Phosphorus is one of macronutrients, indispensable for growth and development of plants. The aim of the proposed project is to gain new knowledge concerning genetic determinants of phosphorus deficiency tolerance in plants using rye (*Secale cereale* L.), a cereal characterized by high tolerance of nutrient deficiency, as a model.

We plan to: 1) understand molecular mechanism of rye's tolerance to phosphorus deficiency by characterization of accompanying changes of gene activity (at the RNA and protein levels) of DNA methylation, 2) determine full genomic sequences of key genes involved in phosphorus deficiency tolerance and analyze their structural features, which can influence expression level, 3) experimentally determine the functions of identified genes, 4) assess allelic diversity of selected genes in rye accessions representing different improvement status and various cultivation environments and identify functional gene variants, which can cause an alteration of phosphorus deficiency tolerance level.

We expect that the project will broaden the understanding of the genetic basis of phosphorus use efficiency in plants. Information obtained in the project will constitute also an important resource for structural and functional genomics studies in rye and a starting point for further research. The assessment of the diversity of selected phosphorus use efficiency related genes in diverse rye accessions will provide insight into allelic richness of rye genetic resources, but will also improve our understanding of influences imposed by different cultivation environments and by breeding activities on the genetic makeup of a crop. The obtained results will also have relevance for future improvement of closely related crops - wheat and barley.