

## **REGULATION OF THE METABOLIC SHIFT TOWARD LIPID ACCUMULATION IN THE DIATOM *PHAEODACTYLUM TRICORNUTUM***

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Diatoms constitute a major group of photosynthetic microalgae. Diatoms have a high biotechnological potential because they produce of biomolecules of high interest for industries in the sector of energy, nutrition, cosmetics, health and well-being. However, the scientific knowledge of biological processes remains too scarce to make the diatom biotechnology a viable source of biomolecules and more research must be carried on to fulfil this gap. Because biomolecules are mostly/exclusively, composed by carbon atoms, the carbon metabolism constitutes the heart of diatom metabolism. Under nonstressful condition, the carbon metabolism produces sugars that are used to sustain growth. Under difficult conditions, such as a decrease in nutrient deficiency, the carbon metabolism is reoriented towards the accumulation of molecules with a high density in energy, typically lipids. Thus, the elucidation of the mechanisms controlling the carbon metabolism is crucial for the understanding of diatom's life and also for the development of biotechnological applications. In this frame, the lecture will address the following aspects of the control of the carbon metabolism in diatoms:

- Does lipid accumulation constitute a default mechanism of the stress response in diatoms? It is usually observed that under stress, diatoms accumulate lipids. This observation is general enough to hypothesize that this reorientation of the carbon metabolism constitutes a default mechanism. Recent data in favour of this hypothesis will be presented.
- Can the regulatory elements controlling the reorientation of the carbon metabolism in diatoms be deciphered?  
The reorientation of the carbon metabolism must involve cellular, biochemical and molecular components. Using high-to-low carbon availability transition, some of these components have been identified among which transcription factors (TF).
- Can the regulation of the carbon metabolism reorientation controlled by transcription factors? The change in the expression levels of TFs measured in progressive N deprivation conditions has been recorded. Physiological, biochemical and molecular analysis coupled with mRNA quantification, have been used to generate gene regulatory networks. As a consequent step, TF genes have been selected for gene editing and generation of mutant strains. The on-going screening and characterization will confirm the function of the selected TFs in the metabolic shift.

