

Background/Objective

- While recent genome analyses in plants reveal many structural variants (SVs), most current studies of crop genetic variation are dominated by single nucleotide polymorphisms (SNPs). Current knowledge of the extent of the impact of SVs on trait variation is limited to a few loci.
- Here, we built an SV dataset based on whole-genome resequencing of 363 sorghum lines from the global Bioenergy Association Panel (BAP). We find new knowledge of allelic variation, including SVs controlling key agronomic traits that can be used in crop improvement.

Approach

In this study, to explore the genetics of SVs within sorghum germplasm, we utilized the Illumina short-read whole-genome resequencing data from 363 global sorghum accessions in the BAP. To enhance the accuracy and sensitivity of SV detection, we developed an ensemble pipeline for SV calling based on five independent algorithms involving different SV detection strategies.

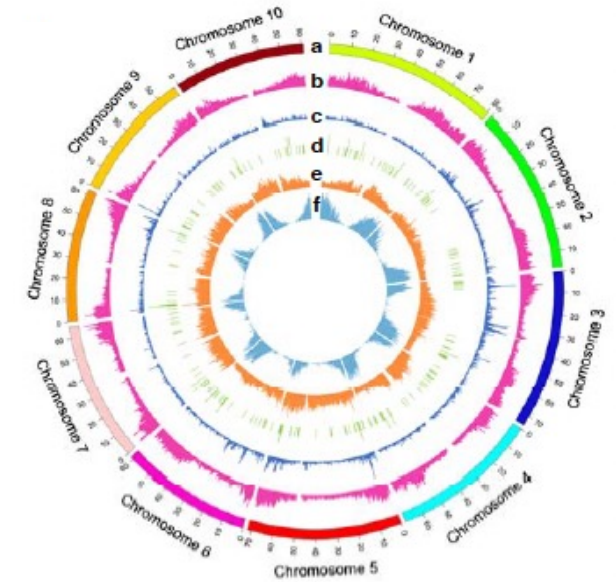
Results

Three-way genome-wide association studies (GWAS) based on whole-genome SNP, SV, and integrated SNP+SV datasets demonstrated substantial associations between SVs and sorghum traits. Addition of SVs to GWAS substantially increased heritability estimates for some traits, indicating their important contribution to functional allelic variation at the genome level. RNA-seq analysis indicated the SVs are strongly associated with heritable differential gene expression.

Significance/Impacts

Our study highlights the complementary contribution of the underexplored SVs in heritability of important traits, reveals their widespread impacts on gene expression, and demonstrates their crucial role in shaping population genetic diversity and trait determination. These results suggest that bioenergy traits, including oil traits, could be enhanced via breeding endeavors, and that specific targeting of SVs via marker-assisted selection could allow modification of gene expression levels in many cases.

Zhang, et al. 2024. "Major Impacts of Widespread Structural Variation on Sorghum." *Genome Research* DOI: 10.1101/gr.278396.123.



Distribution of genome-wide variations in the sorghum Bioenergy Association Panel (BAP).