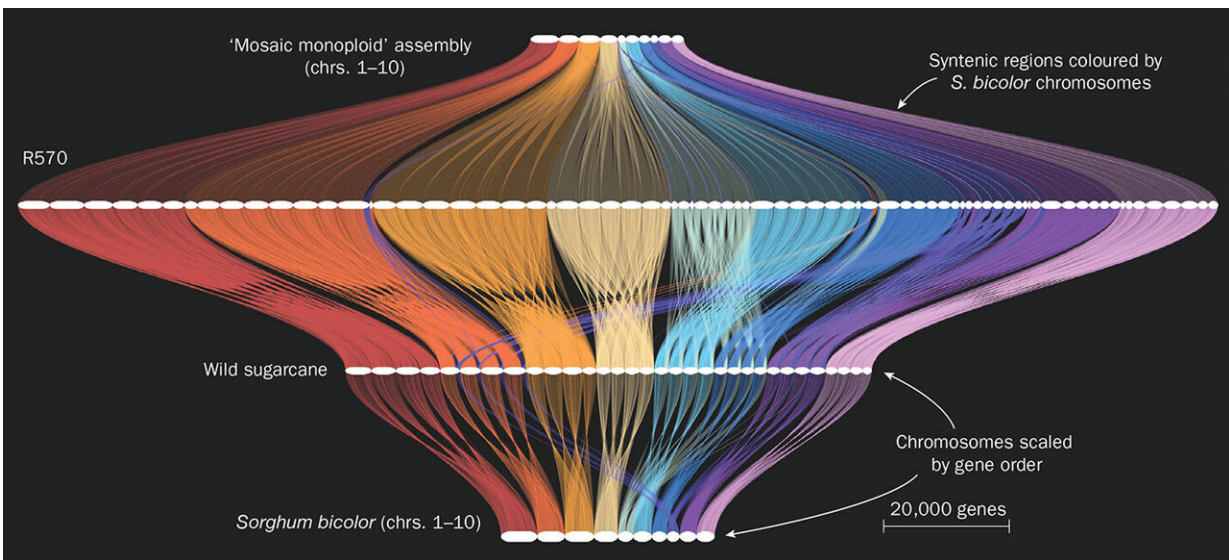


Sweet success: Researchers crack sugarcane's complex genetic code

March 27 2024, by Lauren Biron



A gene order map (created using GENESPACE) that compares genome assemblies among related plant species. The horizontal white lines represent chromosomes, and the colored braids that link them show conserved blocks of genes. This enables researchers to track conserved genes of interest from well-researched crops (such as *Sorghum bicolor*; a specific type of sorghum) into more complex genomes, such as wild sugarcane and cultivar R570, to better understand their function. For contrast, the previous monoploid assembly of R570 is provided on the top row, where multiple chromosome copies in the genome were represented as a single, mosaic assembly. Credit: Adam Healey and John Lovell/HudsonAlpha

Modern hybrid sugarcane is one of the most harvested crops on the planet, used to make products including sugar, molasses, bioethanol, and bio-based materials. It also has one of the most complex genetic blueprints.

Until now, [sugarcane](#)'s complicated genetics made it the last major crop without a complete and highly accurate genome. Scientists have developed and combined multiple techniques to successfully map out sugarcane's genetic code. With that map, they were able to verify the specific location that provides resistance to the impactful brown rust disease that, unchecked, can devastate a sugar crop. Researchers can also use the genetic sequence to better understand the many genes involved in sugar production.

The research was conducted as part of the Community Science Program at the U.S. Department of Energy Joint Genome Institute (JGI), a DOE Office of Science user facility at Lawrence Berkeley National Laboratory (Berkeley Lab). The study is published today in the journal [Nature](#), and the genome is available through the JGI's plant portal, [Phytozome](#).

"This was the most complicated genome sequence we've yet completed," said Jeremy Schmutz, Plant Program lead at the JGI and faculty investigator at the HudsonAlpha Institute for Biotechnology. "It shows how far we've come. This is the kind of thing that 10 years ago, people thought was impossible. We're able to accomplish goals now that we just didn't think were possible to do in plant genomics."

Sugarcane's genome is so complex both because it is large and because it contains more copies of chromosomes than a typical plant, a feature called polyploidy. Sugarcane has about 10 billion base pairs, the building blocks of DNA; for comparison, the human genome has about 3 billion.

Many sections of sugarcane's DNA are identical both within and across different chromosomes. That makes it a challenge to correctly reassemble all the small segments of DNA while reconstructing the full genetic blueprint. Researchers solved the puzzle by combining multiple genetic sequencing techniques, including a newly developed method known as PacBio HiFi sequencing that can accurately determine the sequence of longer sections of DNA.

Having a complete "reference genome" makes it easier to study sugarcane, enabling researchers to compare its genes and pathways with those in other well-studied crops, such as sorghum or other biofuel crops of interest, like switchgrass and miscanthus. By comparing this reference to other crops, it becomes easier to understand how each gene influences a trait of interest, such as which genes are highly expressed during sugar production or which genes are important for [disease resistance](#).

This study found that the genes responsible for resistance to brown rust, a [fungal pathogen](#) that previously caused millions of dollars of damage to sugarcane crops, are found in only one location in the genome.

"When we sequenced the genome, we were able to fill a gap in the [genetic sequence](#) around brown rust disease," said Adam Healey, first author of the paper and a researcher at HudsonAlpha.

"There are hundreds of thousands of genes in the sugarcane genome, but it's only two genes, working together, that protect the plant from this pathogen. Across plants, there are only a handful of instances that we know of where protection works in a similar way. A better understanding of how this disease resistance works in sugarcane could help protect other crops facing similar pathogens down the road."

Researchers studied a cultivar of sugarcane known as R570 that has been used for decades around the world as the model to understand sugarcane

genetics. Like all modern sugarcane cultivars, R570 is a hybrid made by crossing the domesticated species of sugarcane (which excelled in [sugar production](#)) and a wild species (which carried the genes for disease resistance).

"Knowing R570's complete genetic picture will let researchers trace which genes descended from which parent, enabling breeders to more easily identify the genes that control the traits of interest for improved production," said Angélique D'Hont, last author of the paper and a sugarcane researcher at the French Agricultural Research Center for International Development (CIRAD).

Improving future varieties of sugarcane has potential applications in both agriculture and bioenergy. Enhancing how sugarcane produces sugar could increase the yield farmers get from their crops, providing more sugar from the same amount of growing space. Sugarcane is an important feedstock, or starting material, for producing biofuels, particularly ethanol and other bioproducts.

The residues that remain after the pressing of sugarcane, referred to as bagasse, are an important type of agricultural residue that can also be broken down and converted into biofuels and bioproducts.

"We are working to understand how specific genes in plants relate to the quality of the biomass we get downstream, which we can then turn into biofuels and bioproducts," said Blake Simmons, Chief Science and Technology Officer for the Joint BioEnergy Institute, a DOE Bioenergy Research Center led by Berkeley Lab.

"With a better understanding of sugarcane genetics, we can better understand and control the plant genotypes needed to produce the sugars and bagasse-derived intermediates we need for sustainable sugarcane conversion technologies at a scale relevant to the bioeconomy."

More information: Adam Healey, The complex polyploid genome architecture of sugarcane, *Nature* (2024). [DOI: 10.1038/s41586-024-07231-4](https://doi.org/10.1038/s41586-024-07231-4).
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