



Genetic characterization of papaya plants (*Carica papaya* L.) derived from the first backcross generation

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ABSTRACT. The limited number of papaya varieties available reflects the narrow genetic base of this species. The use of backcrossing as a breeding strategy can promote increases in variability, besides allowing targeted improvements. Procedures that combine the use of molecular markers and backcrossing permit a reduction of the time required for introgression of genes of interest and appropriate recovery of the recurrent genome. We used microsatellite markers to characterize the effect of first-generation backcrosses of three papaya progeny, by monitoring the level of homozygosity and the parental genomic ratio. The homozygosity level in the population ranged from 74 to 94%, with a mean of 85% for the three progenies (52-08, 52-29 and 52-34). The high level of inbreeding found among these genotypes increases the expectation of finding more than 95% fixed loci in the next generation of self-fertilization of superior genotypes. The mean proportion of the recurrent parent genome found in first-generation backcross progeny was 50.1%; 52-34 had a larger

genomic region in common with the recurrent genitor and the lowest level of homozygosity. The progeny 52-08 was genetically closest to the donor genitor, and it also had the highest level of homozygosity. We found that linking conventional procedures and molecular markers contributed to an increase in the efficiency of the breeding program.

Key words: Backcross; Microsatellite markers; Parental genome; Inbreeding; Genetic variability