Increasing the yield potential of cereal crops is one of the most important efforts of plant breeding. Yield is a complex trait, which is determined by genotype, environment and agrotechnology. Because of narrow genetic pool of modern cultivars, the abilities of further improvement of yield potential using conventional breeding methods are very limited. As a consequence, very little progress of yield improvement has been achieved in the past decades. The application of new breeding techniques could invert this negative trend, however, it requires the broad knowledge about genetic background of grain yield. A very promising research studies in this field is discovery of mechanisms controlling size and weight of grains, as these traits are strongly determined by the genotype and only slightly by the environment. The genetic background of grain size and weight has been poorly understood in barley, despite that it is the fourth most important cereal crop in terms of production quantity after rice, maize and wheat.

The aim of this project is comprehensive study of genetic determinants of grain size and weight in barley and application of novel genetic engineering techniques for development of barley lines with improved grain yield. The main research tasks will be focused on identification of candidate genes that control grain size and weight and analysis of their molecular function. The genetic variation of identified genes will be analyzed in the population of barley lines that differ in grain size and weight using new generation sequencing. It will allow to assess the influence of candidate genes on the tested grain traits and for development of new molecular markers that could be used in selection of cultivars with the desired traits. Based on obtained results, several candidate genes will be selected for further analyses to confirm their influence on grain phenotype, and to determine their molecular function. Functional analysis of these genes will be performed based on genome editing and transcriptional gene activation technologies. In the first strategy, CRISPR/Cas9 system will be used for induction of loss-of-function mutations in candidate genes. In the second strategy, a modified CRSIPR/Cas9 system will be used for increasing expression of candidate genes by transcriptional activation. Effect of both modifications will be analyzed in plants at the molecular level. Transcriptomic analysis will reveal the mechanisms of regulation of the tested genes and their interaction with other genes. The aim of proteomic analysis will be detection of potential chenges in protein profiles of developing seeds and identification of peptides with a putative regulatory functions in grain development. An important part of the project is the is the development of new barley lines with increased grain size and weight using genome editing and gene activation approaches. For several years, CRISPR/Cas9-based genome editing has been successfully used as a research tool in studies of gene functions and for direct improvement of crop plants. In turn, CRSISPR/Cas9-based transcriptional activation is an innovative method of regulation of gene expression, which has not yet been used for improvement of important agronomic traits in cereal crops. Results of this project can be useful in similar research studies of other cereal crops. It is particularly important for polyploid cereal species, such as wheat, triticale and oat. As a diploid, closely related species, barley is considered as useful model for polyploid cereals.