An appropriate response to various abiotic stresses is critical for plants survival in environmentally adverse conditions. A key step of this response is the re-programming of gene expression enabling adaptation to stress conditions. In eukaryotic cells genome is packaged into chromatin - a nucleoprotein complex build primarily of DNA and histones - that plays fundamental role in regulating the first steps of gene expression. The mechanisms altering chromatin structure are therefore in the centre of scientific interest. Post-translational modifications (PTMs) of histones are among the main players in remodelling of chromatin structure affecting gene expression. The complex patterns of the type and level of histone modification marks encompassing different residues are often described as a "histone code". Alterations in histone marks can be spread across wide areas of chromatin or positioned locally at specifically regulated genes. Although the role of post-translational histone modifications in gene regulation has been studied for several decades the large variety of histone marks and constellation complexity of various modifications leaves many open questions concerning their impact on gene expression. This notwithstanding, it is now widely accepted that in eukaryotes histone modifications are critical for gene reprogramming required for cellular response to external and internal cues. Studies in mammalian cells have demonstrated an importance of a particular type of chromatin mark, the phosphorylation of histone H3, in coupling signal transduction to transcriptional regulation of signal-inducible genes. The results of our group showed that in plants, similarly as in animals, different stress-induced signalling pathways are accompanied by dynamic and transient modifications of core histones, commonly termed as “nucleosomal response”. In particular, we showed that rapid and transient phosphorylation and phospho-acetylation of serine 10 and lysine 14, respectively, observed on histone H3, is strictly correlated in time with up-regulation of genes induced in response to stress in plants. The published work of others proved a direct involvement of H3 phospho-acetylation in regulation of different stages of transcription in animal cells.

In higher Eukaryotes including a model plant *Arabidopsis thaliana*, the majority of intron-containing genes undergo splicing often resulting in production of various forms of mRNA from a single gene. This enables an increased transcriptome diversity followed by increase in corresponding proteome complexity. It has been established that in plants the alternative splicing plays a key regulatory role in regulation of gene expression in response to environmental changes. Numerous studies demonstrated that splicing is coupled to transcription and that the pattern of alternatively spliced mRNA isoforms is influenced by chromatin structure.

Our preliminary results suggest that in Arabidopsis occurs a protein complex that is recruited to phospho-acetylated histone H3. This putative Arabidopsis “histone reader” is composed of proteins which are structurally and/or functionally strictly connected with the process of splicing. While in both animals and plants certain stable histone modifications important for mRNA processing by splicing have been described, there are no reports that the modulation of splicing events can also depend on the stress-related highly dynamic modifications like phospho-acetylationof histone H3. **The main goal of this project is to explain the role of the connection between stress induced transient phospho-acetylation of histone H3 and gene splicing in response of Arabidopsis thaliana to high salinity.**

Our project has a potential to document a so far undescribed direct connection between stress signaling in plants, chromatin and alternative splicing and thus uncover a new layer of gene regulation involved in response of plants to adverse conditions.

This project will bring a better understanding about mechanisms crucial for plant adaptation to their environment. Recognizing an important players of gene regulation during plant response to stress can open up a new possibilities for improving plant and crop phenotypes.