Phosphorus (P) is one of key elements essential for growth and development of plants. P-deficiency is a major constraint to agricultural production. Development of crops, which yield satisfactory under P-insufficient conditions is crucial to help ensure food security of the rapidly growing human population. The changes caused by P-deficiency in plants occur at different, molecular and morphological levels and there are multiple response mechanisms, universal and species-specific.

Rye (*Secale cereale* L.) is a popular cereal important for Polish agriculture. Rye has a much higher tolerance of nutrient stress, including P-deficiency, than its close relatives wheat and barley, and can be expected to have highly efficient mechanisms of adaptation to low P-availability, which could be used in improvement of other cereals. However, very little is known about molecular mechanisms or rye P-deficiency response.

The aim of the project is to precisely characterise various aspect of rye P deficiency response with the overall goal of identifying the key components (genes) involved in the molecular regulation of this process.

We propose to (i) gain precise information on the patterns of rye P-deficiency response by analysis of expression levels of selected genes over time and in different plant organs, (ii) perform observations of root anatomical and architectural traits to understand how root system responds to P-deficiency and what root traits differentiate rye inbred lines with contrasting P-deficiency response, (iii) uncover the regulatory role of miRNA and lncRNA in rye P-deficiency response using next generation sequencing, (iv) experimentally determine function of selected rye genes related to P-deficiency response, for example, by finding out where their expression products (transcripts, proteins) are located (within tissue or cell), and (v) discover how plant growth promoting rhizobacteria (PGPR) influence performance of rye inbred lines with defined P-deficiency tolerance and the expression of selected P-deficiency response related genes.

All the aspects of P-deficiency response we propose to address have not been studied in rye yet. Therefore, we expect that this research will be a break-through moment in the understanding of the molecular mechanism of P-deficiency response of rye, providing sufficient evidence for identification of specific regulatory networks. We expect that, due to its comprehensive nature, the proposed project will expand significantly the general understanding of stress response mechanisms in plants and in further perspective - contribute to development of crops that will thrive in low-P conditions.