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Segregation analysis of microsatellite (SSR) markers in sugarcane polyploids

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ABSTRACT. No information is available on segregation analysis of DNA markers involving both pollen and self-progeny. Therefore, we used capillary electrophoresis- and fluorescence-based DNA fingerprinting together with single pollen collection and polymerase chain reaction (PCR) to investigate simple sequence repeat (SSR) marker segregation among 964 single pollens and 288 self-progenies (S_1) of sugarcane cultivar LCP 85-384. Twenty SSR DNA fragments (alleles) were amplified by five polymorphic

SSR markers. Only one non-parental SSR allele was observed in 2392 PCRs. SSR allele inheritance was in accordance with Mendelian laws of segregation and independent assortment. Highly significant correlation coefficients were found between frequencies of observed and expected genotypes in pollen and S_1 populations. Within the S_1 population, the most frequent genotype of each SSR marker was the parental genotype of the same marker. The number of genotypes was higher in pollen than S_1 population. PIC values of the five SSR markers were greater in pollen than S_1 populations. Eleven of 20 SSR alleles (55%) were segregated in accordance with Mendelian segregation ratios expected from pollen and S_1 populations of a 2n = 10x polyploid. Six of 20 SSR alleles were segregated in a 3:1 (presence:absence) ratio and were simplex markers. Four and one alleles were segregated in 77:4 and 143:1 ratios and considered duplex and triplex markers, respectively. Segregation ratios of remaining alleles were unexplainable. The results provide information about selection of crossing parents, estimation of seedling population optimal size, and promotion of efficient selection, which may be valuable for sugarcane breeders.

Key words: *Saccharum* spp. hybrids; Polyploidy; Microsatellite DNA marker; Pollen; Self-progeny