

## **New elements of ABA signaling pathway as an effect of structural and functional divergence of genes in the *Brassica* genus**

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In most angiosperm plants, whole-genome duplication (WGD) have been observed in their evolutionary history. Polyploidization followed by diploidization and gene loss have become important processes for speciation and stress adaptation of plants. The genetic modifications such as mutations and chromosomal rearrangements as well as epigenetic mechanisms have contributed to expression variation of duplicated genes. It is assumed that these changes in function of duplicated genes can broaden the plasticity response of polyploids compared to their diploid ancestor. The effects of these events can be observed on two levels. First of them is genomic plasticity, when multiple sets of genetic material combine in the same nucleus. The second is functional plasticity of duplicated genes, which modulate gene expression to adapt plants to the specific environment conditions.

I am particularly interested to understand the evolutionary mechanisms responsible for structural and functional divergence of duplicated genes and their impact on the adaptation of plants to different environmental conditions, which is an important challenge for evolutionary biology. In our studies, we have focused on the analysis of functional diversification of *ABII*-like genes in the *Brassica* species (oilseed rape, vegetable cabbages). The structural and functional studies have clearly showed that the maintenance of all copies of the *ABII* gene had an effect on its function during abiotic stresses and the position of adjacent genes in the corresponding syntenic chromosomal regions in the *Brassica* species. The process of functional divergence of *ABII* paralogs followed WGD, probably by subfunctionalization and neofunctionalization, and these processes were independent in the *Brassica* lineage. The main mechanism was based on changes in the promoter sequences (including regulatory motifs) and proteins of ABIs, which affected their functions at the transcript level, but may possibly also affect their interactions with other proteins. Our results indicate that a regulatory network exists under *ABII* control in response to abiotic stresses in the Brassicaceae family.