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Quantitative Trait Loci Analysis in Multiple Sorghum Mapping Populations Facilitates the Dissection of Genetic Control of Drought Tolerance Related Traits in Sorghum [Sorghum bicolor (Moench)]

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Abstract : The genetic architecture of drought tolerance is expected to involve multiple loci that are unlikely to all segregate for alternative alleles in a single bi-parental population. Therefore, the identification of quantitative trait loci (QTL) that are expressed in diverse genetic backgrounds of multiple bi-parental populations provides evidence about both background-specific and common genetic variants. The purpose of this study was to map QTL related to drought tolerance using three connected mapping populations of different genetic backgrounds to gain insight into the genomic landscape of this important trait in elite Ethiopian germplasm. The three bi-parental populations, each with 207 $F_{2:3}$ lines, were evaluated using an alpha lattice design with two replications under two moisture stress environments. Drought tolerance related traits were analyzed separately for each population using composite interval mapping, finding a total of 105 QTLs. All the QTLs identified from individual populations were projected on a combined consensus map, comprising a total of 25 meta QTLs for seven traits. The consensus map allowed us to deduce locations of a larger number of markers than possible in any individual map, providing a reference for genetic studies in different genetic backgrounds. The mQTL identified in this study could be used for marker-assisted breeding programs in sorghum after validation. Only one trait, reduced leaf senescence, showed a striking bias of allele distribution, indicating substantial standing variation among present varieties that might be employed in improving drought tolerance of Ethiopian and other sorghums.

Keywords : Drought tolerance , Mapping populations, Meta QTL, QTL mapping, Sorghum
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