Abstract for the general public

In stressful conditions, we can navigate to avoid stress – plants do not have such an opportunity. Therefore, the stress responses of plants have to be rapid and efficient and are thus extremely complex. The capacity of plants to turn a set of genes that alter plant physiology and morphology on or off allows them to tolerate, escape or avoid drought stress. One key question is: the role and the mechanism of action of a given gene in these signaling pathways? And going further: How can we use this knowledge to control the stress responses of plants to engineer stress-resistant crops? The latter is of utmost importance since the percentage of arable land affected by drought stress has doubled during the last 40 years according to FAO. Moreover, 80% of drought-induced economic losses in developing countries are due to losses in the agricultural sector.

In the proposed project we undertake the survey for unraveling barley Cap-binding Complex (CBC) role in abscisic acid (ABA) signaling and stress at different stages of development through single-molecule real-time sequencing (PacBio technique) combined with physiological analyses. CBC consisting of two subunits CBP20 (Cap-binding Protein 20) and CBP80 is involved in basic cell machinery - RNA metabolism. In agreement with expectations the genomic and protein sequences of both subunits are highly conserved amongst Eukaryote, from veast to plants. Strikingly, plant mutants in the CBP20 and CBP80 exhibited ABA-hypersensitivity during seed germination and drought tolerance in several species including Arabidopsis, potato, and barley. In previously conducted research we deciphered a potential mechanism of drought tolerance during early stage of development dependent on CBP20 in barley. Although we linked the CBP20 action with better water-saving mechanism that partially derived from faster stomatal closure and a higher wax deposition under stress, we could not pinpoint the exact mechanism of CBC action, and still many questions remain unanswered. ABA is a pivotal regulator in plant drought response. Despite the fact that understanding of the molecular basis of ABA action is constantly increasing, the knowledge regarding genes encoding CBC and their role in ABA signaling is not fully covered in many agronomically important species including barley. It is still unclear what is the molecular mechanism of CBC role in ABA signaling generally and at different stage of development.

Up till now we investigated the role of each subunit using mutants in *CBP20* or *CBP80*. Here, in addition to single barley mutants we will use unique double mutant in both genes as an object together with their wild type. Thus, it will allow us to distinguish among disturbance in stress signaling due to the impairment of each of the CBC subunits as well as whole complex.

Each of the proposed research tasks in the project targets different stage of development (seed germination, seedling development and pre-flowering phase) in terms of CBC role in ABA signaling to get a full picture of molecular changes dependent on CBC. In each research task we will perform deep sequencing of transcriptome to get insight into alternative splicing events dependent on CBC in each of the tested phase of lifecycle and treatment applied. Beside transcriptomics, we will analyze morphological changes (such as stomatal density), physiological reactions (stomatal conductance and photosynthesis performance) together with the concentration of endogenous phytohormones in each genotype studied.

We assume that results obtained in the proposed project will serve as a toolkit for further and more detailed studies on ABA and drought response in barley. Taking into account high level of CBC conservation across the species it is highly possible that obtained knowledge will serve for translation to other crops and thus may lead to identification of smart-climate change plant genotype. It is worth noting that the significance of these studies is fully justified in the present climate change scenarios, where water deficit is the main environmental stress that negatively influences crop yield.