**Master 2 2023-2024**

Protein Maturation, Cell fate and Therapeutics

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**Challenging how a better understanding of RuBisCO might contribute to better feed the world and solve climate changes**

This Master2 project is at the forefront of research on RuBisCO protein modifications in the context of climate change. RuBisCO, is a key enzyme allowing to uptake carbon dioxide by taking advantage of solar light energy supplied by photosynthesis and to synthesize novel biological compounds. RuBisCO make photosynthetic organisms able to feed on inorganic matter including water.

RuBisCO is a sophisticated macromolecular catalyst only retrieved in photosynthetic organisms (plants, algae, bacteria…). RuBisCO plays a crucial role in converting carbon dioxide into biological carbon. It is therefore the major and most efficient carbon dioxide removal machine and is essential – directly or indirectly - for the food (crop, meat, milk) humans and cattle daily consume. RuBiSCO is not to say the least a natural biological compound and the most abundant protein on Earth. However, this enzyme is remarkably inefficient, hindering our efforts to address climate changes and ensure global food issues in the frame of a growing human population. To overcome both challenges, we need a comprehensive understanding of RuBisCO and its complex maturation mechanism, particularly the intriguing modifications at the N-terminus of the large subunit (RbcL).

In this project, we aim to unravel the mysteries surrounding the plastid machinery involved in the intricate maturation mechanism of the N-terminus of the large subunit (RbcL) of RuBisCO. By unraveling the role of this RbcL N-terminal protein modifications, we hope to contribute to our long-term objective of comprehending the consequences of these modifications under changing environmental conditions. In other terms, by shedding light on these protein modifications, we can lay the foundation for future endeavors focused on enhancing RuBisCO's efficiency and accumulation under changing environmental conditions.

The M2 student will be involved in the genetic characterization of N-terminal protein modifiers and the analysis of the impact of N-terminal protein on RuBisCO in the *E. coli* reconstituted system and in planta. They will construct plasmid vectors expressing the different plastid modification enzymes featuring (i) the four activities (PDF/MetAP/APP/NAA) which the group has identified in *Arabidopsis thaliana* and (ii) the RbcL- mimicking recipient target. They will be trained to use our in-house pipelines/methods for the proteomics N-terminal characterization and quantification of the different modifications. Based on the data, mutations on the target or the modification enzymes genes will be achieved to assess how much they contribute to the balance of the system. This study will be completed with the *in vivo* characterization of Arabidopsis mutant lines devoid of one or more components involved in N-Terminal RuBisCO maturation. Together, the student will investigate how each modification plays its part in plant responses to conditions that mimic the challenges posed by climate change, such as temperature fluctuations, high light intensity, flooding, and salt stress.

The Master student will be involved in a vast international project supported by ANR, DFG and Labex SPS funding in the frame of the MOPGA program (MAKE Our PLANET GREAT AGAIN, a program launched by President E. Macron in 2017 to combat and understand climate changes).

One expected outcome of this research is to link RuBisCO N-terminal modification to the regulation of its activity under environmental stresses similar to those that climate changes will dictate.

Join our international research team and take the opportunity to delve into the important and fascinating filed of protein modifications and their implications for the environment. Together, let's unlock the secrets of RuBisCO and pave the way for a greener, more sustainable future.

References:

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3. Millar, H.A., Heazlewood, J.L., Giglione, C., Holdsworth, M.J., Bachmair, A., Schulze, W.X. (2019) The scope, functions, and dynamics of posttranslational protein modifications. Annual Review of Plant Biology, 70:119-151.