

## DESCRIPTION FOR THE GENERAL PUBLIC

Drought stress, among all abiotic stresses, is pointed as a greatest thread to crops. One can address a question whether the drought stress related research is fully justified in Poland? The answer comes with the report from 2015 prepared by The Institute of Soil Science and Plant Cultivation in Puławy that **state a risk of agricultural drought in Poland**. It clearly showed that there is a pressing need of conducting studies focused on understanding the basis of plants response to drought stress and further translation to crop species. Plants response to drought is a very complicated network that consists of many branches that interact with each other at many different points and lead to their adaptation to water stress conditions. Crucial factor in the stress response is abscisic acid (ABA). Its involvement in a plant's stress response is considered to be a universal stress-sensitizing signal. ABA turns on the various genes that are necessary for triggering a rapid and effective response to drought stress.

One of the most interesting groups of genes that are related to drought response, and that are also the target for genetic manipulation, is the group of **the negative regulators of ABA signaling**. Mutations in the genes that encode the negative regulators of ABA signaling were documented as enhancing drought tolerance, e.g., the genes that encode – two subunits of cap binding complex: CBP20 and CBP80. CBC is involved in molecular 'core machinery' of the cell and both genes encoding the subunits of CBC are highly conserved among Eukaryotes. The role of CBP20 is to directly interact with the cap and to target the CBC to the nucleus. What attracts the most in terms of drought stress, is better performance under water deficit stress of knock-out mutants in CBC genes. It raises questions about the mechanism and the elements of CBC signalosome engaged in drought response.

**Here, we would like to focus on the role of CBP20 under drought. We hypothesized that CBP20 (together with CBP80) can be a 'master controller' of drought and ABA response, that through modulation of basic life processes influences ABA/ drought response network. We presumed that the CBC through negative regulation inhibits the action of positive regulators of ABA signaling.** Thus, under drought stress in *cbp20* mutant, that lacks the aforementioned 'molecular brake' – CBC, the positive regulators of ABA can play its role and transduce the ABA signal till the tolerance to drought is achieved. **The main goal of the proposed project is to decipher the mechanisms underlying the action of CBP20 in response to drought in barley taking advantage from translational genomics.**

Arabidopsis and barley will be used as model systems to study the mechanism of CBP20 signalosome action under drought stress. In Arabidopsis we will use *cbp20* knock-out mutant while in barley TILLING *hvcbp20.ab* mutant identified in our Department. We plan to realize the project taking advantage from translational genomic approach. **We will use a combination of cutting-edge molecular techniques such as RNA-Seq and smallRNA-Seq supported by phylogenetic studies together with phenotyping analyses under drought stress and functional analysis of genes potentially involved in CBP20 signalosome in order to understand the mechanism of CBP20 action in barley.** Using Arabidopsis and barley simultaneous analysis of global profile of expression the 'gene space' will be discern in accordance with the main assumption of the translational genomics. Then it will be extended to a more detailed research that are planned in further research tasks of proposed project: such as the functional analysis of selected differential expressed genes from RNA-Seq in Arabidopsis using T-DNA lines and investigation of the level of mature miRNA triggered by drought (and potentially related to CBP20) and their precursors in order to get the insight into the biogenesis process related to CBP20 in Arabidopsis and barley (using RT-qPCR technique). Finally, we will exploit the function of CBP20 signalosome in barley using TILLING approach for selected differentially expressed genes from RNA-Seq. The phenotype of identified homozygous mutants will be investigated in terms of their drought response.

The results of analyses that are planned within the scope of this project will contribute to a better understanding of the molecular mechanism of the CBP20 action under drought stress. **We also assumed that obtaining such a detailed and multi-level data from two mutants in two species will provide a tool that will enable the drought stress response in plants to be controlled.** The great potential of CBP20 in terms of further research using crops and their better performance under drought increases the value of studies proposed in the scope of that project.