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.