

Environmental stresses are one of the most important factors affecting the growth and development of plants. Understanding the mechanisms that regulate the response of plants to environmental stresses can help to improve plants and make them resistant to adverse environmental conditions, and thus can have a huge impact on agriculture. Novel research will provide new possible strategies to improve economically important crops. A field of research that potential has not been fully utilized in agriculture is epigenetic. Recent studies have shown that DNA methylation is an important mechanism of acquisition of plant tolerance to adverse environmental conditions.

In recent years, DNA methylation phenomenon has been widely studied. However, we still know too little about the mechanisms that enable the induction of new changes at specific sites in the genome. Currently, it is assumed that induction of changes in methylome is triggered by small RNAs, which may induce changes in DNA methylation at specific loci through a process called RNA-directed DNA methylation (RdDM). Thanks to the research undertaken in recent years on the model plant *Arabidopsis thaliana* our knowledge about the RNA-directed DNA methylation increased significantly. However, we still know very little about the role of this process in the response to abiotic stresses. The aim of the presented project is to analyze of the dynamics of changes in *Arabidopsis thaliana* methylome under heat stress conditions and to investigate whether these changes are associated with expression of small RNAs. Our research hypothesis assumes that a substantial part of the changes occurred in the methylome under stress is induced by small RNAs through a RdDM.

In order to analyze the relationships between expression of small RNAs and DNA methylation under stress, the heat stress experiment on model plant *Arabidopsis thaliana* will be conducted. During the experiment the level of DNA methylation and small RNA expression will be measured in seven time points, including three key stages: under control conditions, during stress and after stress. DNA and RNA will be extracted from leaves of analyzed plants and then sequenced using the Illumina platform HiSeq 1500. The data will be analyzed using available software and scripts and programs prepared for the project.

Approach proposed by us will allow to answer questions about how epigenetic response is regulated under heat stress conditions. The analyses that take into account multiple time points will help to understand the dynamics of changes formation and will allow to determine the speed of response of plants to adverse environmental factors. Simultaneous analysis of DNA methylation and small RNAs expression level will enable to find the relationship between increased expression of specific small RNAs and DNA methylation in the genomic sequences complementary to this small RNAs. The results obtained thanks to the realization of the presented project will contribute to a better understanding of the plant response to stress conditions and will enable better understanding of the mechanism of RNA-directed DNA methylation, and also will make a major contribution to the development of this field of research.