

DESCRIPTION FOR THE GENERAL PUBLIC

The main goal of the presented project is to discover a new function of the *HvSNAC1* (*Stress responsive NAC 1*) gene in the regulation of aquaporins in barley during abiotic stress. Currently, great effort has gone into identifying the genes involved in the response of plants to abiotic stresses. Among those that have been identified, among others, the *SNAC1* gene in rice, which quickly became the object of great interest in the quest to obtain improved drought and salt tolerance by creating lines with its overexpression in different plant species. We plan to test the binding specificity of a native form of *HvSNAC1* and two altered forms encoded by alleles that carry a mutation in the NAC domain to the *cis*-regulatory sequences present in the promoter of genes encoding aquaporins using the yeast one-hybrid assay. Then, we plan to carry out experiments treating barley seedlings with various abiotic stresses and treatment with methyl jasmonate (MeJA), followed by transcriptomic analysis, which will be performed to establish the gene expression profiles of *HvSNAC1* and the selected aquaporins. The information that is obtained as a result of this project has a chance to demonstrate a new function of *HvSNAC1* in the regulation of the aquaporin genes that lead to the closing of the stomata during drought stress. Stomata control CO₂ uptake and water use efficiency, thereby playing crucial roles in abiotic stress tolerance. Finding a new pathway in which *HvSNAC1* regulates AQPs in barley could add special value to research aimed in long term to improve resistance to stress major crops including barley.