Description for the general public

For many years, transcription and RNA maturation were studied independently. However, current data show that synthesis of RNA precursors and their processing are strongly related processes, which should be considered and examined together. One of the most important mechanisms of gene expression regulation, alternative splicing, is indicated as one of those processes whose mechanism of action and the final effect is dependent on the chromatin structure and RNA Polymerase II (RNAPII) elongation rate. Moreover, recent data indicates that biogenesis of small RNAs is co-transcriptional as well. Both of those pathways are very important elements in RNA maturation. Small RNAs are one of the main negative regulators of plant genes expression and are responsible among others for leaves, roots and flowers development as well as participate in response to all the stresses that plants deal with. Alternative splicing increases the coding potential of the genome. The same pre-mRNA molecule is a potential source of several different mature mRNAs. In humans, approximately 95% of the genes containing introns is subjected to alternative splicing. In the case of *Arabidopsis thaliana*, this value is around 60%. More than 75% of alternative splicing events occur within coding sequences of genes, which gives a potential opportunity to generate proteins with modified structures and functions.

Our previous results point to the important role of AGO1 in the regulation of transcription of two genes: *MIR161* and *MIR173* when Arabidopsis plants were treated with high salt concentration. In salt stress conditions AGO1 localize on those genes and leads to premature termination of transcription by RNA Polymerase II resulting in decreased level of both: pri-miRNA161 and pri-miRNA173. Further studies indicates that this mechanism is likely dependent on miRNAs and connected with phosphorylation status of CTD domain of RNA Polymerase II. Moreover, our data indicates that AGO1, beside role in small RNA pathway, takes part in the regulation of alternative splicing.

The mechanism of the *A.thaliana* nuclear AGO1 action in small RNAs biogenesis is still unknown. It is not known how AGO1 cooperates with RNA Polymerase II, whether and how AGO1 has influence on chromatin structure as well as on splice sites selection. The main goal of this project is characterization of the AGO1 in the context of salt stress. For this purpose, techniques allowing for detailed testing of AGO1 action will be applied. Moreover, high throughput sequencing methods will be used to monitor whole genome distribution of AGO1 and to correlate AGO1 localization and changes in RNAPII distribution on affected genes.