

## **A Molecular Switch for Oxygenic Photosynthesis and Metabolism in the Emerging Oleaginous Model Green Alga *Chromochloris zofingiensis***

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**Project Goals: Our overarching research goal is to design and engineer high-level production of biofuel precursors in photoautotrophic cells of the unicellular green alga *Chromochloris zofingiensis*. Our strategy involves using large-scale multi-‘omics systems analysis to understand and model the genomic basis for how the energy metabolism of the cell is redirected partitioning based on the carbon source. Enabled by cutting-edge synthetic biology and genome-editing tools, we will integrate the systems data in a predictive model that will guide us in the redesigning and engineering of the metabolism in *C. zofingiensis*. This presentation focuses on understanding regulation of photosynthesis and metabolism, which will enable bioengineering of microalgae for improved production of biofuels and bioproducts.**

### **Abstract:**

Microalgae have the potential to become a major source of biofuels and bioproducts without exacerbating environmental problems. Photosynthetic microbes can utilize solar energy, grow quickly, consume CO<sub>2</sub>, and be cultivated on non-arable land. However, there are presently considerable practical limitations in the photosynthetic production of biofuels from microalgae, resulting in low productivity and high costs. Insight into regulation of photosynthesis and metabolism will enable bioengineering of microalgae to maximize production of biofuels and bioproducts.

In this study, we show that the emerging oleaginous model green alga *Chromochloris zofingiensis* has a glucose-dependent photosynthetic and metabolic switch that includes rapid reversible changes in photosynthesis, the photosynthetic apparatus, thylakoid ultrastructure and energy stores including lipids and starch (1). With glucose in the light, *C. zofingiensis* shuts off photosynthesis and accumulates large amounts of commercially relevant bioproducts including

triacylglycerols (TAGs) and the high-value nutraceutical ketocarotenoid astaxanthin, while increasing culture biomass. We used our recently published high-quality transcriptome (2) to show reversible, specific, coordinated gene expression changes in carotenoid, photosynthetic and metabolic pathways. Moreover, we used forward genetics and our chromosome-level genome assembly (2) to reveal that this photosynthetic and metabolic switch is mediated by the glycolytic enzyme hexokinase (HXK1), which likely functions as a glucose sensor that regulates algal photosynthesis, astaxanthin synthesis, and carbon metabolism (3). Our data suggest that HXK1 initiates a signaling cascade resulting in repression of photosynthetic genes. Sugars play fundamental regulatory roles in gene expression, physiology, metabolism, and growth in plants and animals, and we introduce a relatively simple, emerging model system to investigate conserved eukaryotic sugar sensing and signaling at the base of the green lineage. Advancing the basic science underlying regulatory ‘switches’ between growth and lipid production will likely be critical to developing economically viable algal biofuels.

## References

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