communities, seaweeds show a wide-ranging use in many industries. The Mediterranean Sea, even though representing the 0.82% of the world's oceans, is a seaweeds biodiversity hotspot, and is at the same time the area affected by the introduction and spread of alien marine species. In Italy, the seaweed industry does not appear a widespread sector; furthermore, the harvesting and exploitation of macroalgae have always had a character of extreme sporadicity. However, the coastal habitats can offer an opportunity to enhance the endemic and alien species as a resource in the Bio-based Circular Economy framework. In this context, the objective of our research is a screening on the applicative potential of endemic and alien seaweeds from two Italian coastal sites: The Strait of Messina and the Lagoon of Venice. Among the investigated species, ethanolic extracts from the red alga *Asparagopsis taxiformis* and sulphated polysaccharides from the alien brown algae *Undaria pinnatifida* and *Sargassum muticum* have shown interesting results in the veterinary-pharmaceutical and energy sectors. The possibility of exploiting these seaweeds for industrial uses would at the same time to manage the biomass proliferation of alien species and to promote a new economic sector, thus diversifying the fishing activity, allowing to increase local production and the valorization of the resources within the framework of a Bio-based Circular Economy process.

Keywords: Italian coasts, seaweed uses, veterinary-pharmaceutical applications

E-Poster

SCAVENGING GENES ASSOCIATED WITH THE BIOSYNTHESIS OF SCYTONEMIN AT THE GENOMES OF CYANOBACTERIA ISOLATED FROM BRAZILIAN SODA LAKES

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Cyanobacteria from the Brazilian soda lakes at the Pantanal biome endure harsh abiotic conditions. Apart from the salinity, due the fluctuation in depth of the lakes, they are continuously exposed to high doses of ultraviolet radiation (UV) in both winter and summer solstices. As many other species of cyanobacteria, it is expected that the strains inhabiting these soda lakes are capable of producing photo-protective pigments. While an ample range of organisms can produce mycosporine-like amino acids (MAA's), the biosynthesis of scytonemin, an extra-cellular matrix pigment with the capacity to absorb light at the wavelength of 370 nm (UVA), is restricted to cyanobacteria. Therefore, the main goal of this study is to explore the presence of 20 genes related to the metabolic pathway of scytonemin in 6 Brazilian strains isolated from the Pantanal soda lakes (*Limnospira* sp. CENA 597, *Limnospira* sp. CENA 650, *Geminocystis* sp. CENA 526, *Pantanalinema rosanae* CENA 516, *Alkalinema pantanalense* CENA 528 and *Anabaenopsis elenkinii CCIBt3594*). Each genome was automatically annotated using BLAST and Prokka software's. Then, a manual annotation was made with Artemis based on libraries created with sequences from several species of cyanobacteria present in NCBI and described in the literature as relevant to scytonemin. Most of the genes were found and had their location on the genomes settled. Only two strains present all genes and none had them organized as a continuous cluster. Finding these genes is relevant to unravel the genomic complexity of the scytonemin biosynthetic pathway, which is not yet completely described.

Financing: Doctoral scholarship from CAPES (Finance code 001) and CNPq (140892/2020-6).

Keywords: Photo-protective pigments, gene annotation

E-Poster

INNOVATIVE SEAWEED EXTRACTION FOR AGRICULTURAL PURPOSES

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The global population is predicted to grow by more than a third by 2050. Due to this increase, worldwide food production is facing a considerable challenge. Currently, cultivation practices mainly use mineral fertilizers to promote plant growth. However, short- and long-term negative impacts on the environment are already described. Thus, the challenge is to search for a new generation of sustainable agro-products. Among the marine flora encountered in Europe, some seaweeds can become proliferative and induce adverse ecological impacts. Due to their unique composition, this underexploited biomass can be used to manufacture agricultural products. The conventional techniques of algal compounds extraction include maceration, Soxhlet extraction, hydrodistillation. However, their major disadvantages include low extraction yield, higher operational time and hazardous nature of solvents. In the case of seaweed biomass, extraction processes need to be optimized to improve extraction efficiency and purification of compounds of interest. Thus, we aim to develop a biorefinery concept, based on the application of European macroalgae as a raw material, to take advantage of the whole biomass. Thereby, the obtained extracts will be applied as biostimulants for crops, and algae itself and the post-extraction residue will be used as a biosorbent of heavy metal ions from contaminated soil/wastewater. We have focused our project on three species: *Solieria* sp. (Rhodophyta), *Ulva* sp. (Chlorophyta) and *Fucus* sp. (Ochrophyta). The results will enable to choose the best seaweed candidate for the production of algae-based products for agriculture by the use of sustainable technologies for algal biomass valorization.

Keywords: Seaweed, biostimulant, bioremediation

E-Poster

CHEMICAL COMPOSITION AND BIOACTIVE PROPERTIES OF *PADINA BORYANA* THIVY AS POTENTIAL SOURCE OF SKIN LIGHTENING ACTIVE INGREDIENT FOR COSMETIC APPLICATION

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The chemical composition, antioxidant, tyrosinase inhibition, and antibacterial properties of the brown macroalga *Padina boryana* Thivy were studied. The seaweed contains a total phenolic content of 1.40 ± 0.02 mg GAE g-1. Antioxidant efficiency of *P. boryana* are characterized by having potent DPPH scavenging activity and high copper reducion capacity with IC50 value of 31.2 µg GAE ml-1 and 11.43 µg GAE ml-1 respectively, more effective than ascorbic acid. Phenolic profile analysis using reverse phase high performance liquid chromatography (HPLC) showed the presence of gallic acids and other flavonoids. The seaweed extract exhibited potent antibacterial activities against bacterial pathogen such as *Staphylococcus epidermidis* (MIC = 125 µg ml-1), *Micrococcus luteus* (MIC = 125 µg ml-1), and *Staphylococcus aureus* (MIC = 250 µg ml-1). *In vitro* study of tyrosinase inhibition properties showed that *P. boryana* extract have potent inhibitory activity with IC50 of 40.50 µg GAE·mL-1 as compared to kojic acid with IC50 of 109.8 µg·mL-1. Results showed proximate composition of *P. boryana* to have high carbohydrate (40.81 ± 0.49%) and ash (21.80 ± 0.33%) content. Elemental composition of the alga showed a decreasing order of Fe > Ca > K > Mg > Na > Mn > Zn > Cu > Pb > Cd > Cr. The current investigation is the first report in the Philippines that shows the potential of *P. boryana* as source of polyphenolic compounds important for the development of novel skin lightening ingredient for cosmetic application.

Financing: National Institute of Molecular Biology and Biotechnology (BIOTECH), University of the Philippines Los Banos

Keywords: Biological activities, polyphenols, seaweeds

E-Poster

NEW APPLICATIONS FOR *GELIDIUM CORNEUM*: ANTIMICROBIAL AND ANTIOXIDANT ACTIVITY WITHIN A BIOREFINERY CONCEPT

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There are more than four hundred endogenous seaweeds that occur in Portugal, and red seaweeds (Rhodophyta) are the most abundant. Among these, *Gelidium corneum*, common in the Atlantic coast of Portugal, is currently being collected in the wild, in S. Martinho do Porto, exclusively for the extraction of agar. During the summer season this species is harvested from the bottom of the ocean, dried and sold, representing an important economic local activity. Yet, besides agar, this species is important for its bioactivities, namely for its antioxidant and antimicrobial capacities, thus most of the biomass is currently being disregarded as an important marine resource. Therefore, to further research the potential of *G. corneum* as a source of bioactive compounds, the biomass was seasonally harvested and characterized (protein, ash, moisture), and different extract were made (aqueous and ethanolic). These extracts were analyzed for the antioxidant potential (DDPH, ABTS, TPC and FRAP), and for antimicrobial capacity (against *Escherichia coli, Bacillus subtilis, Candida albicans, Saccharomyces cerevisiae* and *Staphylococcus epidermidis*). Preliminary results show that there are seasonal variations in the chemical composition of the biomass. Extracts tested also show interesting free radical scavenging capacity and antimicrobial activity against some of the strains tested. The attained results demonstrate that the biorefinery concept should be implemented to the agar industry, valuing the seaweeds' biomass so to allow its use in other industries, such as textiles or cosmetics.

Financing: This study had the support of FCT UIDB/04292/2020 and Mar2020 project LIMO DO CAIS -MAR-04.03.01-FEAMP-0101

Keywords: *Gelidium corneum*, antioxidant, antimicrobial

E-Poster

POTENTIAL SOURCE OF COSMECEUTICAL BIOACTIVE(S): UNRAVELLING UVB RADIATION PROTECTIVE POTENTIAL OF BROWN ALGA *PADINA AUSTRALIS*

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Seaweed-derived biometabolites are receiving global attention as safe and potentially sustainable ingredients for skincare products. This study aimed to evaluate antioxidant and ultraviolet (UV) protective effect of ethanol and aqueous extracts of *Padina australis* from Malaysian waters. UVB protective activity was tested on an experimental model using HaCaT human keratinocytes. Since antioxidant activity is known to suppress the detrimental effects of UVB damage, the project was initiated with the attempt to evaluate the antioxidant activity of ethanol & aqueous extracts. It was surprisingly to observe that ethanol extracts exhibited a stronger antioxidant activity when compared to aqueous extracts when being examined by DPPH and reducing power activity assays. In fact, it was interesting to observe the ethanol extract was consisted with a high level of phenolics (76 mg GAE/g) and flavonoids (50 mg QE/g) which might give rise to the notion that ethanol extract is a promising candidate for us to move forward with. Further experimentation was done, in order to evaluate the protective effect extracts against UVB-induced cell damage and result shown ethanol extract was far more superior than aqueous extract with stronger a fold in term of its efficacy (400 μg/mL). In addition, Liquid Chromatography–Mass Spectrometry analysis revealed that ethanol extract consists of sugar alcohol, carbohydrate, carotenoids and fatty acids. In summary, extract/biometabolites derived from *P. australis* have shown to possess great antioxidant and promising UVB protective activity which therefore, would be deemed as a great promising candidate to be developed as a novel cosmeceutical ingredient.

Keywords: Algae, cosmeceuticals, UV-protective

E-Poster

UNRAVELLING THE ANTI-NEUROINFLAMMATORY ACTIVITY OF THE MALAYSIAN RED MACROALGA *KAPPAPHYCUS MALESIANUS* IN LIPOPOLYSACCHARIDES-STIMULATED BV2 MICROGLIA

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Neuroinflammation is a hallmark for neurodegenerative diseases due to high oxidative stress produced by activated microglia and astrocytes. Overproduction of cytotoxic factors will increase oxidative stress and lead to neuronal degeneration and neuronal death. It has become increasingly evident in recent years that the biometabolites derived from seaweeds possess numerous biological activities including neuroprotective activity. *Kappaphycus malesianus* is a newly described species in Malaysia, which is an important source of raw material for carrageenan production. To the best of our knowledge, no study has been reported on the pharmacological properties of *K. malesianus*. Therefore, this study aimed to investigate the anti-neuroinflammatory activity of *K. malesianus* extracts (ethyl acetate, ethanol and methanol) on Lipopolysaccharides (LPS)-stimulated BV2 microglial cells. Cell viability assay was used to examine the cytotoxic of all *K. malesianus* extracts and it was found that methanol extract had an IC50 of 6.67 ± 0.61 mg/mL, showing the least cytotoxic effect. The nitric oxide inhibition activity was determined by using Griess assay and the expression of iNOS and COX-2 was evaluated by Immunoblot analysis. All extracts reduced the nitric oxide production in concentration-dependent manner, and methanol extract demonstrated the highest nitric oxide inhibition activity. Immunoblot analysis showed that methanol extracts inhibited iNOS and COX-2 production in a dose dependent manner. Our findings indicate that *K. malesianus* possesses anti-neuroinflammatory activity by inhibiting the production of pro-inflammatory mediators.

Keywords: *Kappaphycus malesianus*, anti-neuroinflammatory effect, pro-inflammatory cytokines

E-Poster

SEQUENTIAL EXTRACTION OF PHYCOBILIPROTEINS AND AGAR FROM AGAROPHYTON CHILENSE

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The main application currently given to *Agarophyton chilense* (Pelillo), red macroalgae, is agar extraction. Instead, phycobiliproteins (PBPs) are intracellular photoreceptor protein pigments which can be also extracted from this red macroalgae. It has been reported that PBPs have antioxidant and antitumor properties, among others, being attractive for the pharmaceutical and biotechnology industries. PBPs are divided into three main groups: Phycoerythrin, Phycocyanin and Allophycocyanin, which are composed of two main subunits, alpha and beta, and in some cases gamma, with molecular weights in the range between 16 to 20 kDa. The main aim of this research is to provide an added value product from *Agarophyton chilense*, by means of the sequential extraction of PBPs and agar from the residual matter, after PBPs extraction. To carry out our purpose, *Agarophyton chilense* was incubated with PBS buffer and proteins were precipitated with ammonium sulfate. PBPs were purified from dialyzed protein fractions using anion-exchange chromatography. Agar was extracted after alkali treatment and neutralization of algae residue. Results demonstrate that it is feasible to recover agar from the residual matter after PBPs extraction. The recovery of PBPs from crude extract was ca. 10% and agar yield from dry algae was approximately 25%. Additionally, no differences were found in agar quality (gel force) from samples treated with and without a previous PBPs extraction step.

Financing: Centre for Biotechnology and Bioengineering (CeBiB) FB-0001 and Fondecyt Grant Number 1180794

Keywords: *Agarophyton chilense*, phycobiliproteins, agar extraction

E-Poster

AN INVESTIGATION ON GROWTH PERFORMANCE AND NANO-BIOTECHNOLOGICAL EXPLOITATION OF *HALAMPHORA SUBTURGIDA* (HUSTEDT) LEVKOV

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A marine pennate diatom *Halamphora subturgida* (Hustedt) Levkov was isolated from Eastern India and its growth performance was investigated based on biochemical parameters at different nitrate concentrations. Maximum value of chlorophyll (14.95 ± 0.04 µg/ml), fucoxanthin (25.70 ± 0.03 µg/ml), total carotenoids (26.92 ± 0.05 µg/ml) and protein (87.49 ± 0.06 mg/g) contents were recorded when subjected to double nitrate (1,764 µM) as compared to control (882 µM) and half nitrogen concentration (441 µM) after 12 days of growth period. Furthermore, for nano-biotechnological exploitation of *H. subturgida*, acid-digested nano-siliceous frustule powder was used for making Metal-oxide Semiconductor (MOS) capacitor employing vapor-liquid-solid (VLS) method. Fabricated MOS capacitor were tested by measuring leakage current (~ 43 ± 8 × 10–11 A µm–2 at +2 V), capacitance-voltage, constant current (0.1 µA), and voltage stress (at – 2 V). Processed nanoporous frustules were again subjected to silver solution (9 mM) at pH 4. The resultant biosynthesized conjugate nanodendrites were characterized using conventional methods. Electron photomicrographs provided mechanistic view with the formation of isotropic hybrid nanospheres (20 nm) internally and continued to develop anisotropic nanocrystals with time. The nanodendrites externally formed on the siliceous frustules acting as a template, were characterized by the distinct trunk (100 nm in width, 1-2 µm in length) with branches on either side (200–220 nm in length, 70–100 nm in width). Both the externally derived hybrid nanodendrites and internally synthesized nanospheres possessed superior stability with zeta potential value of -35.7 mV and -24.8 mV respectively.

Keywords: Diatom, growth performance, nano-conjugate

E-Poster

EXPLORATION OF CYANOBACTERIA AS NANOIRON BIOFACTORY AND ITS APPLICATION IN CR (VI) REMOVAL

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The present study is focused on green synthesis of nanoiron using different Cyanobacterial strains like *Leptolyngbya valderiana* (Gomont) Anagnostidis & Komárek, *Lyngbya birgei* G.M.Smith, *Arthrospira platensis* Gomont, *Anabaena spherica* Bornet & Flahault, *Tolypothrix* sp. Kützing ex Bornet & Flahault etc. followed by potential strain selection for Cr (VI) removal process. Biotransformation of Fe3+ to Fe0 was recorded at intracellular and extracellular levels by active cyanobacterial culture within 4 days of incubation in 0.01M FeCl3 in an ecofriendly way. Synthesized nanoiron particles by the biomasses were characterized using UV-Vis spectroscopy, Scanning Electron Microscopy (SEM), Transmission Electron Microscopy (TEM), Dynamic Light Scattering

(DLS), Fourier Transform Infrared spectroscopy (FTIR), X-Ray Diffraction (XRD). Synthesized particles were monodisperse in nature, having a size range of 20-50nm x 7-12nm with spindle shaped structure. Quantifications were done and *L. valderiana* has been selected as the highest productive strain (40-60 mg/g biomass). Free as well as cyanobacterial biomass loaded with nanoirons were used as nanosorbents and tested for their Cr(VI) removal potency against 5-20mg/L Cr (VI) solutions at different dosages (2-10g/L) with varied incubation times (1-48h). Reaction kinetics along with adsorption isotherm analysis showed that biomass loaded nanoiron was following chemisorption process satisfying Freundlich isotherm whereas free nanoirons (intracellular and extracellular) were followed physisorption process satisfying Langmuir isotherm for Cr (VI) removal from solution. It has been found that biomass loaded nanoirons had higher adsorption capacity (0.0439 L/mg) and thus more efficient in Cr (VI) removal than that of their free form.

Keywords: Cyanobacteria, nanoiron, Cr (VI) removal

E-Poster

GRACILARIA MANILAENSIS YAMAMOTO & TRONO EXTRACTS IN ATTENUATION OF LIPOPOLYSACCHARIDE-STIMULATED NEUROINFLAMMATION IN BV2 MICROGLIA

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Lipopolysaccharide (LPS)-stimulated BV2 microglia is known as a stable model for anti-neuroinflammatory activity studies. *Gracilaria manilaensis* is an agarophyte commonly cultivated in Malaysia which has received increasing attention for its antioxidant and neuroprotective activities. This study aimed to investigate how *G. manilaensis* extracts attenuate the neuroinflammatory activities in LPS-stimulated BV2 microglia. Hot aqueous, methanol and ethanol extracts were prepared from the *G. manilaensis* sampled at Kuala Muda, Kedah, Malaysia. BV2 microglial cells were treated with extracts for 2 h and then stimulated with LPS O55:B5 16 – 24 hr. Nitric oxide production and cell viability were measured by Griess assay and dimethylthioltetrazolium bromide (MTT) assay respectively. Inflammatory mediators expression were analysed by the Western blot. pro-inflammatory cytokines expressions were analysed by Enzyme-linked immunosorbent assay (ELISA). The profile of possible biocompounds was analysed by Liquid chromatography-mass spectrometry analysis (LCMS) with Q-TOF. Methanol and ethanol extracts showed significant anti-nitric oxide activity ($p \le 0.05$) without interrupting the cell viability. Ethanol extract was selected for protein expression study as it poised the strongest anti-nitric oxide activity. iNOS expression of LPS-stimulated BV2 microglia was downregulated with no effect on β-actin expression and COX-2. Further ethanol extract inhibits interleukin-6 (IL-6) and tumor necrosis factor alpha (TNF-α) production in LPS-stimulated BV2. LCMS analysis detected 2-hydroxyhexdecanoic acid, Cyrneine A and Eplerenone with anti-neuroinflammatory activity in ethanol extract. Our findings indicate that ethanol extract has the highest anti- neuroinflammatory activity which was closely linked with iNOS, IL-6 and TNF-α abrogation.

Keywords: *Gracilaria manilaensis*, LPS-stimulated BV2 microglia, neuroinflammation

E-Poster

SCREENING OF DIATOMS FOR THEIR EFFICACY TO SYNTHESIZE GOLD-SILICA AND SILVER-SILICA NANOCONJUGATES

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The main objective of nanobiotechnology is to synthesize non-toxic metal nanoparticles which consider "biological systems" as a potential, eco-friendly source. The metal-silica nanocomposites are very useful in medical applications especially in photothermal therapy and multimodal imaging for cancer detection. Diatoms are well known as "Natural silica-nanofactories" and considered as efficient bioreagent for biogenesis of metal-silica nanocomposites. In the present communication a screening program has been completed in relation to bioconversion of gold-silica and silver-silica nanoconjugates from auric chloride and silver nitrate solutions respectively exploiting different diatoms like *Melosira lineatae, Phaeodactylum tricornutum, Nanofrustulum shiloi, Navicula korzeniowskii, Gedaniella mutabilis*. Each of the selected diatoms was exposed to $HAuCl_4$ and $AgNO_3$ solution separately for 72 h. The biosynthesized nanoconjugates were extracted from the nanoparticle loaded biomass using nanoparticle capping agent, sodium citrate solution. The nanoconjugates were characterized using Uv-Vis spectroscopy, Energy-dispersive X-ray (EDAX) analysis, scanning (SEM) and transmission (TEM) electron microscopy. In Uv-vis spectroscopy, gold-silica and silver-silica suspension showed the characteristic absorption bands ~530 nm and ~420 nm respectively. Energy-dispersive X-ray (EDAX) analysis confirmed the presence of Au/Ag and SiO_2 nanoparticles in a composite form. The SEM study revealed that composite particles were deposited on the siliceous frustules of diatom cells. The TEM analysis confirmed the synthesis of different shaped metal-silica nanoconjugates with variable size ranges. It can be concluded that diatoms are good potential source for the rapid biosynthesis of biocompatible metal-silica nanoconjugates due to their high growth rate and high metal uptake capacity.

Keywords: Diatoms, biogenesis, nanoconjugates

E-Poster

PHYCOREMEDIATION OF TANNERY WASTE USING CYANOBACTERIA AS BIOREAGENT AND EXPLOITATION OF SPENT BIOMASS AS BIOFERTILIZER

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Economically feasible Cyanobacteria-based remediation of Tannery waste water was carried out along with application of spent biomass as biofertilizer for crop plants. Tannery wastewater carry heavy pollution load due to high organic and inorganic substances. Characterization of this water from inlet point source showed high level of BOD (1234.33 mg/L), COD (1706.64 mg/L), TDS (6984 mg/L), Sulfide (140.8 mg/L) and Ammonia (134.5 mg/L). From the present investigation it was found that from tannery wastewater Cyanobacteria efficiently removed toxic metals in one hand and nutrient loads on the other. In this investigation both marine and freshwater strains *Leptolyngbya* and *Arthrospirawere* grown in diluted tannery wastewater. Both of them were found to be potent in removing in removing BOD, COD and Ammonia by 90%, 96% and 84% respectively. Dissolved Oxygen increased by 10 folds. The growth performances of exposed biomass were measured in terms of dry weight. The ability of spent biomass to improvise plant growth was demonstrated for both dicotyledonous (Cicer arietinum) and monocotyledonous (Oryza sativa) plants. The N (nitrogen), P (Phosphorus), and K (Potassium) contents were recorded from Soil, Soil mixed with Chemical Fertilizer (SCF), and Soil mixed with Cyanobacterial Biomass (SCB). Results showed, SCB raised N, P, K contents in both shoots and roots. An increase in root length, shoot length and dry weight were also noticed. Germination rate and vigour index were improved. These results of SCB were almost comparable to the chemical fertilizer therefore spent cyanobacterial biomass would be very effective in organic cultivation.

Financing: Applied for IPC fund for Delegates; Applied for Global Seaweed Star Capacity Building Fund

Keywords: Cyanobacteria, biofertilizer, wastewater

E-Poster

POTENTIAL FOR LIPIDS PRODUCTION OF BENTHIC DIATOMS FROM THE COASTAL ZONE OF THE POMERANIAN BAY (BALTIC SEA)

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The aim of this study was to determine the potential of the selected Baltic Sea diatom taxa for the production of lipids and to determine their theoretical biogeographical zones in the Baltic Sea. Growth kinetics, biomass productivity and lipid content were tested for: *Halamphora cf. hybrida, Navicula korzeniewskii, Navicula gregaria, Nitzschia supralitorea, Stauroforma* sp. 1 and sp. 2. For diatoms cultivation, f/2 medium was used with different salt concentration (3, 5, 7 and 10‰). Malassez counting chamber was used for cell counting and growth rate determination. Diatoms strains were kept in a cultivation chamber at a temperature of 200C, day:night cycle (12:12 h), with a PAR value of 100 molxm2xs2. Harvesting of biomass took place on the 14th day of the experiment. Collected biomass was dried and weighed. Lipid fraction was extracted by the continous extraction method using methanol:chloroform (2:1) as organic solvents. The highest growth rate was observed in *N. gregaria*, and the lowest in H. cf. hybrida. The largest amount of biomass was collected from *N. gregaria* (0.0159 g, 10‰ medium), and the smallest from Stauroforma sp. 2 (0.0003 g, 5‰ medium). The largest amount of the lipid fraction was obtained from *N. gregaria* (92.97% dry mass volume, 5‰ medium), and the smallest amount was obtained from *Stauroforma* sp. 2 (26.59% dry mass volume, 7‰ medium). Diatoms isolated from the Pomeranian Bay have features which allows them to be considered as potentially useful in the biofuel context (fast growth rate, high productivity of biomass and crude oil, wide salinity tolerance).

Keywords: Diatomology, bioprospecting, biofuels

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EFFECTS OF SALINITY AND TEMPERATURE ON BIOMASS ACCUMULATION IN THE MARINE DIATOM *GEDANIELLA FLAVOVIRENS*

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Chitosan was found in the marine diatom *Gedaniella flavovirens*, hence the species could have a biotechnological potential. We conducted ecophysiological experiments, focused on the temperature and salinity effects on *Gedaniella flavovirens* growth. A series of three experiments were conducted on this strain, beginning with determination of growth kinetic parameters. The strain was cultivated for 22 days under the following conditions (further - standard condition): temperature 17-21oC, light intensity 100 μmol s-1 m-2 and 12:12 day: night light cycle, in a f/2 medium with 7‰ salinity. Biomass was harvested on 2nd, 4th, 8th, 16th, 18th and 22nd day of experiment, centrifuged, dried and weighed. A growth curve was determined and growth kinetic parameters (time of exponential growth (texp=6 days), time of maximal growth (tmax=16 days) and growth rate (μmax=0,38 d-1, R2=0,77) were estimated. Secondly, experiment was conducted on the strain in f/2 medium with different salt concentrations of 0, 1, 3, 7, 10, 15 and 20 g/L under standard conditions. Thirdly, the strain was again cultivated in standard f/2 medium under a range of temperatures at 15, 20, 25 and 30oC. After 16 days (tmax for this strain) of cultivation, the biomass from the second and third experiment was harvested, centrifuged, dried and weighed. Student's t-test analysis showed that there was no significant increase in biomass accumulation with salt enriched medium (at 10, 15 and 20 g/L salt) and under higher temperature (25oC and 30oC). The lowest growth was achieved at 0, 1 and 3 g/L salt and 15oC temperature (t-test, α=0,05).

Financing: Project № POIR.04.04.00-00-1792/18-00 BIOG-NET, Zaawansowane biokompozyty dla gospodarki jutra BIOG-NET, financing by Foundation for Polish Science

Keywords: Ecophysiological experiments, diatom culturing, diatom bioproducts

E-Poster

ANTIOXIDANT PROPERTIES AND ELEMENT LEVELS OF TWO COMMERCIAL *ARTHROSPIRA* STRAINS

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This study aimed to determine the total phenolic, flavonoid contents, mineral contents of *Arthrospira platensis* and *Arthrospira maxima*, and the effects of extraction solvents on their free radical scavenging activities. Water, phosphate buffer (pH 7.5), ethanol, acetone, and ethyl acetate were used for extraction. DPPH free radical-scavenging assay was used to determine the best extraction solvent for antioxidant activity. The total phenolic and total flavonoid contents of groups were measured according to Djeridane et al. (2006) and Quettier-Deleu et al. (2000). The element compositions of examples were determined analyzed via ICP-AES (Nordisk Metodikkomité for Næringsmidler, 2007). The highest antioxidant activity was determined in phosphate buffer for *A. platensis* and water for *A. platensis* with low IC_{50} values. The lowest flavonoid content in *A. platensis* was determined used acetone and phosphate-buffer groups ($p \leq 0.05$). The highest flavonoid content was found in water used as solvents in A. maxima ($p \leq 0.05$). The highest value of total phenolic content was found in the phosphate buffer group for A. platensis and the acetone group for A. maxima ($p \leq 0.05$). According to the element evaluations, it was determined that all values were below the limits of the FAO (Food and Agriculture Organization) and WHO (World Health Organization) for human consumption. However, it was determined that the Na content of A. platensis was higher than that *of A. maxima*, while the P, K, and Fe values were low.

Keywords: *Arthrospira*, antioxidant properties, minerals

E-Poster

ANTIMICROBIAL ACTIVITY OF MACROALGAL EXTRACTS AGAINST SEVERAL *LISTERIA MONOCYTOGENES* STRAINS FOR THE APPLICATION IN FOOD PRODUCTION

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Macroalgae are a source of compounds used for a long time in human affairs; some algal species are more used than others, as they possess molecules with antibacterial, antiviral, antifungal and immunostimulant activity. These molecules are often extracted from algal species which are invasive and, therefore, their use is also advisable in the perspective of environmental management, to eliminate large unwanted biomasses. In the present research, we evaluated the antimicrobial activity of Asparagopsis extracts against different *Listeria monocytogenes* strains. Ethanolic extracts prepared from lyophilized algal material were tested against 6 different strains of *Listeria monocytogenes*: 3 ATCC (13932, 7644, 1911) and 3 wilds isolates from food matrix. A mean value of 22±5 mm was reported for all the strains with the disk-diffusion assay (disk 6 mm) of the extracted compound. Furthermore, the Minimal Inhibiting Concentration (MIC) and Minimal Bactericidal Concentration (MBC) were performed by microdilution method. A value of 0.05% was established for all strains both for MIC and MBC. These results represent a very promising finding for the application of *Asparagopsis* extracts in food production as natural preservatives against *Listeria monocytogenes.*

Keywords: *Asparagopsis*, antibacterial activityt, *Listeria monocytogenes*

E-Poster

UTILIZATION OF GREEN SEAWEED WASTE FROM ALGAL BLOOMS USING A TERRESTRIAL FUNGI FOR PRODUCTION OF PROTEIN-ENRICHED FEEDS

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Single-cell protein (SCP) corresponds to edible unicellular microorganisms grown on biomass to be used as an ingredient for protein-rich foods. Green algae biomass of *Ulva rigida* harvested from marine eutrophicated coastal areas is a lignin-free cellulosic-rich waste with a good nutritional profile and a high potential for feeds production. Because of *Ulva rigida* cellulose contents, a saccharification step prior to microbial fermentation is required. *Trichoderma reesei* RUT-C30 is a terrestrial fungi that hyper secretes cellulases, which could be used for transforming waste biomass from different sources into protein. Therefore, the aim of our work is to transform *Ulva rigida* from 'green tides' affecting sea coasts into SCP using the cellulolytic fungi T. *reesei* RUT-C30 for saccharification and fermentation of Ulva rigida in a single step. For this purpose, the fungi T. *reesei* RUT-C30 was grown in liquid cultures using *Ulva rigida* as the single carbon source for 11 days at 30 °C. Dry biomass, protein contents and reducing sugars were studied to characterize cultures, and the nutritional profile of the fermented product was characterized by proximal analysis and amino-acid composition. We found that T. *reesei* RUT-C30 was able to grow using Ulva rigida as carbon source, producing the same amount of biomass and proteins after 72 h of culturing, when compared to fungal fermentation in 2% glucose after 48 h. In addition, the fermented product resulted in an increase in protein contents and essential amino acids, when compared to raw seaweed.

Financing: Fondecyt Grant 1180794 and CeBiB Basal Grant FB-0001.

Keywords: *Ulva rigida* seaweed, *Trichoderma reesei*, Single-Cell Protein (SCP)

E-Poster

COMPARATIVE CHARACTERIZATION OF *TETRASELMIS CHUII, CHAETOCEROS CALCITRANS* AND *ISOCHRYSIS GALBANA* STRAINS AS SOURCES OF FOOD SUPPLEMENTS

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Species of the genera *Tetraselmis* (Chlorophyta), *Isochrysis* (Haptophyta) and *Chaetoceros* (Bacillariophyta) have been traditionally used as a valuable nutritional source in aquaculture for their high fatty acids content. In recent years, several microalgae have been incorporated also in food products. Here we evaluated the potential of five microalgal strains to produce polyunsaturated fatty acids (PUFA) with interest for their use as nutraceuticals. Two strains of *Tetraselmis chuii* were freshly isolated from Guanabara Bay in Brazil (TCBG-1 and TCBG-2). The other strains: *T. chuii* (CCAP 8/6), *Chaetoceros calcitrans* (ICMAN-CSIC) and *Isochrysis galbana* (ICMAN-CSIC) were acquired from collections. All strains varied in their PUFA content with culture age. Total fatty acid content (% dry weight) ranged from a minimal 9.3 % DW to 32.18% DW. The biomass productivity obtained from the 3 strains of *T. chuii* was greater than those of the other strains tested and the yield by cell fatty acids and PUFA was 10 times higher than in *I. galbana* and *C. calcitrans*. All strains produced significant quantities of specific omega-3-fatty acids with interest as nutraceuticals and PUFA production ranged from 36 % to 71 % of total fatty acids. Particularly, strain TCBG-1 produced arachidonic acid (ARA) and EPA at the exponential growth phase, while TCBG-2 produced DHA at exponential and EPA at the late exponential growth phases. A two-stage growth system using co-cultures of these two Brazilian *T. chuii* strains in photobioreactors is proposed as an optimal model for PUFA production.

Financing: We are grateful to the mobility internship of Fundación Carolina (G. Moser) and project FICOEXPLORA (RTI2018-101272-B-I00), Spanish National Research Plan.

Keywords: Polyunsaturated fatty acids (PUFA), eicosapentaenoic acid (EPA), docosahexaenoic acid (DHA)

E-Poster

EFFECT OF SALT CONCENTRATION AND COMPOSITION ON THE RHEOLOGICAL AND MECHANICAL PROPERTIES OF K/I-CARRAGEENAN GELS: OPTIMIZATION USING RESPONSE SURFACE METHODOLOGY

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Carrageenans are sulphated polysaccharides of red seaweed used as gelling, thickening and stabilizing agents by the food industry. Particularly, κ/ι-carrageenan gels show unique properties and have received increased interest in recent years. Gelation occurs in the presence of cations, typically potassium in κ- and calcium in ι-carrageenan. The aims of this study were to 1) analyse the effect of cation concentration and composition on the rheology, texture and syneresis of food grade κ/ι-carrageenan gels, and 2) optimize the structural properties of these gels. Response surface methodology (RSM), small composite design (SCD) was used to evaluate the effects of three factors (carrageenan concentration, salt concentration, and KCl fraction in a mixture of KCl and $CaCl_2$) on the following responses: elastic modulus at 1 Hz (G'), hardness (H), rupture strength (R) and syneresis (S). Regression analyses indicated that the quadratic model was the most appropriate to explain all responses. Carrageenan concentration positively affected G', H and R, while salt concentration negatively influenced these responses, indicating that higher carrageenan and lower salt concentrations improved gel firmness. Higher KCl fractions also resulted in increased H and R. Syneresis was reduced with the increase of carrageenan concentration and KCl fraction, while it was augmented by high salt concentrations. To optimize the structural properties of the gels, G', H and R were maximized and S was minimized, achieving a global desirability of 0.895 with the following combination of factors: carrageenan concentration = 1.74% (w/w), salt concentration = 0.07 M and $KCl/(KCl + CaCl_2) = 0.85$.

Financing: PIP-CONICET: 112-2015 01-00510

Keywords: Carrageenan gels, rheology, texture

E-Poster

HAEMATOCOCCUS PLUVIALIS STRAIN FOR SUSTAINING PROFITABLE AGRICULTURAL PRODUCTION

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Agricultural land degradation and natural resource depletion are accelerated by population growth. To overcome this challenge, an intensive search for alternative sources is needed. Microalgae are considered one of the most promising sustainable sources for the production of a high variety of molecules, such as valuable unsaturated fatty acids, proteins, vitamins, and carotenoid secondary metabolites. *Haematococcus pluvialis* (Chlorophyceae, Volvocales) is a freshwater unicellular green microalga and is the richest source of astaxanthin, a natural carotenoid considered one of the strongest antioxidants in nature. Carotenoids are precursors of essential phytohormones required for plant growth and development. Strigolactone and abscisic acid are especially important for plants in response to environmental stresses, both are plant hormones derived from β-carotene. The carotenoid biosynthesis pathway of *H. pluvialis* has been genetically modified to overproduce β-carotene. The endogenous phytoene desaturase coding sequence has been codon-optimized and overexpressed in the chloroplast of *H. pluvialis*. Genetically engineered strains and non-transformed *H. pluvialis* biomass were used as biostimulants for the growth of *Arabidopsis thaliana*. Microalgal extracts in the form of seed primer were able to trigger faster germination and enhance shoot and root length compared to the untreated seeds. Thus, *H. pluvialis* and carotenoid overproducer strain extracts represent a potentially sustainable alternative as an environmental-friendly biostimulant for promoting ecological agriculture.

Financing: Lab. Genética e Inmunología Molecular-PUCV

Keywords: *H. pluvialis*, β-carotene, biostimulant

E-Poster

NUTRITIONAL ANALYSIS OF THE NATIVE NEW ZEALAND SEAWEED SPECIES *MACROCYSTIS PYRIFERA*

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The marine environment represents a vast, relatively untapped resource for sustainable bio-compound sourcing. Global population growth has put considerable pressure on food production, specifically, the present need for protein to supply global requirements has increased 5-fold since 1961. *Macrocystis pyrifera* is a native species of brown seaweed in New Zealand, Australia and is also found, on the west coast of the US, South America, and South Africa. In comparison to other brown seaweeds such as Laminaria digitata, *Macrocystis pyrifera* has not been studied in as much detail for its potential to produce bioproducts. Previously reported *Macrocystis pyrifera* protein content values range from 9-17% depending on location and environmental factors including the season of harvest. Protein sourced from seaweed can contain all essential amino acids, which account for almost half of the total amino acids and the protein profile of some species is similar to that of egg protein. Initial nutritional analysis using AOAC standard protocols of wild harvested *Macrocystis pyrifera* from Tory Channel, in the South Island of New Zealand, found dry weight % values of 12.2% crude protein, 30% total dietary fibre, and 1.9% total lipid. Further analysis of fatty acid profiles detected essential fatty acids, and the highest content was found for arachidonic acid (AA) at 9% followed by eicosapentaenoic acid (EPA) at 6.5%, linoleic acid (LA) was 6.1%, and alpha linoleic acid (ALA), was 4.4%.

Further analysis of the protein including amino acid profile and the carbohydrates, such as total polysaccharides and degree of sulphation is being carried out.

Financing: Research Leaders 2025 programme co-funded by Teagasc and the European Union's Horizon 2020 and Marie Skłodowska-Curie grant agreement number 754380

Keywords: Nutritional, analysis, *Macrocystis pyrifera*

E-Poster

USING CHIMERIC KELP PRODUCTION AS NATURE-BASED SOLUTIONS (NBS) FOR ECOSYSTEMIC SERVICES RESTORATION

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Climate change is pushing kelp dominant habitat-forming species into decline, with negative effects in many aspects such as adaptability and biodiversity. Therefore, kelp cultivation for aquaculture, restocking or ecosystem restoration could be effective actions in climate change mitigation as Nature-based Solutions. However, lack of consideration for genetic diversity, such as using just one or non-native strains, could reduce population adaptability. Here, we selected strains of *Lessonia spicata* and built chimeras (Patent N°2017-1827) to evaluate their relationship with fitness and resilience capabilities at different scales, including in-laboratory or hatchery, and transplantation to field at pilot scales. Additionally, we quantified natural chimera frequency, and their relationship with the role of chemicals and invertebrates in ecosystem services. Building chimeras increased local genetic diversity fivefold, together with survival rates (1.2 to 3 times), biomass (1.2-1.6 times), and the number of axes (7-10 times) compared to homogeneous individuals. Additionally, experiments showed chimeric recruits to be more robust and resilient than homogeneous individuals under stressful temperature conditions (18ºC). In natural populations, 47-67% of plants were chimeras, which showed higher levels of photosynthetic pigments (Chl a, Chl c, and Carotenoids), compared to homogeneous plants, but did not affect phenols and alginic acid yield. They also exhibited greater invertebrate richness and abundance. Considering kelp's foundational role in natural ecosystems, the use of chimeras can enhance the health of the affected population by anthropogenic disturbance or climatic change, as well as produce a diverse range of services on which human wellbeing depends, as an example of a Nature-based Solution.

Financing: FONDEF ID17I10080 - ID20I10167

Keywords: Chimera, kelp, ecosystem services

E-Poster

EVALUATION OF THE FUNCTIONAL PROPERTIES OF *POLYSACCHARIDES* PRESENT IN SEAWEEDS FROM VERACRUZ-BOCA DEL RÍO, MEXICO

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Algae are organisms widely studied for their diversity of bioactive compounds, among these are the polysaccharides they contain. For this reason, in the present work, the content of dietary fiber was determined, as well as its functional properties in coastal algae from the Port of Veracruz. For this study, *Ulva lactuca, Hypnea cervicornis, Hypnea musciformis, Gracilaria bursa-pastoris* and *Padina gymnospora*, collected in Veracruz, Mexico, were analyzed. They were washed and taken to constant weight in a drying oven at 60 °C. The method proposed by AOAC (2000) was used for their analysis of soluble (SDF), insoluble (IDF) and total (TDF) dietary fiber. The determination of swelling capacity, water retention and oil retention were followed the methodology of Gómez-Ordoñez (2013). The results show an abundant FDT content having a range of 34.4-66.7 g/100 g of dry algae, highlighting red algae. SDF and IDF content varied between 9.6-25.4 g/100 g and 24.4-46.6 g/100 g of dry seaweed, respectively, highlighting *H. cervicornis* and G. bursa-pastoris in SDF and IDF. The ratio of SDF/IDF was found to be 0.4-0.84 g/g, highlighting *P. gymnospora* and *G. bursa-pastori*. For the functional properties, it was found a good capacity of water retention (9.71-12.4 g/g) which provides a potential capture of hydrosoluble substances, on the other hand, oil retention showed a potential of hydrophobic substances capture (0.64-2.35 g/g). It is concluded that algae found in the Gulf of Mexico present attractive functional properties as a source of functional ingredients.

Financing: We are grateful to the National Technological Institute of Mexico (TECNM) for its financial support with project 9039.20-P

Keywords: Dietary fiber, functional properties, seaweed

E-Poster

BIOREFINERY APPROACH APPLIED TO THE BIOMASS OF THE DIATOMS *STAUROSIRELLA PINNATA* AND *PHAEODACTYLUM TRICORNUTUM*

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Biorefinery approach, which relies on sequential extraction of multiple products from a single biomass, allows for cost and impact reduction of microalgal biotechnology although application to diatom biomass is still limited. In this work, a cascade extraction was applied to a native diatom strain of *Staurosirella pinnata* and to the model organism *Phaeodactylum tricornutum*. Biomass of the two strains was intensively cultivated in indoor, 30 l photobioreactors and extracted to obtain i) crude extracts, ii) lipids, iii) biomethane. The products were thus characterized and tested for their biomedical and energetic potential. Nuclear Magnetic Resonance (NMR) analysis of hydrophilic fractions of the crude extracts identified 52 metabolites while their bioactivity tests on human melanoma and keratinocytes cell lines revealed that *S. pinnata* extract exhibit a strong and selective cytotoxic activity on melanoma, whereas *P. tricornutum* extract showed significant cell death levels only at the highest doses. Gas Chromatography and Mass Spectrometry (GC-MS) analysis of lipidic extracts from the residual biomass evidenced that cis-9-hexadecenoic and eicosapentaenoic acids were the most abundant fatty acids in *S. pinnata*, while eicosapentaenoic, docosanoic and hexadecanoic acids, prevailed in *P. tricornutum*. We tested the metabolic effect of the diatoms' lipids on insulin resistance and obesity treating human Brown Adipose Tissue (BAT) cells. Western Blot and rtPCR analysis revealed that *P. tricornutum* extract modulated the thermogenesis pathway of BAT, prospecting an anti-diabetic activity. Finally, the exhausted biomass of the two diatoms was evaluated for its Biochemical Methane Potential pointing to a suitable substrate for biomethane production.

Keywords: Microalgae, diatom, biorefinery

E-Poster

ANALYSIS OF GROWTH AND EXOPOLYSACCHARIDES PRODUCTION OF THERMAL CYANOBACTERIUM *PHORMIDIUM* SP. ETS05

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Phormidium sp. ETS05, a filamentous cyanobacterium, is the most abundant species identified among themicrobiota that grows on the Euganean Thermal District (Italy) during the mud maturation process (Gris,2020). This traditional method carried out by spas combines virgin clay and thermal water at 40 °C, obtaining after two months a therapeutic mud. The efficacy of the mud in healing the chronic pain of arthro-rheumatic pathologies is related to heat, presence of electrolytes, and presence of bioactive molecules produced by the microbiota. Monogalactosyldiacylglycerol and digalactosyldiacyl glycerol extracted from *Phormidium* sp. ETS05 have been tested in vitro and in vivo for their anti-inflammatory activity (Bruno, 2005; Ulivi 2011). Recently, having observed a conspicuous presence of mucilaginous substances forming the microbial mats, exopolysaccharides (EPS) obtained from *Phormidium* sp. ETS05were investigated and have been demonstrated to have anti-inflammatory activity in vivo (Zampieri, 2020). The cyanobacterium was cultivated at different light intensities using a lab-scale photobioreactor to evaluate which was its optimal growth condition. EPS production for each condition was measured, to understand which condition leads to higher EPS productivity. We observed higher biomass growth at 50μmol m -2 s -1, while EPS were more abundant at 100 μmol m -2 s -1. From literature, information on EPS assembly and export pathways in cyanobacteria are limited. Putative genes of a Wzy-dependent pathway identified in *Phormidium* sp. ETS05 genome were investigated and correlated to light intensities tested. Further analysis will widen our knowledge on this aspect, leading to the possibility of biotechnologically boost EPS production.

Keywords: Thermal cyanobacteria, exopolysaccharides

E-Poster

RNA-SEQ ANALYSIS OF DIFFERENTIALLY EXPRESSED GENES IN *SOLANUM LYCOPERSICON* L. IN RESPONSE TO *SARGASSUM* BIOSTIMULANT

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Seaweeds have been used in the industry for several purposes for several decades across the world. Seaweeds contain a number of plant growth-stimulating compounds. Seaweed Liquid Extract (SLE) is used as a nutrient supplement or biofertilizer in agriculture to increase plant growth and yield. Puerto Rico tourism and coastal environment is severely affected by the abundance of seaweed, *Sargassum fluitans*, on its coastal areas. We hypothesized that the waste of *Sargassum fluitans* collected from the coastal areas of Puerto Rico can be utilized to locally produce eco-friendly biofertilizer. We measured the effect of varying concentrations of *S.fluitans* SLE on growth of tomato seedlings. Ectopic application of 5% SLE increased the shoot length when compared with controls indicating a potential role of SLE in plant growth and development. We further assessed if the bacterial microbial communities are affected with varying concentrations of SLE. Our preliminary data suggests that application of SLE changes the bacterial communities of the host plant treated with SLE and consequently SLE may enhance the growth of the plant by controlling the association of microbial communities. We studied the changes in gene expression of

tomato plants after they were treated with SLEs. Our results show that genes associated with growth and development were significantly up-regulated in plants treated with SLEs. In future, the use of bio-fertilizers from seaweed would provide an ecofriendly alternative method of keeping the coasts of Puerto Rico clean by converting the waste into wealth.

Financing: The research work has been funded by National Science Foundation HSI-STEM grant (Award No. 1928792) awarded to Alok Arun

Keywords: Seaweeds, biofertilizer, RNA-seq

E-Poster

MINERAL AND HEAVY METAL CONTENT OF DRIED SEAWEEDS FROM THE CHILEAN COAST AND HEALTH RISK ASSESMENT TO HUMAN CONSUMPTION

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Seaweeds are a rich source of minerals and functional compounds, but they can also accumulate toxic heavy metal ions. This study investigated the concentration of macroelements (Na, K, Ca, Mg, P), microelements (Fe, Mn, Zn, Mo, Se) and heavy metals (total As, Cd, Pb, Hg, Cu, Cr, Al) in 10 species of Chilean seaweeds and estimated the possible health risk upon ingestion by hazard index (HI). A wide range of element concentrations were observed between the species analyzed. Among seaweed groups, brown seaweeds (*Lessonia trabeculata, Lessonia berteroana, Lessonia spicata*, Macrocystis sp., and *Durvillaea incurvata*), showed higher mean concentrations of Na, Ca, P, and Cr, whereas red seaweeds (*Agarophyton chilense, Sarcodiotheca gaudichaudii, Chondracanthus chamissoi*, and *Cryptonemia* sp.) had higher contents of K, Mn and Zn. The green seaweed Ulva sp. had the highest content of Mg. In the case of main heavy metals, the highest mean contents of total As (between 15.0 and 35.6 mg Kg-1) and Cd (between 2.4 and 6.2 mg Kg-1) were observed in brown seaweeds. No variation among seaweed groups was observed in the level of Hg (between 0.009 and 0.02 mg Kg-1) whereas Pb content was below the detection limit (<0.01 µg Kg-1). The health risk assessment indicated that HI at mean level was less than the threshold of 1. It indicated that consumption of the Chilean seaweed species poses a low risk for humans with regard to heavy metals including in the analysis.

Financing: CORFO Cod. 16BPER-66977; ANID - PAI 79160069; Fondo Postdoctorado Universidad Católica del Norte N°001

Keywords: Northern Chile, raw seaweed, value-added

E-Poster

CHEMICAL AND MICROSTRUCTURAL CHARACTERIZATION OF THREE SPECIES OF SEAWEED FROM TWO LOCALITIES FROM VERACRUZ, MEXICO

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Seaweed is an important source of compounds, distributed throughout their tissues, which can be studied using histochemical and microscopy techniques. This aim was to characterize chemical composition and microstructure and evaluated the localization and distribution of carbohydrates and proteins, besides quantified those considered toxic minerals in the tissue of *U. lactuca (UL), S. cymosum (SC), G. subpectinata (GS)*. The chemical composition was determined and microstructural analysis was carried out by optical microscopy, image analysis, scanning electron microscopy and atomic absorption spectrometry. Through histochemical techniques, carbohydrates and proteins were evidenced using Schiff and Coomassie Blue reagents, respectively and determining the shape and size of the cells of *SC* and *GS* cortex tissues, and UL blade, as well as the distribution and density of the protein bodies (PB), and was observed that the largest size shown by the cells and PB corresponded to those of cortex *SC* and blade *UL*. In *GS*, the PB had a greater area and density. The chemical composition of the three species showed values between 44-73% of carbohydrates, 13-45% ashes, 5-16% of proteins, and minerals (Cu, Cd, Cr, Ni, Pb, Zn, and Hg) did not reach the toxicity limits. The used techniques showed similarity in the obtained data in the seaweed tissue.

Keywords: Protein bodies, histochemical and microscopy techniques

SYM16: OTHER

Oral presentation

TRACING THE EVOLUTION OF SILICA SCALES IN THE FRESHWATER GENUS *SYNURA* (STRAMENOPILES)

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A high degree of morphological variability is expressed between the ornately sculptured siliceous scales formed by species in the chrysophycean genus, *Synura*. In this study, we aimed to uncover the general principles and trends underlying the evolution of scale morphology in this genus. We assessed the relationships among thirty extant *Synura* species using a robust molecular analysis that included six-genes, coupled with morphological characterization of the species-specific scales. The analysis was further enriched with addition of morphological information from fossil specimens, and by including the unique and rare modern species, *Synura punctulosa*. We inferred the phylogenetic position of the morphologically unique *S. punctulosa*, to be an ancient *Synura* lineage related to *S. splendida* in the section Curtispinae. Some morphological traits, including development of a keel or a labyrinth ribbing pattern on the scale appeared once in evolution, whereas other structures, such as a hexagonal meshwork pattern, originated independently several times over geologic time. We further uncovered numerous construction principles governing scale morphology and evolution, as follows: 1) scale roundness and pore diameter decreased during evolution; 2) elongated scales became strengthened by a higher number of struts or ribs; 3) as a consequence of scale biogenesis, scales with spines possessed smaller basal holes than scales with a keel and; 4) the keel area was proportional to scale area, indicating its potential value in strengthening the scale against breakage.

Financing: Funded by the Czech Science Foundation (20-22346S) and the United States National Science Foundation (EAR-1725265, EAR-1940070).

Keywords: Chrysophytes, morphology, phylogeny

Oral presentation

STAR WARS: PHENOLOGY OF *NITELLOPSIS OBTUSA* (STARRY STONEWORT) IN TWO MICHIGAN, USA DROWNED RIVER MOUTH LAKES

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Invasive species have been introduced into new areas through anthropogenic interactions causing economic, environmental, and social impacts because of their unique ecological engineering strategies, including: aggressive competition, habitat degradation and declines in native species. This study is focused on the growth of a newly introduced aquatic invasive species, *Nitellopsis obtusa* (starry stonewort). *Nitellopsis obtusa* is a dioecious freshwater green macroalga from the Characeae family native to Eurasia, but relatively uncommon in much of its native range. Considered invasive in North America, *N. obtusa* is a rapid colonizer that spreads through an asexual reproductive bulbil and is capable of outcompeting other aquatic macrophytes/macroalgae by creating large monotypic meadows. The focus of this study is to document the timing of the peak biomass of *Nitellopsis obtusa* in Pentwater and Muskegon Lakes in Michigan, USA and relate this peak to light, temperature, and the biomass of other species present. For biomass sampling, six quadrats were placed randomly at each site (0–3 m depth) and all macrophytes/macroalgae in each quadrat were destructively harvested by snorkeling, sorted by species, and subsequently dried and weighed to obtain a growth curve. Preliminary results indicate *N. obtusa* peaked at different times at each site. The relationship between the growth curves of *N. obtusa* and abiotic/biotic factors will be discussed. These results may allow us to better understand the factors that influence the growth of *N. obtusa* and therefore, assist in the management of this invasive species.

Keywords: Macroalga, aquatic invasive species, biomass growth

Oral presentation

ENDOSYMBIONT-CONTAINING DIATOMS FROM RHOPALODIACEAE FAMILY AS INDICATORS OF CHANGES IN NUTRIENT CONDITIONS OF LOWLAND RESERVOIRS

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Increasing phosphorus load upon aquatic ecosystems leads to a decline in nitrogen-to-phosphorus-ratio. Under such conditions competitive edge is acquired by nitrogen-fixing algae, such as planktonic heterocyst-forming Cyanobacteria (Bulgakov, Levich, 1999). As regards benthic and epiphytic communities, diatoms from *Rhopalodiaceae* family may develop under low N:P-ratio (Trapp et al., 2012). It is because their cells contain nitrogen-fixing endosymbionts tracing their origin to Cyanobacteria from *Cyanothece* genus and providing diatoms with nitrogen compounds (Nakayama et al., 2010). The aim of the research was to test the hypothesis that *Rhopalodiaceae* diatoms gain competitive advantage in epiphytic communities of the Dnieper water reservoirs under current N:P-ratio reduction. For this purpose, we plotted the cumulative biomass of *Rhopalodiacea* diatoms in epiphytic communities on common reed against the N:P-ratio data, published by the Ukrainian State Water Resources Agency. The relationship between these parameters was inverse logarithmic with R2 = 0.41 for the *Rhopalodiaceae* algae's absolute biomass and R2 = 0.50 for their share in the total epiphytic algae biomass. That is, when the N:P-ratio reduces, species from *Rhopalodiaceae* family with endosymbionts gain a competitive edge in epiphytic communities. For example, when N:P-ratio is above 15, the biomass of

Rhopalodiaceae diatoms makes up 0.083 mg×10 cm–2 (<1% of the total biomass). When N:P-ratio is equal to 4, their biomass reaches 2.325 mg×10 cm–2 (13%). Thus, an increase in biomass of *Rhopalodiacea* algae may serve as a reliable biological indicator of low N:P-ratio. This pattern may have a practical application for assessing aquatic ecosystems' water quality.

Keywords: *Rhopalodiaceae*, endosymbionts, nitrogen-to-phosphorus ratio

E-Poster

DINOTOMS AND ITS EVOLUTIONARY RELATION WITH ECOLOGY AND SYSTEMATICS

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Durinskia baltica is a dinotom dinophyta with a wide ecological distribution that has undergone a complicated taxonomic history based on morphology that does not seem to be related entirely to populations' different eco-physiological characteristics reported around the world. For this reason, molecular approaches are useful to understand these taxonomic and ecological overlaps. Based on the phylogenetic inferences obtained from the 18S rRNA ribosomal gene of a Mexican freshwater strain of *Durinskia baltica* and the *rbc*L gene of its endosymbiont nucleus, we performed a relative time analysis with sequences of dinotomes and their hosts from marine and freshwater environments. The construction of each time tree used two-time constraints as calibration. The resulting host time trees were consistent with those estimated for endosymbionts. Sequence divergence times that identified species from freshwater environments were more recent than those from saline environments. Results show that the genetic information and the history of the endosymbionts are essential keys to understand the ecology and the evolutionary line of dinotomes since their eco-physiological differences are not only explained with the type of habitat but with the evolutionary history of the endosymbiont given the possibility of serial endosymbiosis in at least some of the species of this genus. For this reason, it is necessary to extensively document and adjust the dimensions of the ecology, physiology, and genetics of dinotomes, within the framework of their systematics.

Keywords: Dinophyte, endosymbionts, timetrees

E-Poster

FROM COMMERCIAL SAND DIGGING TO DIATOMS "HOTSPOT"

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The artificial sandpit lake "Peskara" is located between the two saline lakes, Lake Velika Rusanda and Lake Mala Rusanda, in the protected zone of Rusanda Nature Park (Vojvodina, Serbia). The lake was created by human activity for the exploitation of sand. The depression (on average 4.4 m deep, around 205 m long, and 107 m wide) was filled with water that can be classified into sodium bicarbonate chemical type. Over time a stable diatom community developed. During observations of the samples collected from the sand and reed during 2019 and 2020, 111 diatom taxa belonging to 37 genera were recorded. 14 diatom taxa and one genus (*Seminavis*) were noted for the first time for the diatom flora of Serbia. Fresh alkaline waters with elevated concentrations of electrolytes (1860–1950 µS/cm) enabled the development of freshwater diatoms (e.g. *Achnanthidium minutissimum, Gomphonema parvulum*) but also diatoms characteristic for brackish and coastal waters, such as *Bacillaria paxillifera, Entomoneis costata, Haslea duerrenbergiana, Pleurosigma salinarum, Staurophora brantii, Seminavis strigosa*, etc. Many of these species have not been found in saline lakes and ponds in the Vojvodina province, which makes "Peskara" a significant "hotspot" from the aspect of diatom biodiversity. This artificial sandpit lake requires more detailed research in order to obtain a certain degree of legal protection and to prevent possible backfilling and habitat loss for many diatom species.

Keywords: Diatoms, artificial sandpit lake, subsaline water

E-Poster

ALGAL COMPOSITION OF *KYPHOSUS VAIGIENSIS* (PERCIFORMES, KYPHOSIDAE) DIET IN SUBTROPICAL ROCKY REEFS OF THE GULF OF CALIFORNIA, MEXICO

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Rocky reefs of the Gulf of California are covered during spring by luxuriant Sargassum beds that disappear in summer. Therefore, the organisms that feed on it must find another alternative food source. The brassy chub *Kyphosus*

vaigiensis is a circumtropical fish species associated with rocky reefs that feeds mainly on Sargassum. This study describes the diet of *K. vaigiensis* from stomach content analyses of 62 organisms captured off Santa Rosalía (Punta Gorda and Los Frailes) on the western coast of the Gulf of California, Baja California Sur, México during May and September 2015, coinciding with the maximum and minimum *Sargassum* biomass. The Prey-Specific Index of Relative Importance (%PSIRI) was calculated using the percentages of frequency of occurrence, specific abundance, and weight of each identified item in stomach contents. A total of 30 macroalgal taxa were identified, of which 19 were from the *Phylum Rhodophyta*, seven from Ochrophyta, and four from Chlorophyta. Of these components, 14 were found in May and 22 in September. The main diet components (%PSIRI > 10%) were *Sargassum* and *Padina* in May, while the red seaweeds *Gracilaria, Grateloupia, Prionitis*, and *Chondracanthus* were predominant during September. These results showed that *K. vaigiensis* diet changes seasonally with seaweed availability. However, the species seems to have a preference for *Sargassum*, probably because the genus is a vital component of the rocky reefs in both localities and *K. vaigiensis* has the necessary adaptations for its assimilation.
Financing: CONACyT project CB2012-179327

Keywords: Brassy chub, herbivorous, Santa Rosalía

E-Poster

MACROALGAE IN THE DIET OF THREE SEA URCHIN SPECIES IN SUBTROPICAL ROCKY REEFS OF THE GULF OF CALIFORNIA

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Sea urchins graze abundantly on seaweeds in rocky reefs. They also consume invertebrate species and could be facultative omnivores depending on the availability of macroalgae. In the Gulf of California, the three species, *Eucidaris thouarsii, Echinometra vanbrunti*, and *Tripneustes depressus*, coexist in *Sargassum* beds. This study determines their diet by stomach content analysis and calculated the prey-specific index of relative importance (PSIIR%). The organisms were collected in three *Sargassum* beds off Santa Rosalía, Baja California Sur, México, on May and October 2013, coinciding with *Sargassum* highest and lowest biomass. Although sea urchin species feed mainly on red and brown macroalgae, the relative importance of the macroalgae genus in the diet was different. The main items (>10%PSIRI) of *E. thouarsii* were the red articulated coralline *Amphiroa*, brown alga *Sargassum*, and the invertebrate group Briozoa. *E. vanbrunti* main prey were red coralline algae, red alga *Chondracanthus*, brown algae *Padina, Cluteria* and *Sargassum*, and the green algae *Cladophora* and *Caulerpa*. While *T. depressus* main items were *Padina, Sargassum* and *Amphiroa*. This study found that *E. vanbrunti* and *T. depressus* are fundamentally herbivorous while *E. thouarsii* could consume invertebrates in times when algae are not abundant.
Financing: CONACyT project CB2012-179327

Keywords: Stomach content, *Sargassum* beds, herbivores

E-Poster

PREDICTING MACROALGAL SPECIES DISTRIBUTIONS ALONG THE THAI-MALAY PENINSULA

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Seaweed ecosystems provide many essential and valuable ecosystem services in coastal waters. Understanding the environmental variables affecting their large-scale distribution is challenging but crucial for the proper management and conservation of macroalgae. The aim of this study is to predict the potential distribution of the green alga *Halimeda macroloba* Decaisne and the brown algae *Padina boryana Thivy, Sargassum plagiophyllum* C.Ag. and *Sargassum polycystum* C.Ag. along the Thai-Malay Peninsula. Occurrence data was obtained from field observations and literature. Five species distribution models were developed for each species based on sea surface temperature, sea surface salinity, pH, dissolved oxygen, chlorophyll-a concentration, and bathymetry. The results suggested potential suitable habitats for *H. macroloba* along the coasts of the Gulf of Thailand and the Malacca Strait. The models predicted suitable habitats for *P. boryana* along the entire west coast (Andaman Sea and Malacca Strait) and the entire coast of the Gulf of Thailand. Suitable habitats of *S. plagiophyllum* and *S. polycystum* were clearly separated, with *S. plagiophyllum* potentially occurring along the west coast of Thailand and extending into Malaysia and Myanmar, while *S. polycystum* potential habitats occur only along the east coast of Thailand and Malaysia. The importance of the environmental variables differed between the models and species. Using a modeling approach, the potential suitable and unsuitable distributional areas of these species were defined, as well as the variables affecting them. These findings provide encouragement for its use in future climate-related studies as well as sustainable conservation and management.
Financing: RDG613002, TRF Thailand Research Fund

Keywords: Species distribution modelling, geographic distribution, coastal ecosystem

E-Poster

BENTHIC MACROALGAE FROM THE SISAL REEFS, YUCATAN, MEXICO

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Reefs are ecosystems that provide multiple ecosystem services, and the macroalgae as a primary group help to a better understanding of these areas. The Sisal Reefs are located on the shores of the Campeche bank under the influence of the Gulf of Mexico. There are few phycological studies on this area, specifically the Sisal reefs. In order to contribute to the study of macroalgae inhabiting Yucatan, the first taxonomic list of these reef banks was made. Sisal Reefs are made up of three shallow banks: Bajo Diez, Madagascar, and Serpientes. Sampling was done through SCUBA diving at 2-4 stations per site. The samples were preserved in 4% formalin and identified at the lowest taxonomic level. With the data, a matrix of presence-absence of species per station and site, the frequency of species per station, and a similarity analysis (UPGM) with the Bray-Curtis index was performed. The three reefs have 123 species (28 Phaeophyceae, 43 Chlorophyta, and 52 Rhodophyta) and the most frequent taxa between the sites were *Aspargopsis taxiformis*. There is a greater similarity between sample stations than between sites. The richness of Arrecifes de Sisal is much greater than previous reports from the Banco de Campeche. Sisal reefs have diverse substrates, which translates into great diversity like the reef areas of the Mexican Caribbean. These reefs can function as reservoirs of diversity and allow species to disperse, so it is vital to conduct more studies to understand the Spatio-temporal dynamics of these ecosystems.

Keywords: Reefs, macroalgae, richness

E-Poster

A SURVEY OF THE DISTRIBUTION OF STRUCTURAL COLOUR IN THE RED ALGAE (RHODOPHYTA)

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Structural colour occurs across a wide range of seaweed species (red, green and brown macroalgae). Unlike pigmentation, which is based on chemical composition, structural colour results from the physical organisation of the surface layers at the nano- or mesoscale. These structure cause interference in the reflected light, the physics behind the iridescent features observed in many organisms. Structural colour has been extensively studied in terrestrial organisms, but there is still much to discover about the phenomenon in marine algae. Previous studies show that two of the mechanisms responsible for structural colouration in nature have been found among iridescent seaweeds: multi-layered structures and iridescent bodies. The phenomenon is a key component of the seaweed's interaction with sunlight and is considered a potential photoprotection mechanism against harmful light intensities. As a first step in a project aimed at understanding the role of structural colour for light management in macroalgae, we are carrying out a review of the geographical, ecological and phylogenetic distribution of structural colour mechanisms within the Rhodophyta. Initial results hint at a strong concentration of species within three taxonomic orders: Ceramiales (seven families), Gigartinales (four families), Rhodymeniales (five families). Observation records show a larger concentration of iridescent red algae in the Southern hemisphere: Caribbean Islands, South America, South Africa, Middle-East, and Australasia; and some records for Europe and North Pacific (West and East).

Financing: Horizon 2020 Research and Innovation Framework ITN "BEEP"

Keywords: Biogeography, light management, photoprotection

E-Poster

ROCKY REEF MACROALGAE OF THE NORTH COAST OF YUCATAN, MEXICO

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The study of macroalgae in reef environments in Yucatán has been limited to coral reefs of the Bank of Campeche such as Arrecife Alacranes, however, there are many rocky reef banks near the north coast of Yucatán that have not been studied. The present work focuses on three rocky reefs: Sisal, Chicxulub and Río Lagartos. This is the first description of the composition and richness of the benthic macroalgae communities. The samples were made at different times, (winter 2012, 2013, summer 2017 and 2019) using autonomous diving (SCUBA) and general collections were made at different points of the reef area. The specimens were pressed, and preserved in 4% formaldehyde, the vouchers were deposited in the Alfredo Barrera Marín herbarium collection at UADY. 87 species are reported, and the largest number of species is the Phylum Chlorophyta (38) followed by the Rhodophyta (30) and the Phaeophyceae (Ochrophyta) (19). The *Caulerpa* and *Udotea* genera are those with the highest number of species. Nine new records were found for the State and of these, *Sargassum pteropleuron, Platoma* *gelatinosum* and *Nemacystus howei* are new records for the Peninsula. The number of species reported in this area is higher than what has been found in the coastal area, which is consistent with previous studies, which have shown that the greatest diversity of algae occurs in reef environments. Therefore, it is important to continue studying these environments since they are very important centers of diversity that are home to very diverse communities of flora and fauna.

Financing: Universidad Nacional Autónoma de México which supported the Program for Projects for the Innovation and Improvement of EducationPAPIME PE207317

Keywords: Diversity, rocky reefs, macroalgae

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