Abstract for the general public

Transmission of genetic information depends on not only on the genetic code, but also on the effective regulation of expression of its functional products, *i.e.* RNAs and proteins. Moreover, gene expression is carefully monitored by specific quality control mechanisms at all stages, from transcription, through RNA processing and export to translation. One crucial feature of RNA in eukaryotic cells that has a strong impact on its fate is the cap structure at the transcript 5' end. Therefore, 5' cap surveillance mechanisms are critical for gene expression regulation.

The synthesis and biological role of the canonical m^7G cap has been already widely investigated with respect to transcripts stability, cellular localisation and efficient translation. Other cap variants with different properties conferred by various chemical modifications, including hypermethylation or 2' ribose methylations, also exist in eukaryotic cells and have diverse effects on mRNA stability, localisation, interactions and functions. In turn, transcripts with incomplete 5' caps are recognized and eliminated by proteins from the DXO family.

One of the most exciting recent discoveries in this field was identification of cellular transcripts carrying 5' nicotinamide adenine dinucleotide (NAD^+) cap in prokaryotes and eukaryotes. It has been soon established that the function of the NAD^+ cap in human cells is to promote mRNA degradation, also by DXO proteins. Although it has been speculated that NAD^+ might be attached to mRNA by RNA polymerase II during transcription or post-transcriptionally by other mechanism, its synthesis still largely remains unknown. Also other aspects regarding the structure-function relationship of this cap are not recognized yet, especially in plants, where these similar studies have not been carried out.

Our preliminary results confirmed the presence of NAD^+-capped RNAs in a model plant *Arabidopsis thaliana*, while studies on the enzymatic activity of plant DXO homolog (DXO1) revealed that, in contrast to its mammalian counterpart, DXO1 has very weak activitities towards canonical and incomplete 5' caps, but is a robust deNADding (i.e. NAD^+ decapping) enzyme. These preliminary data strongly suggest that one of DXO1 cellular function may be related to this activity.

The major objectives of this project are to verify the existence of NAD^+-capped RNAs in *Arabidopsis*, analyse the level, stability and translation efficiency of these molecules and assess their functional classification. We will also investigate the role of DXO1 in degradation of NAD^+-capped RNAs and look for other factors, possibly DXO1 interactors, that are involved in the regulation of these transcripts. We also plan to check whether there are other non-canonical 5' RNA cap structures in plants.

Investigating the metabolism of NAD^+-capped RNA molecules in plants, determining which cellular processes are regulated by this unusual class of transcripts and understanding their physiological impact will significantly add to the state of knowledge related to this newly discovered cap and contribute to understanding the complexity of RNA metabolism pathways in eukaryotic organisms.