

The observed climate changes such as global warming, droughts and environmental pollution can significantly reduce crop production. It is also expected that the reserves of phosphates (Pi) (mainly from Morocco) used for the production of fertilizers may be exhausted by 2050. It could be a serious problem for food production in particular in the context of the anticipated growth of the human population. It is expected that it may reach the number of 9.2 billion people by 2050. Phosphates represent an accessible form of phosphorus (P) for plants. P is essential for proper plant growth. It is necessary for the nucleic acids and phospholipids biosynthesis, furthermore ATP hydrolysis supplies energy to cells and phosphorylation of proteins regulates the functioning of many metabolic pathways. All these factors prompted us to investigate the influence of abiotic stresses such as high temperature or shortage of Pi on the functioning of barley plants. We have observed that the high temperature mostly downregulates the expression of Pi-related genes, which are necessary for Pi acquisition and transport. However, despite significant changes in Pi-related genes expression, the Pi concentration in barley shoot and roots remains stable (with few exceptions). Barley adapts to the high temperature by downregulating the gene encoding Pi transporter (*PHT1*) what is accompanied by the downregulation of another gene encoding Pi transporter (*PHO1*), that loads Pi to the xylem in the roots. Thus Pi content is kept stable in roots. Our previous research focused on the analysis of changes in genes expression. In the proposed work we would like to check the status of Pi-related proteins, like PHO2, NLA, PHT1 and PHO1, and to verify if their level really decreased in roots during heat stress. We will also analyse the protein levels in barley shoots. Our analyses will be performed in normal and Pi-limited conditions. We assume that some of the changes in protein levels may be the result of ubiquitin-dependent protein degradation. In our project we will analyse PHO2 (ubiquitin-conjugating E2 enzyme) and an identified by us barley NLA (E3 ubiquitin-protein ligase) influence on other Pi-related proteins. Using modern techniques, like yeast two-hybrid screening, FRET-FLIM and SAXS (Small-Angle X-Ray Scattering) analyses, we will identify potential partner proteins which can be bound by the complex of PHO2/NLA. Based on the SAXS experimental data we will create a model of the structure of PHO2 and NLA proteins. Finally we will obtain the data showing how proteins regulate Pi level in barley during heat stress and if the expression of Pi related genes is mostly regulated transcriptionally or the post-translational level of regulation exists in Pi homeostasis maintenance. The obtained results can help in introducing new varieties of plants and in developing new ways of barley (cereals) breeding that would be more tolerant to high temperature and Pi-limitation conditions.