

Mapping of loci associated with drought tolerance in chromosomes 2A and 2D of bread wheat and the search for responsible candidate genes

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The study of the genetic mechanisms of wheat adaptation to environmental conditions is necessary for successful selection of cultivars tolerant to abiotic stress factors, drought being the most harmful. The study of the genetic architecture of traits that affect drought tolerance is of great, if not crucial, importance for overcoming the negative impact of drought on crop yields. All of them have a polygenic control and provide coordination of many physiological and biochemical processes. Analyzing the associations between the alleles of molecular markers and target traits in bi-parental mapping populations or by association mapping is the most effective strategy in studying the genetic control of polygenic traits. In our work, the both approaches were used to identify the regions associated with the tolerance of photosynthetic apparatus to water deficiency in chromosomes 2A and 2D. Using the introgressed lines Chinese Spring (Synthetic 6x) for D-genome the two regions in chromosome 2D were identified associated with photosynthetic parameters and the activity of antioxidant enzymes under stress conditions. Regions were marked within the *Xgwm455-Xgwm261* and *Xgwm1419-Xgwm539* microsatellite markers, respectively. Using the substitution recombinant lines Saratovskaya 29 (Yanetskis Probat 2A) the two regions were identified in the long arm of the target chromosome associated with the regulation of stomatal conduction, the rate of photosynthesis, the activity of antioxidant enzymes and the yield components under water deficit conditions. Bioinformatic methods of analysis of these regions have revealed the candidate genes that are homologous to the known Arabidopsis genes involved in the signaling pathways of the hormonal regulation of stress response.

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