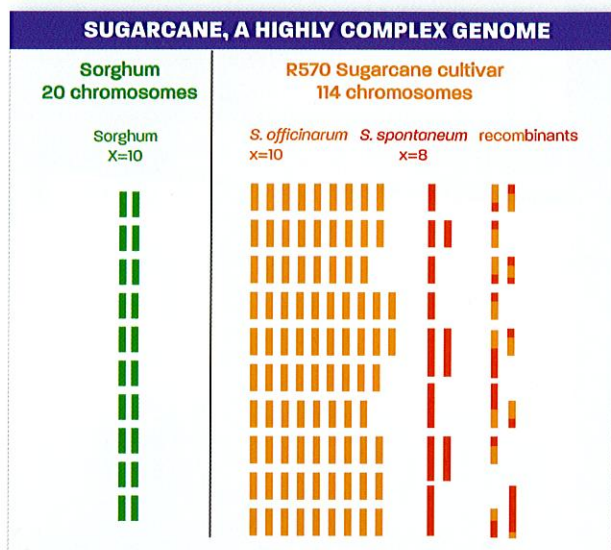


A NEW ERA FOR SUGARCANE BREEDING



SUGARCANE GENOME FINALLY SEQUENCED AND ASSEMBLED

Sugarcane was the last major crop to have its genome sequenced and assembled, due to the huge complexity of its genome. This complexity results from its interspecific origin and polyploidy: each chromosome is present in 10 to 12 copies, with a total of more than 100 chromosomes. In 2018, an international team coordinated by Cirad achieved this milestone in producing the first reference sequence assembly of the sugarcane genome. Sugarcane geneticists will now benefit from modern molecular tools to untangle the complex genetics and origin of sugarcane and initiate molecular breeding strategies.

A NOVEL AND ORIGINAL SEQUENCING STRATEGY

The sugarcane genome is so complex that conventional sequencing methods have proved ineffective. Cirad

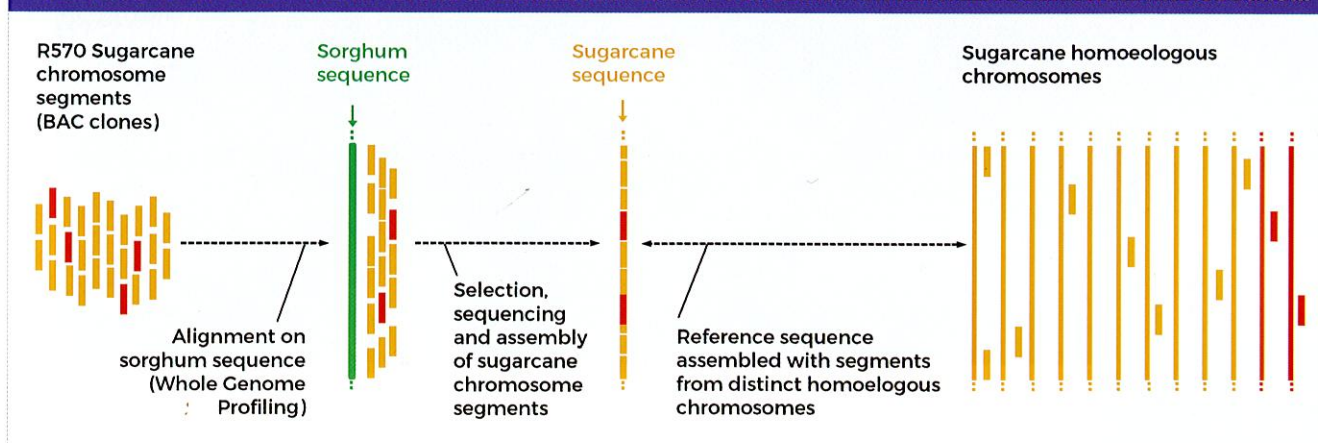
researchers took up the gauntlet using a novel and original sequencing strategy based on a previous discovery: sugarcane and sorghum genomes have a similar organization, with large collinear chromosome segments bearing numerous genes occurring in the same order. The available sorghum genome was thus used as a template to select and sequence around 5,000 sugarcane chromosome segments. Thanks to this original strategy, a reference sugarcane genome was assembled from the well-known cultivar R570, a hybrid created by eRcane in Reunion Island. A new version of the R570 genome assembly including all chromosome copies is underway in collaboration with the Joint Genome Institute (USA). This cultivar has broad adaptability and is still used as genitor in many breeding stations worldwide.

A KEY STAGE TO INITIATE MOLECULAR BREEDING STRATEGIES

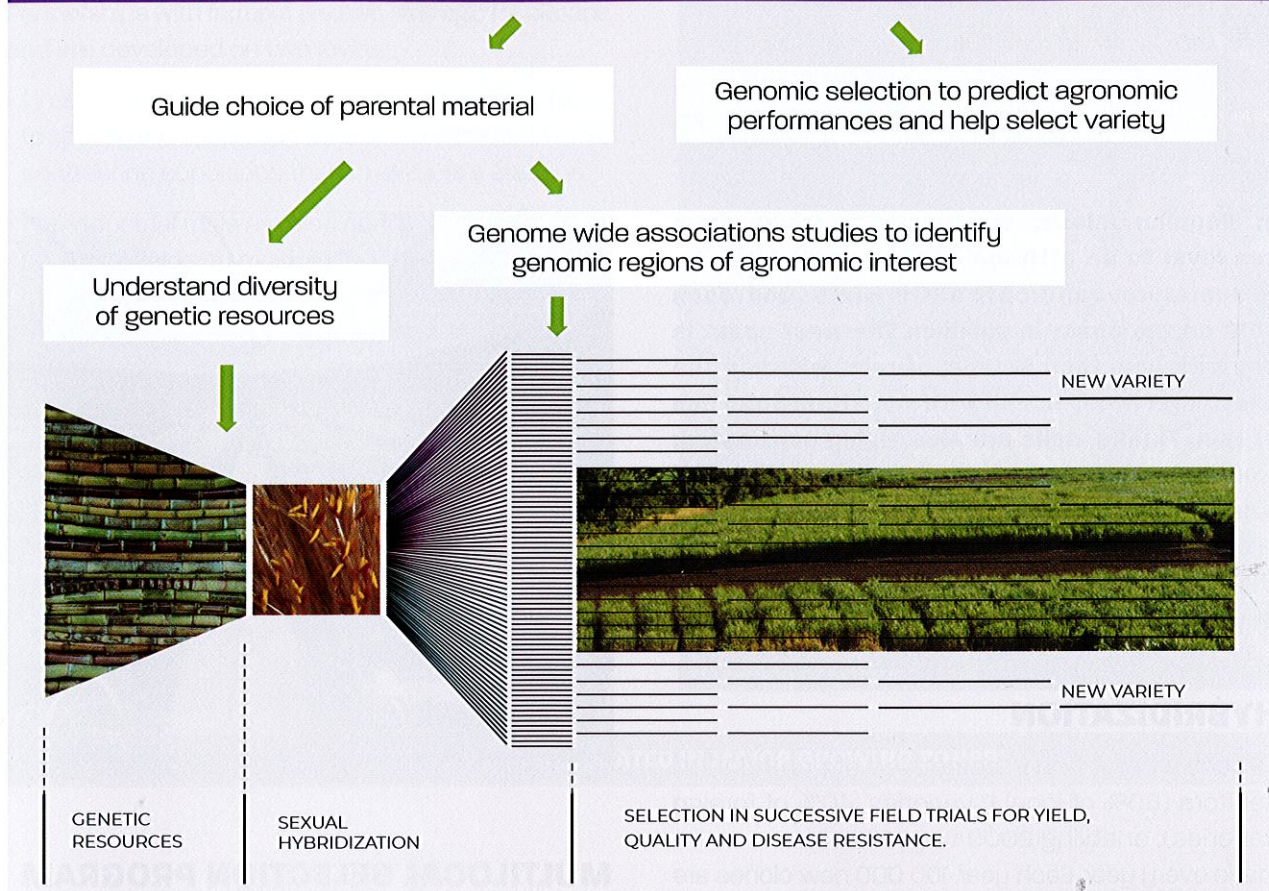
This reference sequence is an invaluable stepping-stone toward developing molecular assisted breeding to speed up genetic progress. It will allow the development of genome-wide molecular marker strategies based on single nucleotide polymorphism (SNP) to:

- understand the genome structure and the diversity of sugarcane genetic resources and guide their use in breeding programs;
- identify genes or chromosome regions involved in important agronomic traits (disease resistance, quality, yield, etc) and keep track of their incorporation in breeding materials;
- develop genomic predictions of agronomic performance, in order to supplement field trials with genomic selection to speed up genetic progress.

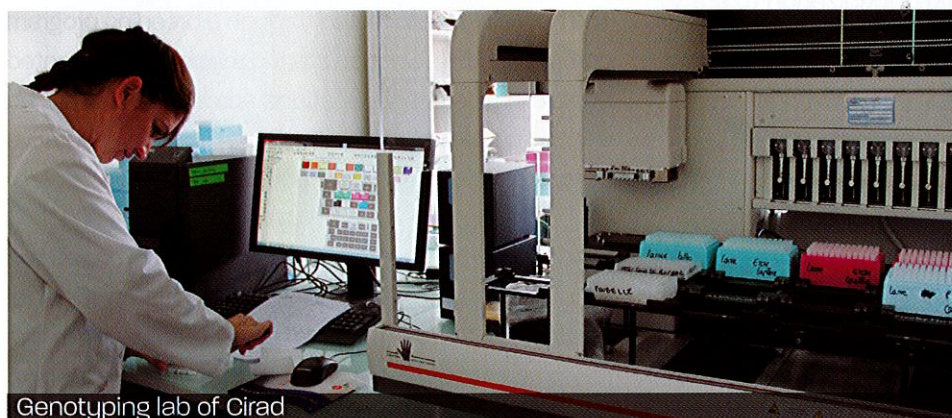
SEQUENCING STRATEGY BASED ON THE OVERALL COLLINEARITY CONSERVATION BETWEEN SUGARCANE AND SORGHUM



PERSPECTIVES OF GENOME WIDE MOLECULAR MARKER APPLICATIONS IN SUPPORT TO BREEDING PROGRAM



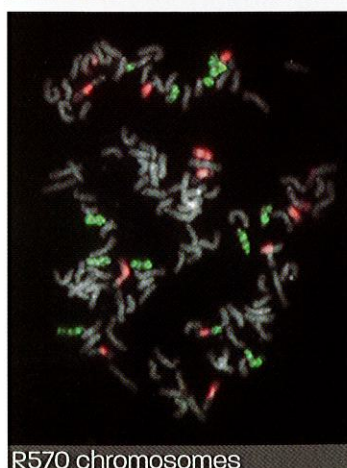
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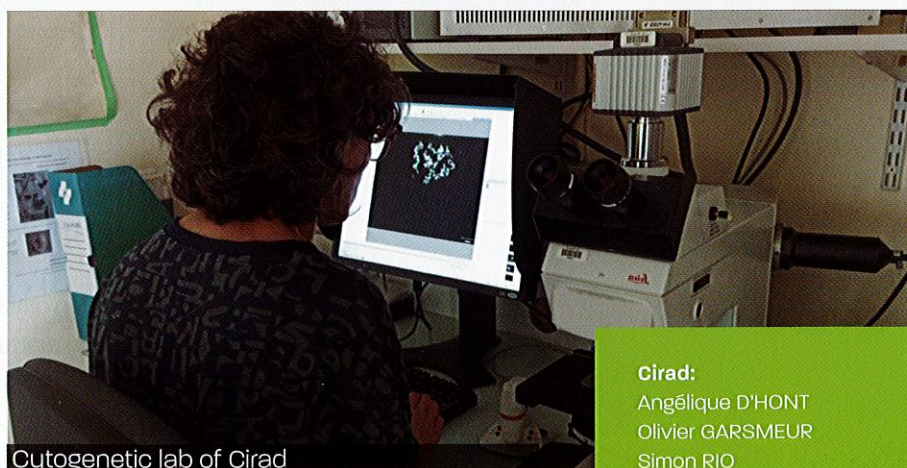
Genotyping lab of Cirad

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TCTGTAATCATAG
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R570 chromosomes



Cytogenetic lab of Cirad

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FRENCH SUGARCANE EXPERTISE

