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W604 : Sugarcane Genome Sequencing Initiative

Comparison Of Seven Homoeologous Haplotypes (BAC) Within The High Polyploid Sugarcane Genome

Carine Charron¹, **Olivier Garsmeur**¹, **Vincent Jouffe**¹, **Stéphanie Bocs**¹, **Sylvie Samain**²,
Arnaud Couloux², **Gaëtan Droc**¹, **Jean-Christophe Glaszmann**¹, **Marie-Anne Van Sluys**³,
Angélique D'Hont¹

¹ CIRAD, UMR 96, Avenue Agropolis, F-34398 Montpellier cedex 5, France

² CEA, Institut de génomique, Genoscope, 2 rue Gaston Cremieux, CP 5706, F-91057 Evry cedex, France

³ GaTE Lab, Instituto de Biociencias, Universidade de Sao Paulo, Rua do Matao 277, Sao Paulo, 05508-090 SP, Brazil

Sugarcane cultivars (*Saccharum* spp.) present one the most complex crop genomes studied to date: highly polyploids (more than decaploids) and aneuploids, with around 120 chromosomes and a genome size of around 10 Gb. In order to investigate the organisation of this highly polyploid genome (% of homology between allele haplotypes, content in repeated sequence...), which is essential for elaborating a whole genome sequencing strategy, we sequenced and compared seven hom(oe)ologous haplotypes (BAC clones) from the sugarcane cultivar R570. These haplotypes showed a very high colinearity as well as very high gene structure and sequence conservation. A high homology was also observed along the non-transcribed regions to the exception of transposable elements (TEs) which represents between 18 and 53% of the BAC sequence. A high colinearity was also observed in the overlapping regions between sugarcane and sorghum and to a lower extent with rice.

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