

Drought is often accompanied with high temperature and their combined effects are more constrained on yield than effects of each stress alone. Understanding the influence of both stress conditions on plants is a major challenge because of numerous genes are engaged in the response to these stressors. In the most important developmental stage for yield-forming traits the viability of the flag leaf and its efficient photosynthesis activity is of great importance. Our previous studies demonstrated that terminal water shortage imposed in the flag leaf stage was more constrained for yield components compared to the early stress in barley.

There is limited information about the molecular mechanisms and modulations underlying the barley and other cereals tolerance to a multiple abiotic stresses, especially drought and high temperature. There is also relatively little research in molecular characterization of the flag leaf traits in barley. All these points formed the basis of the proposal. The aim of the project is to describe and integrate changes in transcriptome and proteome of stress-susceptible and stress-tolerant barley genotypes under combined drought and heat stresses. The integration of data from different experimental approaches will allow us to decipher molecular characterization of barley response to abiotic stress.

Our research is driven by the following general hypothesis: changes in the transcript level are not always corresponding with changes in protein expression level under a combination of drought and heat stresses. The second hypothesis is based on morphological and physiological observations that these changes are different in each stress alone than in combined effects of both drought and heat stress considered at the genome-wide level.

Employment of the appropriate research methods as well as selection of the specific plant material ensure the objective achievement and the project hypotheses verification. We will run a series of complementary and coordinated experiments with chosen barley forms: two stress-tolerant and two stress-susceptible recombinant inbred lines (RILs F₁₀ M_{Cam}). This choice is based on our previous projects which investigated the influence of abiotic stresses on barley growth and productivity. The proposed project will comprise the pilot experiment in which recognition of expression of selected abiotic stress-related genes by Real Time PCR will be performed. Along with the phenotyping in the fully controlled conditions (under control, drought, heat and combined drought and heat stresses) and at the fully flag leaf development stage the genome-wide genes expression analysis at transcript level via RNA-Seq will be studied. The elucidation of quantitative differences of protein contents between the studied genotypes and conditions will be performed using the iTRAQ technology. Data processing and integration for up- and down-regulated genes under abiotic stresses, gene ontology analysis and identification of novel transcripts, evolutionary sequence conservation and evaluation of correlation between up- and down-regulated transcripts and proteins will be employed in the project.

The integrated research and collected knowledge in the project may serve as a basis for the biological advances and methods of barley and other crop plants improvement since barley is becoming the model plant. Results obtained in the project will significantly affect the broadening of the current knowledge on plant molecular adaptation to abiotic stresses.