

EVOLUTIONARY DYNAMICS OF HOM(OE)OLOGOUS HAPLOTYPES (BACS) WITHIN THE HIGHLY POLYPLOID SUGARCANE GENOME

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Sugarcane (*Saccharum* spp.) has been recognized as one of the world's most efficient crops in converting solar energy into chemical energy and having the most favorable input/output ratio. Beside its importance for sugar production it is thus also a primary energy crop. Sugarcane also presents one the most complex crop genomes studied to date. Modern sugarcane cultivars derive from the combination of two polyploid species: *S. officinarum*, the domesticated sugar-producing species with $x=10$ and $2n=8x=80$, and *S. spontaneum*, a vigorous wild species with $x=8$ and $2n=5x=40$ to $16x=128$ and many aneuploid forms. Both species are thought to have an autopolyploid origin. Modern sugarcane are highly polyploid (more than decaploid) and aneuploid, with around 120 chromosomes and a genome size of around 10 Gb. They typically display 70 to 80% of chromosomes entirely derived from *S. officinarum*, 10 to 20% from *S. spontaneum* and a few chromosomes derived from interspecific recombination. Their meiosis mainly involves bivalent pairing and chromosome assortment results from a combination of polysomy and preferential pairing.

We investigated genome dynamics in this highly polyploid context by analyzing the sequence of hom(oe)ologous haplotypes (BAC clones) from the sugarcane cultivar R570. We first analyzed two homoeologous haplotypes from a gene-rich region bearing the *Adh1* gene (Jannoo et al 2007), knowing that this region has been thoroughly studied within the Poaceae family. We then analyzed seven hom(oe)ologous haplotypes from a second gene-rich region. Our results indicated that the two *Saccharum* species diverged 1.5-2 mya from one another and 8-9 mya from sorghum. The sugarcane hom(oe)ologous 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). Conversely, TEs that represent in average 33% of the BAC clones studied, were not conserved between hom(oe)ologous haplotypes. Compared to sorghum, the sugarcane haplotypes displayed a high colinearity and a remarkable homology in most of the non-coding parts of the genome. On this basis, the high ploidy of sugarcane does not seem to have induced a major reshaping of its genome (at least at the gene level). In addition, the coexistence of potentially in average 12 hom(oe)ologous alleles at each locus does not seem to induce a decrease of conservative selection at the gene sequence level.

Keywords: Sugarcane, BAC sequence, hom(oe)ologous haplotypes, evolutionary dynamics