DESCRIPTION FOR THE GENERAL PUBLIC

Abiotic stresses, such as drought and salt, are the main causes of crop losses in the world. Taking into account the problem of global warming and continuous increase of population, the development of new crop cultivars with the improved level of drought tolerance is an urgent issue. Many studies have been already dedicated to reveal mechanisms of adaptation ensuring better tolerance to abiotic stresses. However, there are still many aspects of these processes which are poorly understood.

Abscisic acid (ABA) is the main phytohormone involved in regulation of abiotic stress responses. ABA signaling includes action of many components, which in turn leads to adaptation to unfavorable environmental conditions. ABI5 is a transcription factor and one of the components belonging to ABA signaling pathway. In Arabidopsis, it regulates expression of stress-related genes which enable adaptation to water shortage. ABI5-regulated genes take part in photosynthesis inhibition, lipid biosynthesis and reactive oxygen species detoxification.

Barley is one of the most widely cultivated cereals in the world. The barley equivalent of ABI5, HvABI5, has been identified but its role remains elusive. We have identified a mutant in *HvABI5* gene, *hvabi5.d*, which showed changed physiological parameters and differential expression of many genes compared to its parent variety under drought stress. Taking into account data on ABI5 function in Arabidopsis and our preliminary results for mutant in *HvABI5* gene, we postulate that **HvABI5 is ABA-dependent regulator of abiotic stress responses in barley. We presume** that HvABI5 regulates expression of genes, which are responsible for stress responses, through binding to their promoters. **The objective of the proposed project is to determine the HvABI5 role as the regulator of drought stress response in barley.** We plan to use barley mutant in *HvABI5* gene and its wild-type parent as the plant material in the proposed project. The study of expression pattern of previously selected genes in the mutant and its wild-type under drought and ABA treatment will allow to identify HvABI5-regulated genes. Their action will be confirmed in *in vitro* system for DNA-protein interactions. Moreover, parallel analysis of physiological response of analyzed genotypes in the presence of drought will enable to understand HvABI5 action at the physiological level under stress in barley.

To realize the objective of proposed project, we plan to analyze expression pattern of *HvABI5* and their potential targets genes using RT-qPCR in the mutant and its wild-type, in the presence of drought and ABA treatment. The potential target genes, co-expressed with *HvABI5* and with differential activity in the mutant and its wild-type, will be selected to analyze DNA-protein interactions in *in vitro* system. Furthermore, the described *in vitro* system will be used to identify ABA-dependent transcription factors regulating *HvABI5* expression. This approach allows to better understand HvABI5 activity in ABA signaling.

We assume that functional characterization of HvABI5 under stress will help to better understand the mechanism of drought tolerance in barley. The proposed studies enable also a more precise description of the mode of ABA signaling. Moreover, the obtained results can be used as the data for creating biotechnological tools useful in creation of new cultivars with higher level of drought tolerance.