Stress Responses Across Scales: From Climate Change to the Evolution of Multicellularity in Green Algae

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Environmental stress responses are central to cellular survival and long-term evolutionary innovation. In this seminar, I present a multi-scale view nutrient stress regulation, cell-cycle control, and the evolution of multicellularity.

In the first part, I summarize a system-wide characterization of the response of *C. reinhardtii* to combined heat and osmotic stress, a condition relevant in the context of climate change. Using an integrated physiological, proteomic, metabolomic, and epigenomic approach, we observed an early reduction in growth accompanied by photoinhibition and oxidative stress. Multi-omic analyses revealed a coordinated acclimation response involving the modulation of photosynthesis-related pathways to counteract excessive ROS production. This response included the accumulation of compatible osmoprotective and antioxidant compounds, together with an increase in cellular respiration to compensate for impaired photosynthetic ATP production. Stress acclimation was further associated with enhanced lipid and carbohydrate metabolism, while amino acid metabolism and protein translation were downregulated, reflecting an optimization of energy expenditure. Epigenomic profiling identified of stress responses in green algae, integrating my PhD work on combined environmental stress in *Chlamydomonas reinhardtii* with a postdoctoral project focused on H3K4me3 as a key activating mark of stress-responsive genes, highlighting the importance which facilitates the integration of epigenetic and multi-omic datasets to uncover stress-associated regulatory signatures.

In the second part, I introduce my postdoctoral project, which investigates how nutrient stress responses are regulated across the cell cycle in unicellular green algae and how such mechanisms may have contributed to the evolution of multicellularity. Within the volvocine lineage, the transition from unicellular species such as *C. reinhardtii* to multicellular organisms with a complete division of labour, such as *Volvox carteri*, represents a major evolutionary innovation. In *V. carteri*, somatic cell fate is controlled by the transcription factor regA, which evolved from a life-history gene present in unicellular ancestors. In *C. reinhardtii*, the closest homolog, RegA-Like Sequence 1 (RLS1), is transiently induced under phosphorus or sulphur limitation, conditions that suppress photosynthesis and cell division to promote survival. This project will combine cell-cycle–resolved physiological analyses with integrated multi-omic profiling to identify regulatory pathways and model how RLS1 couples metabolic state to cell-cycle decisions, providing insight into how stress-regulatory networks may have been co-opted during the evolution of multicellularity.