



12th International Phycological Congress

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Iglesia del Sagrado Corazón de Jesús, Llanquihue Lake and Osorno Volcano in Puerto Varas, Los Lagos, Chile.
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Edited by Alejandro H. Buschmann, Sandra V. Pereda,
Carolina Camus and Olivier De Clerck



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Edited by

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

Copies of the abstracts will be distributed among registered delegates
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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 *SKELTONEMA 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 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$) 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 (ZYGNETOPHYCEAE)

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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, arabinogalactan 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 well 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 aromatic-rich layer in the wall, the latter possibly containing