



Functional molecular markers (EST-SSR) in the full-sib reciprocal recurrent selection program of maize (*Zea mays* L.)

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ABSTRACT. This study aimed to improve grain yield in the full-sib reciprocal recurrent selection program of maize from the North Fluminense State University. In the current phase of the program, the goal is to maintain, or even increase, the genetic variability within and among populations, in order to increase heterosis of the 13th cycle of reciprocal recurrent selection. Microsatellite expressed sequence tags (EST-SSRs) were used as a tool to assist the maximization step of genetic variability, targeting the functional genome. Eighty S_1 progenies of the 13th recurrent selection cycle, 40 from each population (CIMMYT and Piranão), were analyzed using 20 EST-SSR loci. Genetic diversity, observed heterozygosity, information content of polymorphism, and inbreeding coefficient were estimated. Subsequently, analysis of genetic dissimilarity, molecular variance, and a graphical dispersion of genotypes were conducted. The number of alleles in the CIMMYT population ranged

from 1 to 6, while in the Piranão population the range was from 2 to 8, with a mean of 3.65 and 4.35, respectively. As evidenced by the number of alleles, the Shannon index showed greater diversity for the Piranão population (1.04) in relation to the CIMMYT population (0.89). The genic SSR markers were effective in clustering genotypes into their respective populations before selection and an increase in the variation between populations after selection was observed. The results indicate that the study populations have expressive genetic diversity, which corresponds to the functional genome, indicating that this strategy may contribute to genetic gain, especially in association with the grain yield of future hybrids.

Key words: *Zea mays*; Genetic diversity; EST-SSR markers; Reciprocal recurrent selection