

# Sugar Accumulation Enhancement in Sorghum Stem is Associated with Reduced Reproductive Sink Strength and Increased Phloem Unloading Activity

## Background

Sweet sorghum is a promising bioenergy source mainly due to its high biomass and high soluble sugar yield in stems. Studies suggest that loss-of-function *Dry* locus alleles have been selected during sweet sorghum domestication, and decapitation can further boost sugar accumulation in sweet sorghum, indicating untapped potential for improving sugar yields. To maximize sugar accumulation, it is essential to gain a better understanding of the mechanism underlying the accumulation of soluble sugars in sweet sorghum stems beyond the *Dry* locus.

## Approach

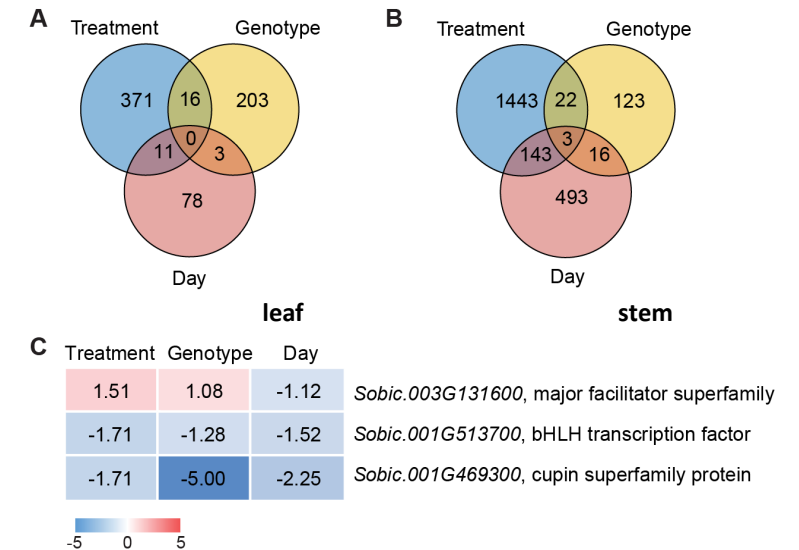
To seek new candidates responsible for sugar accumulation, in addition to the *Dry* (*D*) locus, we conducted transcriptomic data analysis comparing different genotypes (*dd* vs. *DD*), treatments (decapitation vs. control), and stages post anthesis (10d vs. 3d).

## Results

Our analysis revealed that decapitation suppressed photosynthesis in leaves, but accelerated starch metabolic processes in stems. *D* locus gene *SbNAC074A* and other programmed cell death-related genes were downregulated by decapitation, while sugar transporter-encoding gene *SbSWEET1A* was induced and detected in phloem companion cells by the RNA *in situ* assay, which indicates *SbSWEET1A*-mediated hexose flux may contribute to enhancing phloem unloading. Additionally, *SbbHLH093*, a homolog of *AtbHLH093* involved in transitioning from vegetative to reproductive growth, showed a negative correlation with sugar accumulation.

## Significance

This study provides new insights into sugar accumulation enhancement in bioenergy crops, which can be potentially achieved by reducing reproductive sink strength and enhancing phloem unloading. Downregulation or knocking out *SbbHLH093* may further boost sugar content in sweet sorghum. Further study is needed on the extent to which sugar levels can be increased when *SbSWEET1A* is overexpressed in sorghum or other biofuel crops.



**Genes are co-regulated by three factors: treatment, genotype, and day.**