



Selection of high heterozygosity popcorn varieties in Brazil based on SSR markers

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ABSTRACT. We analyzed genetic structure and diversity among eight populations of popcorn, using SSR loci as genetic markers. Our objectives were to select SSR loci that could be used to estimate genetic diversity within popcorn populations, and to analyze the genetic structure of promising populations with high levels of heterozygosity that could be used in breeding programs. Fifty-seven alleles (3.7 alleles per locus) were detected; the highest effective number of alleles (4.21) and the highest gene diversity (0.763) were found for the *Umc2226* locus. A very high level of population differentiation was found ($F_{ST} = 0.3664$), with F_{ST} for each locus ranging from 0.1029 (*Umc1664*) to 0.6010 (*Umc2350*). This analysis allowed us to identify SSR loci with high levels of heterozygosity and heterozygous varieties, which could be selected for production of inbred lines and for developing new cultivars.

Key words: *Zea mays*; Popcorn; SSR locus; Microsatellite; Genetic diversity; Molecular breeding