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Drought tolerance and grain yield are important traits in sorghum [*Sorghum bicolor* (L.) Moench], comprehensively studied and yet their genetic bases remain elusive. We conducted a genome-wide association study (GWAS) in a panel of 200 multi-parent advanced generation inter-cross (MAGIC) inbreds to identify genomic regions associated with drought tolerance, grain yield (GY), yield stability (YS) and 100 seed weight (HSW). Genotypes were evaluated for yield traits across multiple environments, and further assessed for drought-like response under salt desiccation stress.

GWAS using a 79K MAGIC SNPs generated via a high throughput genotyping-by-sequencing (GBS) platform identified four genomic regions associated with drought tolerance (Fig. 1).

A major drought region on chromosome 6 harbored 12 candidate genes, orthologous to *Arabidopsis thaliana*, Mize (*Zea mays*) and Rice (*Oriza sativa*) with functional annotations depicted in abiotic stress defenses (Fig.2).

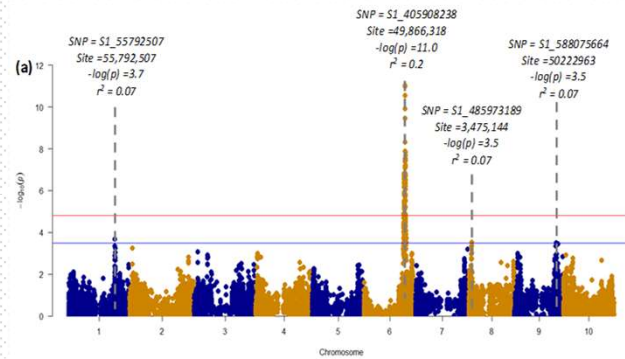


Fig.1. Manhattan plot depicting SNP-drought associations on chromosomes 1, 6, 8 and 9. Statistical strength of association ( $-\log_{10}P$ ) is plotted against genomic position with the 10 chromosomes in different colors. The red horizontal line indicates the genome-wide significance threshold while the blue line is the suggestive cut off.

We further detected three suggestive association signals each for GY, YS and HSW. Previous transcriptomics analysis depicted proximal genes to these regions to be involved in phytohormone pathway, carbohydrate metabolism, sugar transport and stress defense (Fig. 3).

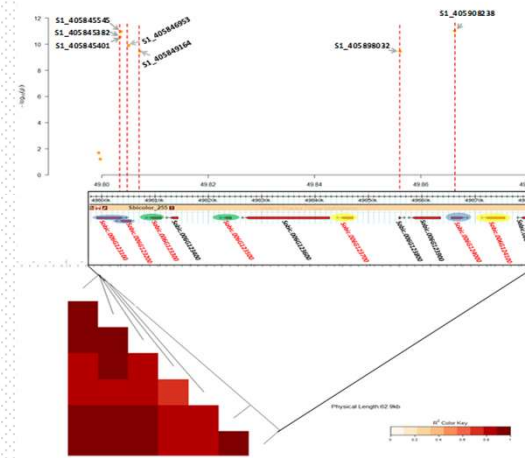


Fig.2. Portion of chromosome six showing a cluster of drought candidate genes localized within 63Kb region. Gene models are shown below the Manhattan plot with the nearest SNPs indicated by the vertical dash lines. Linkage disequilibrium (LD) pattern of all the significant SNPs within this region is shown below the gene models. From the color key provided, strength of color intensity reflects the strength of LD between pairs of SNPs

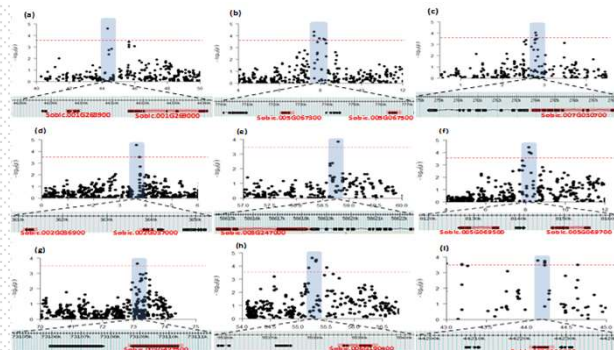


Fig.3. Candidate genes for grain yield, yield stability and 100 seed weight. (a-c) Grain yield genes on chr1, chr5 and chr7; (d-f) yield stability genes on chr2, chr3 and chr5; (g-i) seed weight genes on chr3, chr6 and chr8. Associated genes are highlighted in red. SNP-trait associated genomic regions are shown in vertical blue transparent shades. Significant threshold is indicated by horizontal dash lines.

### Summary;

- The study uncovered novel loci associated with drought tolerance and grain yield.
- The SNP markers linked to each of these four drought loci guided us into genomic regions harboring genes whose functions have been implicated in abiotic stress responses.
- Grain yield and seed weight loci were proximal to genes involved in plant growth and development
- Study added knowledge on the basis of variation for drought and grain yield and offers opportunity for genetic enhancement through genomic selection.