

Under temperate climate conditions, the seeds of winter crops are sown in the autumn and germinate before winter comes. Plants acquire increased freezing tolerance through prior exposure to low, non-freezing temperatures. This is an adaptive process termed cold acclimation. It could be supposed that global warming indicates a lower risk of winter crop exposure to extremely low temperatures. However, the risk of winter damage to crops may not decrease. Winter-warming events cause snowmelt. Lack of snow cover and higher temperature may lead to de-acclimation and reduced plant winter hardiness. De-acclimation is responsible for the occurrence of frost injury when after the warm spell, the temperature decreases rapidly to freezing temperatures. The winter hardiness of cereals is determined by the freezing tolerance of crown (first node above the seed).

We opine that under a climate change scenario, de-acclimation is a particularly critical factor determining overall cereal winter-hardiness. As a model plant, we will use a winter barley cultivar. The objectives of this project will be to 1) gain a deeper understanding of how warming stress, accompanied by other stresses, affects the transcriptional signature, phytohormonal profile, and redox status of the crown during the de-acclimation of winter barley, which are susceptible to this process; 2) selecting of key regulatory genes associated with phytohormones or redox signal transduction pathways. We have hypothesized that in winter barley, de-acclimation-susceptible, warming stress plays a dominant role under simultaneously-acting multiple stresses during de-acclimation, and determines the expression of crucial regulatory genes. In project, after cold acclimation, barley will be subjected to five stresses: warming stress (warm spell) - leading to de-acclimation, high-light stress, soil drought stress, and elevated carbon dioxide concentration stress. These stresses result from climate change, for which agriculture and the food industry are unprepared.

Our research will expand knowledge on a neglected topic in global research on de-acclimation mechanisms in winter cereals. In our project, we will use a systems biology approach, still not widely used in agricultural research. We will not only perform a transcriptome analysis but also create appropriate dynamic models, based on which, together with the results of phytohormone profiling and redox state analysis, we will identify key regulatory genes. Regulatory genes coordinate the expression of other genes and determine plant stress responses. In the project we will use an unprecedented approach to research. The project's goal is cognitive, but the knowledge it will provide can be applied in plant breeding to produce new improved cultivars of winter cereals better adapted to changing environment and to reduce the negative impacts of climate change on agricultural systems.