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Iglesia del Sagrado Corazón de Jesús, Llanquihue Lake and Osorno Volcano in Puerto Varas, Los Lagos, Chile. © 2021 Visit Puerto Varas. All rights reserved. Reproduced with permission.

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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 underinvestigated, 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 O₂. 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 lightharvesting 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.

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Keywords: Diatoms, fatty acids, hypersaline lagoons



We hereby certify that

Laura García Abad

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

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SYM14: Algae at the extremes

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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