

**Do the two barley genes *HvGSK1.1* and *HvGSK1.2* regulate salt tolerance and yield-related traits?**

Brassinosteroids (BRs) are important group of plant growth regulators. They regulate wide range of important processes of plant growth, development and response to environmental factors. This group of regulators was found in practically all plant parts: roots, leaves, flower buds. The highest BRs levels were found in pollen and immature seeds. Exogenous application of BRs was reported to induce plant growth and plant biomass, enhance tolerance to environmental stresses including salinity, tolerance to drought and suboptimal temperatures.

It was also proved that number of important agricultural traits: stress tolerance, plant biomass, number and weight of seeds were dependent on BR regulation. Barley is very important crop and it is also a model species of temperature cereals. As a result of our earlier research we identified a family of 7 *GSK* genes in barley genome. Protein encoded by these genes was reported to function in diverse cell signalling pathways including BRs' signalling.

We showed that barely plants with silenced expression of selected *GSK* genes better tolerated salinity stress, had bigger biomass and developed more seeds of higher weight. In the proposed project we plan to use gene edited plants obtained as a result of CRISPR/Cas9 technology. We anticipate that editing of the two *GSK* genes (*HvGSK1.1* and *HvGSK1.2*) will result in obtaining plants with improved agronomic characteristics. These plants will be used for basic research aimed at understanding functions of both genes in plant development and stress tolerance. Detailed characterization of such obtained plants, including stress tolerance, shoot and root system architecture, parameters of productivity, will be a key scientific goal of the main part of the project.

Gene editing by means of CRISPR/Cas9 is novel and very important technique. It is currently adapted to diverse biological and medical applications. The proposal will allow adapting the method for biological investigations of important cereal species. Obtained results will provide the new knowledge on the method itself and on the function of the two BRs' regulators in barley.