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HIGH HOMOLOGOUS GENE CONSERVATION DESPITE EXTREME AUTOPOLYPLOID REDUNDANCY IN SUGARCANE

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Modern sugarcane (*Saccharum* spp.) has been recognized as one of the world's most efficient crops in solar energy conversion and as having the most favorable input : output ratios. Beside its importance for sugar production, it thus became recently a primary energy crop. Sugarcane also presents one the most complex crop genome studied to date, mainly due to a very high degree of polyploidy ($2n=ca\ 12x=ca\ 120$), together with an interspecific origin. In order to investigate genome dynamics in this highly polyploid context and to provide guidelines for future whole genome sequencing project, we sequenced and compared seven homoeologous haplotypes (BAC clones). Our analysis revealed a high conservation at the gene level (high colinearity and high gene structure and sequence conservation). Remarkably, all homoeo-alleles are predicted functional and no apparent general decrease of purifying selection was observed. Thus the high polyploidy of sugarcane does not seem to have induced a major reshaping of its genome, at least at the gene level. By contrast, transposable elements displayed a general absence of colinearity among homoeologous haplotypes and appeared to have undergone dynamic expansion in *Saccharum*, compared with sorghum, its close relative in the *Andropogonea* tribe. Our data suggest the presence of broad sets of functional homologous alleles in the sugarcane genome, which could explain its unique efficiency, its high phenotypic plasticity and wide adaptation.