

Down regulation of commitment point related genes and the cell cycle progression in
Chlamydomonas reinhardtii

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Growth and cell cycle appear to be coordinated but the responsible mechanism remains unclear. The simplest model system to study the phenomenon are unicellular organisms such as yeast or microalgae. Particularly intriguing models are unicellular algae dividing by multiple fission that maintain stable daughter cell size over wide set of conditions. They grow autotrophically in the light and can divide into 2, 4, 8, 16 or more daughter cells. In model microalga *Chlamydomonas reinhardtii*, reaching critical cell size will lead to attainment of commitment point (CP) that switches on one sequence of DNA replication, nuclear and cellular divisions. In fast growing cells, attainment of CP comes very early after light switch and the CP responsible genes/proteins can not be separated from the light induced ones. *C. reinhardtii* cells grown at low light intensity ($100 \mu\text{mol m}^{-2} \text{s}^{-1}$) attained CP 7 hours later in comparison to cells grown at high light intensity ($500 \mu\text{mol m}^{-2} \text{s}^{-1}$). Transcriptome and proteome data analysis identified a set of genes/proteins with significantly different expression in the two light conditions. Many genes and proteins were expressed differentially in pre-CP, CP and post-CP samples at high light conditions; while there was a lower number of such genes/proteins at low light conditions. We identified five genes with the most stringent change during attainment of CP. They encompass chlorophyll metabolism, chloroplast growth and energy metabolism. We used inducible amiRNA lines of the target genes to analyse phenotypical changes caused by their partial inactivation within the progression of the cell cycle.