



Genomic regions associated with leaf wilting traits under drought stress in spring wheat at the seedling stage revealed by GWAS

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Abstract:

Drought is one of the complex abiotic phenomena that limit wheat production. Improving drought tolerance at the seedling stage is very important as it is a critical stage affecting the subsequent growth stages. In this study, a population consisted of 138 diverse spring wheat genotypes was used to identify the most drought tolerant genotypes and genomic regions controlling drought tolerance at the seedling stage. Three morphological traits were scored: seedling length, days to wilting, and leaf wilting. All genotypes had a high genetic variation in all the seedling traits scored in this study. Moreover, high significant phenotypic and genotypic correlations were found among these traits. Heritability estimates for these morphological traits ranged from 0.59 to 0.86. Nine genotypes from different countries were identified as drought-tolerant genotypes. The genome-wide association study (GWAS) was performed on the population using 407 Diversity Arrays Technology (DArT) markers which were distributed across 21 wheat chromosomes. The results of GWAS revealed 104 significant QTL controlling drought tolerance and susceptibility in wheat. A set of 12 markers was found to be associated with more than one trait. Out of the 12 markers, the WPT-2356 was found to be associated with drought susceptibility in all traits scored in this study. The gene annotation analysis revealed that this marker fell within TraesCS7B02G438200 gene model which encodes to UBA-like superfamily protein (a negative drought regulator). Moreover, four significant DArT markers WPT-6668, WPT-8460, WPT-8124, and WPT-4196 found in this study were previously reported with their association with drought tolerance and susceptibility at wheat seedling stage. The nine genotypes can be used as candidate parents to improve drought tolerance in spring wheat. Moreover, promising validated markers can be used for marker-assisted selection to genetically improve drought tolerance through a breeding program.

Keywords:

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