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A New Chapter in Sugarcane Genomics: Constructing the R570 Reference Genome and the Future of Agricultural Biotechnology

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Wang M., and Fang J., 2024, A new chapter in sugarcane genomics: constructing the R570 reference genome and the future of agricultural biotechnology, Genomics and Applied Biology, 15(1): 8-11 (doi: 10.5376/gab.2024.15.0002)

A paper titled "The Complex Polyploid Genome Architecture of Sugarcane" by A.L. Healey, O. Garsmeur, J.T. Lovell, et al., from institutions including the Hudson Alpha Institute for Biotechnology, CIRAD, and the University of Queensland, was published in the journal Nature on March 27, 2024. This research successfully constructed a polyploid reference genome for the sugarcane (*Saccharum* spp.) variety R570. As the highest-yielding crop worldwide, sugarcane is a crucial source of sugar and biomass production. Despite certain successes in adapting to new environments and pathogens through traditional breeding methods, the increase in sugarcane's sugar yield has plateaued in recent years. By generating a polyploid reference genome for the R570 variety, this study fills a gap in the lack of high-quality reference genomes for modern sugarcane varieties, marking an important step forward for biotechnological advancements in sugarcane.

1 Experimental Data Analysis

The study employed a range of cutting-edge genomics technologies, including high-throughput Illumina sequencing, high-accuracy PacBio HiFi sequencing, and precise chromosome flow sorting, to successfully construct a high-continuity reference genome for the sugarcane variety R570. The genome size is estimated at 10Gb, reflecting the characteristic traits of a modern hybrid variety created through the breeding of two primary parent species of sugarcane: Saccharum officinarum and Saccharum spontaneum. Furthermore, the genome annotation work identified 194,593 genes, significantly enriching our understanding of the complex polyploid genome structure of sugarcane and providing valuable resources for exploring the genetic diversity and functional genomics of sugarcane. The size of this genome and the number of genes reflect the genetic complexity and richness of sugarcane as a significant agricultural and bioenergy plant, laying a solid foundation for further molecular breeding, genetic improvement, and disease prevention research.

Figure 1 illustrates the pedigree and genome structure of the hybrid sugarcane R570. From Figure 1a, it is seen that R570 is a sugarcane variety approximately 4 meters in height. Figure 1b details the breeding pedigree of R570, where pie charts show the genome contributions from wild sugarcane (red) and sweet sugarcane (blue) to R570. The asterisks "*" represent the diploid chromosome transmission in the first two generations, and the "+" indicates the first generation of hybrids. Although the exact pedigrees of ‘R331’ and ‘Co213’ are unknown, they are estimated to be BC2F2 and BC2:BC1 F1, respectively. Figure 1c shows R570 chromosomes prepared after in situ hybridization with wild sugarcane-specific probes, with the red parts marking the chromosomes from wild sugarcane. Figure 1d is the karyotype of R570, with colors corresponding to those in figure 1b. This information helps researchers understand the complex polyploid genome structure of R570 hybrid sugarcane.

Figure 2 presents the genome assembly information for the sugarcane variety R570. Figure 2a is a schematic of the main assembly of the R570 genome, showing that each homologous chromosome has about 12 chromosome copies, but almost identical haplotypes are folded in the genome assembly due to backcrossing and 2n+n chromosome transmission (indicated by different colored shadows). Figure 2b shows the one-to-one orthologous genes between R570's main chromosomes and chromosomes 1 to 10 of sorghum (Sorghum bicolor v.3.1.1), colored according to ancestral contributions in R570. Figure 2c is a homology map between R570 and related genomes generated by GENESPACE, from bottom to top: sorghum, wild sugarcane genotype AP85-441, R570's main genome, and the assembly of R570's haplotype genome. This chart aids researchers in understanding the complex homology between R570 and other species' genomes.

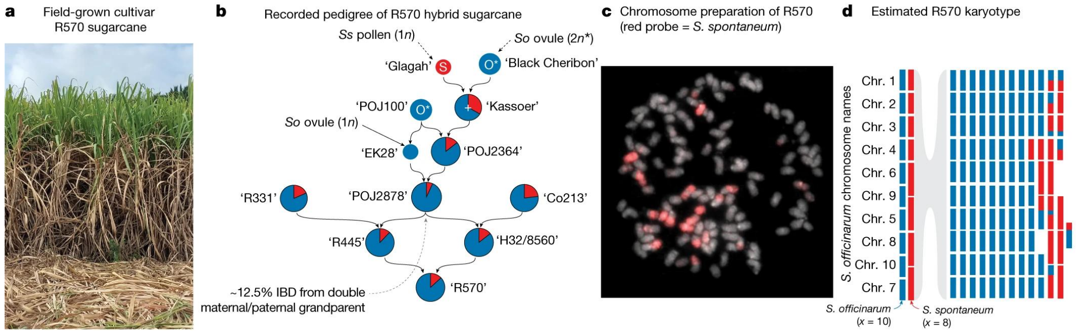

Figure 1 The pedigree and genome organization of R570 hybrid sugarcane

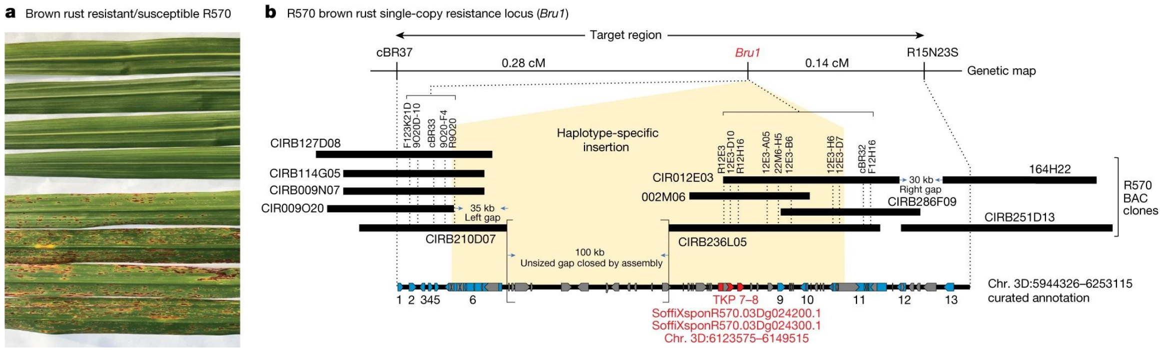

Figure 2 The genome assembly of sugarcane cultivar R570

Figure 3 focuses on the Bru1 gene locus in the sugarcane variety R570, which is associated with resistance to brown rust disease. Figure 3a shows leaves from two selfed progenies of R570: the upper leaf carries the Bru1 locus and exhibits resistance to brown rust disease; the lower leaf lacks the Bru1 locus, showing susceptibility to the disease. Figure 3b displays the filled haplotype assembly, identifying the TKP gene as the candidate causative gene for persistent resistance to brown rust disease. In the diagram, blue pentagons represent organized gene models, and gray pentagons represent large transposable elements. Candidate genes TKP7 and TKP8 for Bru1 are shown in red and marked on the 3D chromosome. This indicates that through detailed gene localization and functional annotation, researchers can identify key genes related to sugarcane's disease resistance traits, which is significant for breeding.

2 Analysis of Research Findings

This study successfully constructed an 870 million base pair polyploid reference genome for the sugarcane variety R570, revealing the complex genome structure resulting from the hybridization of *Saccharum officinarum* and *Saccharum spontaneum*. Identifying 194,593 genes, the study provides a critical foundation for research into sugarcane's genetic diversity and molecular breeding. Through detailed analysis of the R570 genome, the study not only revealed the genetic contributions of parent species to modern varieties, especially in disease resistance and sugar accumulation but also identified candidate genes for the brown rust resistance gene Bru1, offering molecular tools for improving sugarcane's disease resistance in the future. Additionally, the study delved into the structural variations in the sugarcane genome, the diversity of orthologous genes, and the evolution of specific functional genes, uncovering the relationship between sugar accumulation and certain gene families. This research not only deepens our understanding of the complexity of the sugarcane genome but also provides valuable genetic resources for sugarcane breeding, disease management, and biotechnological improvements, marking a new phase in sugarcane genome research.

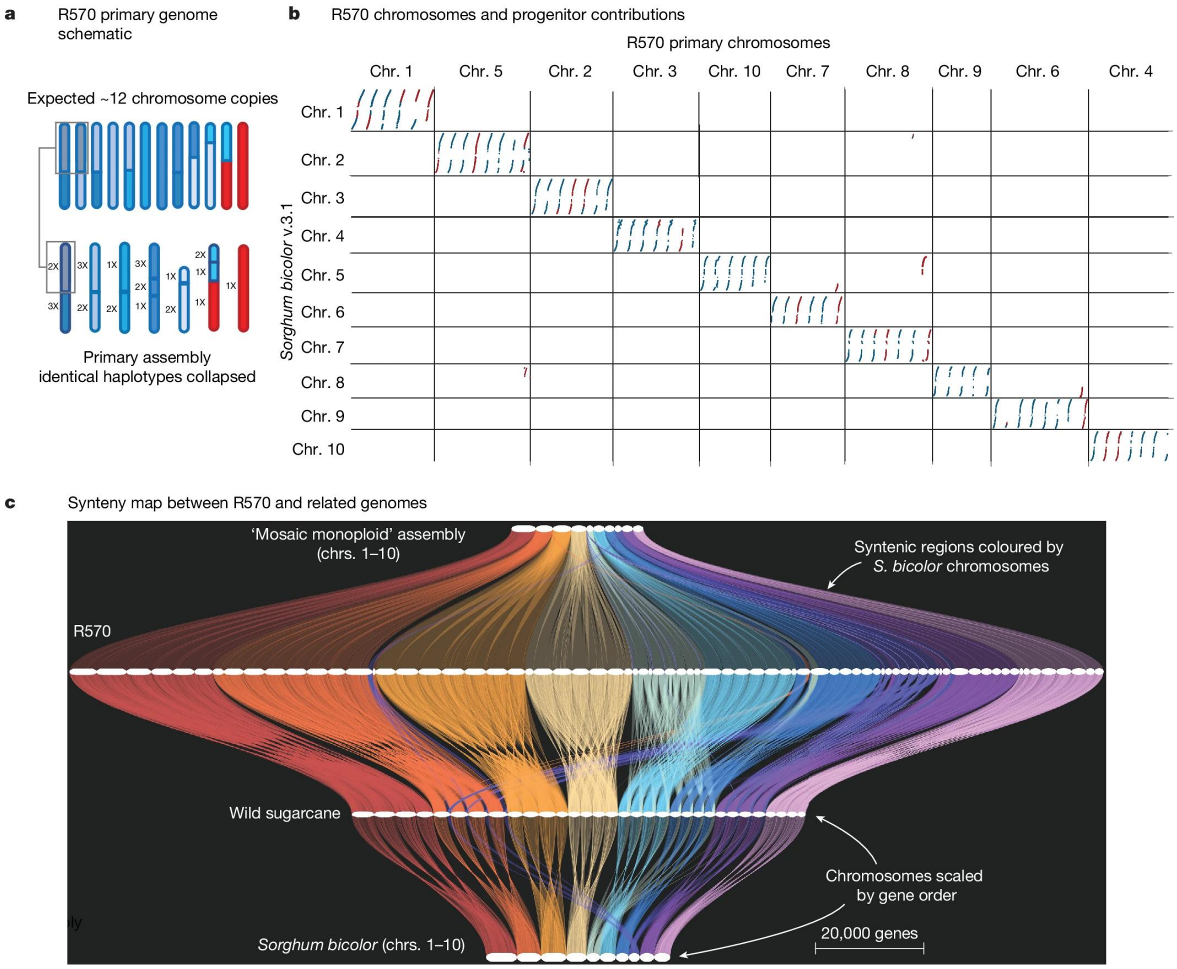

Figure 3 *Bru1* candidate gene locus

3 Evaluation of the Research

This research represents a milestone achievement in the field of sugarcane genomics, constructing a complex polyploid reference genome for the sugarcane variety R570 through highly innovative methods. The findings not only deepen the scientific community's understanding of sugarcane's genetic complexity but also significantly advance the application of genomics in sugarcane research, particularly in improving disease resistance and productivity. By thoroughly analyzing key resistance genes like Bru1, this study provides molecular targets for sugarcane disease-resistant breeding and also offers potential resistance mechanisms for other crops. Moreover, the success of this study demonstrates the power of interdisciplinary collaboration, integrating techniques and knowledge from bioinformatics, molecular biology, genetics, and other fields, reflecting the composite and interconnected nature of modern scientific research. The publication of this study not only provides valuable resources for sugarcane breeding and improvement but also offers clues to solving challenges faced by global agricultural production, showcasing the key role of genomic research in modern agricultural science.

4 Conclusions

The successful construction of the polyploid reference genome for sugarcane R570 marks a milestone in sugarcane genome research, advancing the study of this important economic crop to a new level. Through the use of the latest sequencing technologies and bioinformatics analysis, this work provides an unprecedented detailed view of sugarcane's genetic diversity and complex genome structure, as well as identifying genes controlling key agronomic traits such as sugar accumulation and disease resistance, providing important molecular markers and candidate genes for future molecular breeding and genetic improvement. Moreover, the outcomes of this research pave the way for advances in sugarcane biotechnology, offering scientific evidence and technical tools for developing new disease-resistant varieties and increasing sugarcane sugar yield. Against the backdrop of global climate change and the challenges of sustainable agricultural production, this study not only has profound significance for the sugarcane industry but also provides valuable experience and insights for the genome research and improvement of other crops. By deeply exploring the genetic potential of sugarcane, this research provides a solid foundation for improving the productivity and adaptability of sugarcane, as well as further utilizing this crop as a source of biomass energy.

5 Access the Full Text

Healey, A.L., Garsmeur, O., Lovell, J.T. et al. The complex polyploid genome architecture of sugarcane. Nature (2024). https://doi.org/10.1038/s41586-024-07231-4.

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The authors sincerely thank Nature magazine for providing the research paper by Healey, A.L., Garsmeur, O., Lovell, J.T., et al. on the complex polyploid genome architecture of sugarcane in an open access (OA) manner, allowing for the timely sharing of this important finding with academic colleagues. This act not only exemplifies the spirit of scientific sharing but also deepens our understanding and knowledge of the field.