

Description for the general public

Phosphorus (P), in the form of phosphate (Pi) is an essential macronutrient for all living organisms, including plants. Corresponding phosphate level is underlying for the structural and metabolic needs of plants, is controlled and maintained by the regulatory network of Pi signaling and homeostasis. Global phosphate reserves are not renewable and phosphate is being rapidly depleted. The prediction is that total phosphate reserves could last until 350 years. The natural phosphate resource is being used up increasingly fast, which may lead to the worldwide problems with crop fertilization and food production. Barley (*Hordeum vulgare* L.) is one of the first cereals that were domesticated and began to be used for food purposes. Nowadays, barley takes 4th place for worldwide production of cereals. It is also characterized by large adjustment capacity and high tolerance to cold, salinity and drought as well. However, plants have gained series of evolutionarily adapted strategies that ease or help them to coping when the soil is missing phosphorus. The implementation of these strategies requires molecular and structural changes in their tissues such as: development of lateral roots and root hairs, the induction of high-affinity and some low-affinity phosphate transporters, and the secretion from roots of phosphatases, organic acids, phytohormones to established symbiotic associations with soil microorganisms. The regulation of those processes is performed via the activity of cluster of phosphate stress responses genes encoding various cell components enzymes, RNAs, proteins modifiers or transcription factors. Several genes are up- or down-regulated during phosphate starvation and their expression level is controlled by PHR1 (*PHOSPHATE STARVATION RESPONSE1*) plant specific transcription factor. PHR1 encodes a conserved MYB transcription factor and its homologue in green algae (*Chlamydomonas reinhardtii*), *PSR1* (*PHOSPHORUS STARVATION RESPONSE1*) has been extensively described in terms of phosphate starvation transcription responses. The *PHR1* gene is not the only one molecule involved in the regulation of phosphate stress responses gene expression.

The project is aimed at the experimental verification of the hypothesis, that PHR-like transcription factors regulate the expression of Pi-starvation response genes in barley. We are going to select three different barley cultivars (phosphate starvation tolerant and sensitive) to demonstrate via real-time PCR, that HvPHR1 transcription factor regulates the expression of phosphate stress response genes. We plan to identify novel related proteins, that are involved in the recognition and binding to the specific promoter sequences. Those specific sequences are called P1BS motifs, and they are located in the promoter of most common Pi starvation response genes. The P1BS motifs will be used in the yeast one-hybrid experiment. Then we plan to test the impact and level of DNA methylation in the vicinity of P1BS motifs via bisulfite sequencing technique. Our experiments will answer for another questions if there are any differences in the level of DNA methylation and if the Pi-responses genes might be preferentially promoted for acting. To identify another target genes, which are recognized and binded by PHR-like transcription factors determine whether different Pi regime influence for those PHR1 and PHR2 transcription factors binding efficiency. We are going to establish global experiment via ChIP-Seq (Chromatin ImmunoPrecipitation-Sequencing). This modern experiment will allow us to determine whether different phosphate content influence the binding efficiency of PHR-like transcription factors.

After all, the extent of the role of *PHR1* in Pi starvation responses in crop plant species needs to be established. Due to the limitation of phosphate resources, the data obtained in this project might be helpful to better understand the processes responsible for the adaptation and stress responses in plants. As well as serious environmental problems associated with phosphorus mining and fertilization, an increase in crop phosphorus efficiency is currently receiving greater attention in sustainable agriculture systems. Many questions can be revealed including those about the influence of DNA methylation on transcriptional regulation and efficiency of PHR1-binding during different Pi regime.