Post-transcriptional and post-translational control of gene expression in response to abiotic stress in plants

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Scientific objectives

Plants live in ever changing environment often unfavourable for growth and development. As sessile organisms they must rapidly alter their developmental program to acclimate to stressful situations and survive. To such end they have developed a complex network of sensing and signalling leading to changes in gene expression to switch on protective mechanisms. Our main scientific objectives are to understand how plants acclimate to heat and oxidative stresses through post-translational alterations of protein functions and post-transcriptional reprogramming of gene expression. Stress exposure induces drastic changes in the intracellular redox state of plants. In a first axis we aim at understanding how the modification of Reactive Oxygen Species (ROS) levels, changes the post-translation modification pattern of proteins and reprogram their molecular roles. A second drastic cellular change triggered by stress is the massive downregulation of translation and modification of mRNA lifespan. In a second axis we work to decipher the molecular mechanisms underlying these alterations. Finally, stress directly alters ribosomal production and maturation, creating specialized ribosomes. In a third axis we aim at identifying modifications of ribosomal RNA (rRNA) that affords the most prominent source of ribosome heterogeneity.

Axis 1: Redox modifications of gene expression through ROS homeostasis. ROS produced upon stress conditions impacts massively gene expression but the actors of this regulation are poorly known. Our recent data suggest that redox-modifications of the key chromatin regulators histone deacetylases (HDACs) might take part in the transcription reprogramming by ROS. We will further examine their role biochemically and in different redox genetic accessions. In another approach, we will also study redox modifications of mRNA (e.g. 8-oxo-guanosine) and how these modifications can affect gene expression upon ROS–trigger.

Axis 2: mRNA translation and stability control reprogrammings in response to heat stress. Upon heat exposure, the cell massively downregulates its translation and alters mRNA stability. The determinants of these reprogrammings are poorly known. Recently, chemical modifications, collectively pinned as the epitranscriptome of a cell, were found to play crucial roles in mRNA fate control in animal cells. Methyl groups deposited at position N^6 of internal adenosines (m^6As) are the most abundant of mRNA modifications and attract m^6A reader proteins. Our data support that one of the putative Arabidopsis readers might be involved in the heat triggered mRNA decay process we uncovered few years ago. Other of our data suggests that the m^6A binding activity of another of Arabidopsis readers is regulated by heat-induced phosphorylation. Our current interest is to explore the link that seems to exist between the plant heat stress response and the m^6A epitranscriptomic mark and its readers.

Axis 3: Modifications of rRNA, including methylation and pseudouridylation. Our recent data show that differential rRNA methylation (2'O-methyl ribose) occurs in specific genetic backgrounds and developmental stages in *A. thaliana* (unpublished results). Still, how these (and others like base-methylation) modifications affect ribosome activity remains unexplored in plants. To address these questions, we design and set up large-scale approaches to identify differential rRNA modifications (and subsequently in ribosome translation) in response to environmental conditions and in "*natural accessions"*

TULIP MTR1: organism – abiotic environment interactions. In the context of this MTR, we are exploring the roles of RNA and protein modifications in the acclimation process of the plant to heat and oxidative stresses.

ETPs involved on the project: Team JPR (2 ETP, 1 Non-perm), Team CBA (2 ETP perm, 1 PhD (until dec. 2017), 1 Post-doc (12 months), and 1 ETP postdoc to be hired (36 months)), Team JSV (2 ETP; 1 Non-perm, PhD)