

Allele-defined Genome of the Autopolyploid Sugarcane *Saccharum spontaneum* L.

Background/objective

Sugarcane, which provides 80% of the world's sugar and 40% of its ethanol as the primary sugar and biofuel feedstock crop, has a genome that has been duplicated twice during its evolutionary history. The recently sequenced *Saccharum spontaneum* genome provides a blueprint and history of one of our most important crops.

Approach

- ❖ The sequencing team used long sequence reads of PacBio and a technique called high-throughput chromatin conformation capture, or Hi-C, with a developed algorithm called ALLHiC, to provide a chromosome level assembly of *S. spontaneum* AP85-441.

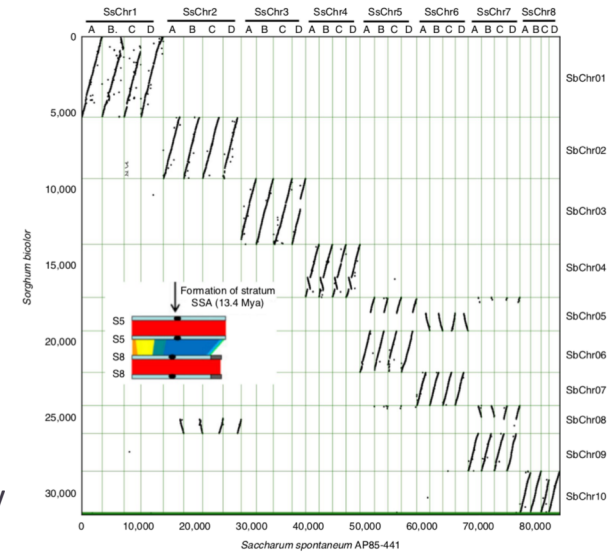
Results

- ❖ Assembled an autotetraploid (quadrupled) genome into 32 chromosomes and realized goal of allele-specific annotation among homologous chromosomes.
- ❖ Identification of 80% of disease resistance genes on rearranged chromosomes suggests that chromosomal rearrangements involved in the reduction of basic chromosome number (10 to 8) might have contributed to the retention of disease-resistance genes.

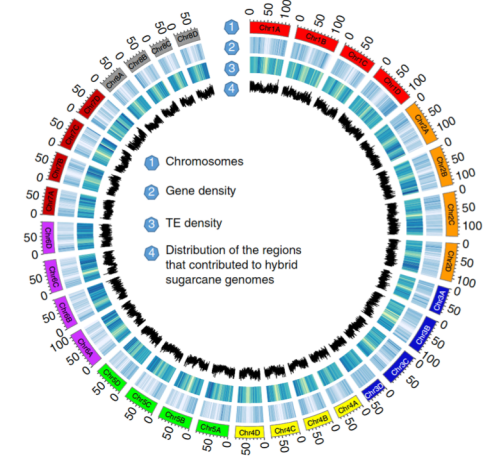
Significance

- ❖ The allele-defined *Saccharum* genome offers new knowledge and resources to accelerate sugarcane trait improvement for bioenergy production.
- ❖ The successful assembly of the sugarcane genome will assist researchers in assembling other complex genomes, such as polyploid Miscanthus.

Ming, R., et al. (2018). "Allele-defined genome of the autopolyploid sugarcane *Saccharum spontaneum* L." *Nature Genetics*, DOI: 10.1038/s41588-018-0237-2



Alignment of *S. spontaneum* AP85-441 chromosomes with sorghum chromosomes.



Distribution of the regions that contributed to the hybrid sugarcane genome in AP85-441.

