In most angiosperm plants, polyploidy and whole-genome duplication (WGD) have been observed in their evolutionary history. Poliploidization and followed by diploidizaion have become important processes for speciation, diversification and stress adaptation of plants. The genetic modifications such as mutations, chromosomal rearrangements as well as epigenetic mechanisms have contributed to the expression variation of duplicated genes. It is assumed that these changes in function of duplicated genes (sub- or neofunctionalization) can broaden the plasticity response of poliploids compared to their diploid ancestors. The problem of functional divergence of duplicated genes and plasticity of stress response in poliploid species are poorly understood due the activity of different mechanisms. The fate of duplicated genes has been studied in many plant species including oilseed rape.

Oilseed rape (Brassica napus L.) is allopolyploid species formed via hybridization between diploid species *B. rapa* (donor A genome) and *B. oleracea* (donor C genome), which are ancient polyploids with triplicated genome structure. Therefore, it is an excellent model to study mechanisms of genomic and functional plasticity of duplicate genes.

The aim of the project is to investigate the plasticity of abiotic stress response in oilseed rape (*Brassica napus* L.). This will be carried out on the example of the involvement of ABI1 protein phosphatases 2C (PP2C, subfamily A) in a control of HB6-dependent gene network under salt and drought stresses. ABI1 is a central negative regulator of the ABA-mediated signaling pathway in Arabidopsis. The phytohormone ABA regulates many processes during plant life cycle and plays an important role in plant adaptation to stresses such as drought, salinity, cold and wounding during vegetative growth. Numerous studies have demonstrated that ABI1 interacts with different proteins as potential targets for its phosphatase catalytic activity. Whereas, HB6 belongs to the plant-specific HD-Zip class I transcription factors, which are involved in regulation of plant growth, development and ABA-related responses.

In this project we will 1) study molecular/physiological background the plasticity of stress response in the poliploid species such as *B. napus*; 2) explore the pleiotropic effects of the binary *ABI1/HB6* system towards up- and down-regulation of selected effector genes involved in plant adaptive response to salt and drought stresses; 3) estimate how many genes are controlled by *BnaHB6* under salinity and drought stress in *B. napus;* 4) study mechanism of transcription regulation genes by analysis of binding the *BnaHB6* transcription factor to the promotor regions of the genes; and 5) investigate and compare the evolutionary fate of the *HB6* orthologues during changing environmental conditions between the related species *B. rapa* and *B. napus*.

Together, the collected data will allow us to determine a cross-talk between salt and drought signaling pathways in Brassicaceae and to establish new stress-specific elements. These aspects of research will be conducted on the basis of complex approaches at the genomic, transcriptomic and proteomic levels using transformation technology, ChIP-qPCR and high-throughput technology such as RNA-seq.

The main effect of this project will be a better understanding of regulatory mechanisms involved in the response and adaptation to salinity and drought stresses in the crop species *B. napus* in the context of the duplicated genes evolution. We should discover novel elements, common for both stresses and/or stress-specific, controlling the plasticity of *B. napus* response. We should also get to know as evolved the various regulation systems controlled by the functional differentiation *BnaABI1* paralogues. The discovery of new interactions between *BnaHB6a* and *BnaHB6b* transcription factors and target genes will open the way for genetic manipulation aimed at the fast and effective to modify the features and create new varieties of oilseed rape.