

Genomics-assisted breeding for drought adaptation of sorghum in the Sahelian region

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Drought and unpredictable rainfall decrease sorghum (*Sorghum bicolor*, L. Moench) productivity in semiarid regions of West Africa. Understanding the genetic architecture of drought tolerance of sorghum germplasm from breeding programs could contribute to efficient molecular breeding in West Africa. This study aimed to dissect the genetic architecture of drought adaptation to develop high-throughput and breeder-friendly markers for rapid introgression of favorable trait-associated alleles into farmers' preferred varieties. First, we used genotyping-by sequencing to characterize 159,101 SNPs across 756 accessions of the West African sorghum association panel assembled from breeding programs of Senegal, Niger, Mali, and Togo. The genetic diversity structured by botanical types and subpopulations within botanical types across countries. Large-effect quantitative trait loci (QTL) for photoperiodic flowering indicate an oligogenic architecture of flowering time in West African sorghum. Secondly, we applied genome-wide association studies using pre- and post-flowering drought response variables from ten managed water stress environments to identify genomic regions associated with drought responses. Significantly positive pleiotropic associations contributed to high phenotypic variance and colocalized with known staygreen (*Stg*) loci. Results suggest the existence of *Stg* alleles in West African sorghum. Three marker loci associated with large-effect alleles were converted into breeder-friendly markers and used in marker-assisted selection for drought tolerance. These resources combined with discoveries from the global scientific community are used to accelerate the development of locally-adapted varieties through efficient genomics-assisted breeding to meet global food demand in semiarid regions of West Africa.