A Day in the Life of Chlamydomonas

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Project goals: The green alga *Chlamydomonas reinhardtii* has become a model organism for many diverse research fields, including photosynthesis research. But our understanding of how gene expression is orchestrated between different organelles is still surprisingly limited. We generated a multilayer data set of the Chlamydomonas cell cycle, using a flat panel bioreactor system to allow reproducible synchronization of *Chlamydomonas reinhardtii*. We monitored transcript abundance from all three genomes during the cell cycle by applying a modified transcriptomic approach. Parallel measurements of select metabolites and pigments, physiological parameters and a subset of proteins offered the opportunity for inferring metabolic events and for evaluating the impact of the transcriptome on the proteome.

During the cell cycle, cell division and DNA replication is initiated at the beginning of the dark period, in S phase. The high demand of the core histones during S phase is met by the coordinated expression of multiple genes encoding the core histones in the green algae Chlamydomonas. Interestingly, we see replication independent expression of two of each genes, serving as emergency histones. The helicase involved in DNA replication (MCM complex), is preceding the expression of core histones, ensuring that newly synthesized nucleosomes can be loaded on replicated DNA. After replication, cells remain in G_0 for the remainder of the night, using stored carbon sources presumably for respiration. But assessment of starch, total organic carbon and respiratory activity suggested that fermentative metabolism may dominate during the night, and co-expression pattern identified FDX9 as participant. During the light period, expression of plastid encoded subunits of photosynthetic complexes preceded their nucleus encoded counterparts in anticipation of the day. The dark to light transition is accompanied by expression of stress responsive genes. Among these, the pattern of *PSBS* and *LHCSR1* is distinguished from *LHCSR3* expression, whose pattern receives two distinct inputs from light. Although genes for tetrapyrrole biosynthesis are expressed concomitantly with those for chlorophyll-binding proteins,

those for light independent protochlorophyllide oxidoreductases are reciprocally expressed compared to the nucleus encoded, light dependent enzymes. The multi-omics approach offers an unprecedented high resolution systems level view of cellular processes as cells grown in the light period and divide in the dark from one to two cells.

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