



Use of microsatellite markers in molecular analysis of segregating populations of papaya (*Carica papaya* L.) derived from backcrossing

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ABSTRACT. Brazil is the world leader in papaya production. However, only a small number of cultivars are registered for commercial planting, mainly owing to delays in obtaining cultivars and the high costs of the field phase of breeding programs. These costs can be reduced when molecular tools are combined with conventional breeding methods. In the present study, we conducted a molecular analysis of a self-fertilized population of a first backcrossing generation of BC₁S₁ papaya plants via microsatellite markers both to monitor the level of homozygosity and the gene/allele transfer that confers the Golden trait (fruit color) and to assess the parental genomic proportion in the genotypes studied. Based on the analysis of 20 polymorphic microsatellite loci, 19 genotypes with the Golden trait belonging to BC₁S₁ were evaluated in addition to the parental genotypes. Genetic distance was estimated through weighted index. The genotypes were then grouped using the hierarchical nearest neighbor method, and the analysis of principal coordinates was used to measure the proportion of parental genomes in the segregating genotypes. The mean value of the inbreeding coefficient was 0.36. The

analysis of the principal coordinates revealed that on average, 64% of the recurrent parent genome was present in the population. Together, the analyses allowed the selection of 3 individuals for the next backcross cycle (33BC₁S₁-18, 34BC₁S₁-16, and 37BC₁S₁-10). These individuals had a higher proportion of the recurrent parent and were grouped close to the recurrent parent in the cluster analysis.

Key words: Microsatellite marker; Assisted selection; Inbreeding