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Green algae dividing by multiple fission are a diverse group formed by species from unrelated genera. They are connected by a common feature: mother cell under optimal growth conditions divides into more than two daughter cells. This organization of cell cycle represents a potent evolutionary strategy allowing them to exploit maximum of sun light during day for growth without constraints from the cell cycle related processes. The best developed model organism is *Chlamydomonas reinhardtii* but other representatives include biotechnologically important algae such as *Chlorella* sp. and *Scenedesmus* sp. Here, we will summarize the principles governing the cell cycle regulation in algae dividing by multiple fission. Further, we will present an example of possible exploitation of the cell cycle mutants for the study of coordination of cell cycle and response to DNA damage. This work was supported by the GA CR (grant no. 15-09231S), CAS (grant no. M200201205) and by projects Algaman and Algain.

7OR.1

CELL-TYPE SPECIFIC PHOTORECEPTORS AND ASSOCIATED LIGHT-SIGNALING PATHWAYS IN THE MULTICELLULAR ALGA *VOLVOX CARTERI*

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Photosynthetic organisms, e.g., plants including green algae, use a sophisticated light-sensing system, composed of primary photoreceptors and additional downstream signaling components, to monitor changes in the ambient light environment towards adjust their growth and development. Although a variety of cellular processes, e.g., initiation of cleavage division and final cellular differentiation, have been shown to be light-regulated in the green alga *Volvox carteri*, little is known about the underlying light perception and signaling pathways. This multicellular alga possesses at least 13 photoreceptors, i.e., one phototropin (VcPhot), one UV-B photoreceptor (VcUVR8), four cryptochromes (VcCRYa, VcCRYp, VcCRYd1 and VcCRYd2) and seven members of rhodopsin-like photoreceptors (VR1, VChR1, VChR2, VcHKR1, VcHKR2, VcHKR3 and VcHKR4), which display distinct light-dependent chemical processes based on their protein architectures and associated chromophores. The study of *Volvox* photoreceptors was almost always accompanied by questions regarding their cell-type specific functions, because they are mostly expressed in a cell-type specific manner. This gives reason to believe that transcriptome pattern of each cell type could change differentially in response to environmental light. Comparison of the gene expression profiles of the reproductive and somatic cells reported revealed that distinct cell-type specific light signaling pathways underlying gene expression modulate appropriate transcript regulation in response to light. Blue light tends to be effective to accumulate transcripts in the somatic cells; while red light leads to accumulate transcripts predominantly in the reproductive cells. Thus, the data show that each cell type has its own genetically predefined light signaling pathways to modulate expression of genes involved in various cellular and metabolic processes including circadian rhythms and photosynthesis in response to environmental light.

7OR.2

THE CIRCADIAN CLOCK IN THE DIATOM *PHAEODACTYLUM TRICORNUTUM*

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The majority of living organisms evolved circadian clocks, sophisticated mechanisms that synchronize cells with the environmental periodic cues. Although well studied in terrestrial plants and animals, only a few examples of circadian clocks have been described in marine organisms. Diatoms have exceptional adaptation capacities and exhibit circadian behaviors in natural environments. Interestingly, no orthologous of known circadian clock components have been found in the sequenced genomes, suggesting the existence of a diatom specific clock. In order to reconstruct diatom timing mechanisms, we completed high-resolution physiological and transcriptomic analyses of *Phaeodactylum tricornutum* cells grown in diurnal light cycles and free-running conditions. We identified

24 genes showing robust rhythmic expression upon the different treatments, including putative clock inputs, oscillators and outputs, demonstrating a circadian regulation of transcription. Using a mathematical approach, we selected the most rhythmic Transcription Factors (TFs) and explored their function by gene knockdown and over-expression. This allowed the identification of a first clock component, a bHLH-PAS TF, whose deregulation causes growth impairment, loss of circadian gene expression and a negative feedback loop effect on its own transcription. Further characterizations of these and other TF mutants will allow unraveling the circadian clock architecture and its adaptive significance in diatoms.

7OR.3

DESICCATION TOLERANCE IN STREPTOPHYTIC GREEN ALGAE: NEW INSIGHTS FROM TRANSCRIPTOMICS AND FATTY ACID METHYL ESTER (FAME) ANALYSIS

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Terrestrial green algae frequently experience desiccation. We investigated changes to the transcriptome in Klebsormidiophyceae and fatty acid composition in Zygnematophyceae upon desiccation stress. At ~ 83% relative humidity (RH) the effective quantum yield of photosystem II (Y II, PAM 2500) dropped to zero between 4.5 and 7 hours in *Klebsormidium crenulatum (*SAG 2415). The cells were able to recover 95% of the initial values within 40 min. When desiccated over silica gel (final RH ~10%), Y II dropped to zero within 40-50 min and no immediate recovery of Y II was observed. We analyzed the transcriptome under moist and desiccated (2.5 h silica gel, RH ~ 10%) conditions using RNAseq. The reference transcriptome includes about 24,183 sequences (1.5 million reads, 636 million bases). Over 7000 transcripts changed upon desiccation, 169 transcripts were 10 fold upregulated, including known factors involved in desiccation tolerance (LEA, ERD), energy production, ROS metabolism and enzymes involved in biosynthesis of raffinose family oligosaccarids (RFO), however many without known function. 330 transcripts were completely suppressed. In *Zygnema* sp. from polar and alpine habitats desiccation tolerance was only observed in mature cultures that form akinetes, in which Y II dropped to zero within 5-7 h at ~83% RH. The transcriptomic analysis in *Zygnema* sp. (SAG 2419) is underway. We analyzed the fatty acid composition in *Zygnema* B, C and E. In all samples the major fatty acids found were oleic and linoleic acid, except in young cultures that also contained palmitic and linolenic acids. We found significant differences in the fatty acid composition between young cultures and all other samples, however hardly any impact of the desiccation/recovery experiment. We conclude that desiccation tolerance occurs in both algal classes, but different mechanisms (i.e. desiccation tolerance only after maturation in *Zygnema*) may be involved.

7OR.4

THE STRUCTURE AND FUNCTION OF COCCOLITH ASSOCIATED POLYSACCHARIDES: IMPLICATIONS FOR THEIR ROLE IN CALCIFICATION

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Coccolithophores are globally distributed, unicellular marine algae belonging to the phylum Haptophyta. Characterised by internally produced, intricate calcite liths found on the cell surface, they are biogeochemically important due to their role in the transfer of carbon from the upper waters to depth. Research has focused on the mechanisms behind calcification, but exactly how and why they calcify is still unknown. During lith production in the unique Golgi-derived coccolith vesicle, polysaccharides are simultaneously produced and extruded. These coccolith-associated polysaccharides (CAPs) have been shown to play a role in the regulation of calcium carbonate precipitation; and therefore calcification. In this investigation we looked at a range of species of coccolithophores and their CAPs by direct observation and