In response to stress stimuli, plants must shift internal resources from growth and development to processes of adaptation to constrained conditions enabling them to survive. One of the main signal transduction pathways modulating both plant growth and adaptation to stress, including drought, is phytohormones action and their trade-offs. Brassinosteroids (BRs) signaling is suggested to be crucial hormonal pathway in plant development, whereas abscisic acid (ABA) is a primary stress-responsive hormone. Other important players in plant signalosome are heterotrimeric G-proteins which act as messengers through various signaling cascades, including phytohormones perceptions, with the central role of Gα-subunit. Despite the large efforts made to study the complex regulatory mechanisms underlying plant response to stress factors, genetic and environmental regulation of plant adaptations, including barley, to various conditions (e.g. drought) remain largely unrecognized. Throughout the course of evolution, plants have developed various mechanisms to alter the expression of genes governing physiological processes in response to changing environmental conditions. Recently, microRNAs (miRNAs) are suspected to be a main class of gene expression regulators that are important in shaping these processes. Unfortunately, there is still lack of information regarding the network of miRNAs and phytohormones that coordinate the response to drought. All these points formed the basis of the proposal. The aim of the project is to to explore molecular mechanisms underlying complicated crosstalk between mentioned above phytohormones.

Our research is driven by the following general hypothesis: cross-regulation between BRs, ABA and other phytohormones in barley leaves is mediated by miRNAs. Moreover, in response to environmental stimuli, phytohormones enable plant adaptation to stress and part of this reaction is attributed to miRNAs and their targets. We will unravel whether G-protein α-subunit is involved in alternative to receptor BRI1-dependent signaling pathway of BRs during barley exposition to drought, and what specific miRNAs control this process. In addition, we will answer if reduced photosynthesis caused by ABA in response to drought may be compensated by BRs through their alternative signaling pathway mediated by G-protein α-subunit and corresponding miRNAs.

Employment of the appropriate research methods as well as selection of the specific plant material ensure the objective achievement and the project hypotheses verification. We will run a series of complementary and coordinated experiments with chosen barley forms: cv. Bowman (wild type) and its near-isogenic lines BW885 and BW074. The regulation of hormone levels will be investigated by using state of the art NGS-based approaches. Genome-wide transcriptomics will allow identification of genes/miRNAs characterized by expression changed between the barley genotypes or between conditions (treatments) in order to draw gene regulation networks. Furthermore, identification of miRNAs targets will be carried out to understand genotype/treatment-specific transcriptomic associations. Automated image-based phenotyping will be employed in the project to develop a reflectance-based physiological ideotype of barley drought resistance. The integrated analysis and inference on all experimental results will be further supported by GO overrepresentation analyses, gene regulatory network construction, development of miRNAs and hormones network, bioinformatic analyses relating the project results to existing information on hormonal pathways (KEGG) and loci controlling quantitative traits (GrainGenes). Overall, miRNAs role in two important pathways of barley signalosome i.e. phytohormones and G-protein during drought will be investigated in the project.

The integrated research and collected knowledge in the project may serve as a basis for the biological advances and methods of barley and other crop plants improvement since barley is becoming the model plant. The integration of data from different experimental approaches will significantly affect the broadening of the current knowledge on plant molecular adaptation to abiotic stresses and how regulatory sequences in the barley genome determine its development.