

## GENETIC MAPPING AND META-QTL ANALYSIS OF TRAITS ASSOCIATED WITH DROUGHT TOLERANCE IN WHEAT

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Meta-QTL analysis represents a modern tool of genetic breeding, enabling the integration of results from numerous quantitative trait loci (QTL) mapping studies and the identification of stable loci associated with adaptive traits in wheat. Particular attention is given to traits related to drought tolerance, since Kazakhstan belongs to the zone of risk farming, where arid conditions are one of the main limiting factors of yield.

Recent studies demonstrate that the application of meta-QTL analysis significantly reduces the localization range of QTLs and allows the identification of consensus regions associated with drought tolerance traits [1, 2]. In the context of Kazakhstan, it is important to note that domestic research on QTL and marker-associated traits, although limited in scale, provides valuable material for integration into international databases [3, 4].

Accordingly, the aim of this research is to conduct a meta-QTL analysis of traits associated with wheat tolerance to abiotic stress factors, with a particular emphasis on drought tolerance, in order to identify stable and reproducible loci that are promising for use in marker-assisted selection (MAS) and genomic selection (GS).

### Research objectives:

To systematize published data on QTLs associated with drought tolerance and other abiotic stresses (drought, salinity, cold).

To transfer the positions of identified QTLs onto a unified consensus map or the wheat reference genome (IWGSC RefSeq v1.0/2.1).

To use specialized software (BioMercator, MetaQTL, MapChart) for the integration of overlapping QTLs into meta-QTLs.

To identify the most stable loci, reproducible across different studies and explaining a significant portion of phenotypic variation.

To narrow down meta-QTL intervals and identify candidate genes involved in the regulation of drought tolerance mechanisms.

To develop a set of promising molecular markers (SSR, KASP, SNP) associated with meta-QTLs and test their applicability in breeding drought-tolerant wheat varieties.

The analysis is based on a body of literature from the past 15–20 years, including both international and regional publications on QTL analysis of wheat resistance to abiotic stresses. Key traits of drought tolerance include productive tillering under water deficit; root system length and biomass; seed germination rate under water stress; relative water content in leaves (RWC); yield stability index (YSI); as well as physiological parameters such as photosynthetic rate (CO<sub>2</sub> assimilation), stomatal conductance, and the photochemical efficiency of photosystem II (PSII).

Preliminary analysis of published data shows that the largest number of QTL associated with drought tolerance are localized on chromosomes 2A, 2B, 4A, 5A, 6B and 7D. These regions often contain key genes for adaptive responses.

In conclusion, as a result of meta-QTL analysis, we can expect the narrowing of locus intervals to 1–5 cM, which significantly facilitates their practical use.

**Key words:** wheat, meta-QTL, traits.

### References:

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