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Genetic Analysis of Pre-flowering Drought Resistance in Sorghum

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Abstract

Sorghum production is highly restrained by drought stress and this has led to a worldwide yield reduction. In sorghum, drought stress is being characterised at pre-flowering and post-flowering stages. The present study was conducted to evaluate genetic variation and to identify quantitative trait loci (QTLs) influencing pre-flowering drought stress by considering some drought related agronomic traits such as leaf area (LA) and total root length (TRL) using an F5 recombinant inbred line (RIL) population derived from a cross between the drought resistant parental line 1488 and the susceptible genotype. The RIL-population and the parental lines were evaluated for the listed traits under well watered and drought stressed conditions. Phenotyping results obtained from the experiment showed high variation among genotypes for both traits. LA showed a high heritability of 0.78 and TRL had a heritability of 0.57. Analysis of variance was conducted for these traits using Proc GLM of the software package SAS 9.1. Both traits were statistically significant at a probability level of 0.05. Pearson's correlation coefficient was computed for both traits and the result showed that both traits (LA and TRL) were highly correlated with correlation coefficients of 0.5 under well watered condition and 0.5 under drought stressed condition.

For genotyping diversity array technology (DArT) markers, which is a hybridisation-based technology marker system with high reproducibility that allows quick development of hundreds of markers distributed along the genome, was used. QTL analysis for LA and TRL was carried out following the composite interval mapping method using the PLABQTL software package.

Keywords: QTLs, recombinant inbred lines, sorghum