

## Summary

Drought is one of the most adverse abiotic stresses limiting plant growth and development, as well as the major factor influencing yield loss. Among cereals, barley (*Hordeum vulgare* L.) is ranked fourth in terms of harvested acreage and as a staple food is attracting renewed attention, because of its wide adaptation to the harsh environments. Plants have evolved various mechanisms to cope with water deficit at different biological levels. However, there is an enormous challenge to decipher molecular mechanisms influencing particular complex phenotypic traits under water-limiting conditions due to polygenic inheritance controlled by several genes of small effects.

The presented research shows a comprehensive approach for elucidation of molecular basis of drought tolerance in barley. The study includes construction of high-density SNP and SSR-based genetic map with positioned functional candidate genes (CGs), mapping of QTLs for physiological and biochemical traits associated with drought tolerance, projection of QTL confidence intervals on physical barley genome map, and the retrieval of positional CGs, followed by Gene Ontology (GO) enrichment analysis.

The genetic consensus map was constructed using three RIL populations, developed from the crosses between European cultivars and Syrian breeding lines, and was enriched with 64 genes, encoding barley orthologues of functional and regulatory drought tolerance-related genes described in model species, as well as the genes derived from the transcriptome analysis of parental genotypes of the study, performed under water deficit conditions. The genetic map spans 941.86 cM with resolution of 1.1 cM and contains 875 loci clustered into 13 linkage groups, as a result of presence of the genomic regions with markers exhibited significant segregation distortion, clearly separated from neighboring chromosome segments. A total of sixty-six QTLs for 26 physiological and biochemical traits that describe water relations, photosynthetic efficiency, content of osmoprotectants and hormones, and activity of antioxidants, were identified. For the first time, QTLs for ethylene, glucose, sucrose, maltose, raphinose,  $\alpha$ -tocopherol,  $\gamma$ -tocotrienol content, catalase activity, and various photosynthetic parameters have been mapped in barley. All of the 33 detected QTLs for 18 physiological and biochemical parameters under drought conditions and stress indices (SI) were a major QTLs with the value of phenotypic variance exceeding 10%. The mapped QTLs tended to be clustered in particular chromosome regions. Based on overlapping confidence intervals of QTLs,

11 hotspots were identified that enclosed 61% of mapped QTLs. Four of them were localized in chromosome 2H. The existence of hotspots suggests a common genetic background of analyzed physiological and biochemical traits mapped in these regions or presence of closely linked genes that control them. The genetic and physical map integration was based on the position of markers defining boundaries of QTL confidence intervals in barley genome and allowed the identification of 1101 positional CGs within the chromosomal regions of drought-specific QTLs. The GO enrichment resulted in the designation of 143 CGs potentially involved in Biological Processes (BP) significantly over-represented in the gen sets associated with water relations, photosynthetic efficiency, content of osmoprotectants and hormones, and activity of antioxidants, compared with the genome-wide background frequency. Among them were genes encoding antioxidants, carboxylic acid biosynthesis enzymes, heat shock proteins, small auxin upregulated RNAs, nitric-oxide synthase, ATP sulfurylases, and proteins involved in the metabolism of molybdenum cofactor synthesis substrates as well as regulation of flowering time.