

Heat stress is one of the major abiotic stresses that can induce severe plant damage. Heat stress is very often accompanied by drought and these two combined stressful conditions are the major limitations to worldwide food production. Observed in recent decades, global warming is predicted to have a general negative effect on plant growth, development and reproduction mostly due to the destructive effect of high temperature. Plants have developed exceptional abilities to cope with multiple environmental stimuli. One of such mechanisms coping with environment changes is the involvement of small RNA molecules called microRNAs, which play a regulatory role in the stress response and plant development.

Barley and the mechanisms which this crop plant developed to handle heat stress conditions are the research areas of our interest. Barley grain production ranks fourth in global cereal production, indicating the economic importance of this monocotyledonous crop plant. Despite barley being a cereal of great economic importance, little data is available concerning its thermotolerance mechanisms. Our preliminary studies showed that four miRNAs are heat stress up-regulated at the level of mature microRNAs. Importantly, that elevated expression of barley heat-induced microRNAs correlates with down-regulation of the expression of their target genes. The aim of our project is global identification of small RNA molecules involved in the response to high temperature in barley and understanding its role in plant response to this stress factor. To answer our questions, we will focus on the following research tasks:

- 1 – global identification of barley microRNAs involved in response to heat stress in barley variety sensitive and tolerant to this stress factor,
- 2 – we will determine the genomic structure and organization of barley heat-induced miRNA genes and understand a mode of their expression regulation,
- 3 – we will determine which barley genes are regulated by heat-responsive small RNA molecules,
- 4 – we will investigate the impact of barley microRNA regulated in heat stress and their target genes on barley growth and development by silencing their expression.

The understanding of the complex network of heat-responsive barley miRNAs and their respective target genes can help us not only in minimizing the developmental disorders in plants, but also in defeating the disadvantages of the global warming that may influence the crop plants productivity and yield. The elucidation of the mechanisms of heat stress response and the genes involved in this process might be a valuable source of information for farmers and breeders which genes are worth of their interest and should be taken into account in the breeding practice to obtain the new barley varieties with increased tolerance to high temperature stress.