



Inference of genetic diversity in popcorn S_3 progenies

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ABSTRACT. Molecular markers are a useful tool for identification of complementary heterotic groups in breeding programs aimed at the production of superior hybrids, particularly for crops such as popcorn in which heterotic groups are not well-defined. The objective of the present study was to analyze the genetic diversity of 47 genotypes of tropical popcorn to identify possible heterotic groups for the development of superior hybrids. Four genotypes of high genetic value were studied: hybrid IAC 125, strain P2, and varieties UENF 14 and BRS Angela. In addition, 43 endogamous S_3 progenies obtained from variety UENF 14 were used. Twenty-five polymorphic SSR-EST markers were analyzed. A genetic distance matrix was obtained and the following molecular diversity parameters were estimated: number of alleles, number of effective alleles, polymorphism information content (PIC), observed and expected heterozygosities, Shannon diversity index, and coefficient of inbreeding. We found a moderate PIC and high diversity index, indicating that the studied population presents both good discriminatory ability and high informativeness for the utilized markers. The dendrogram built based on the dissimilarity matrix indicated six

distinct groups. Our findings demonstrate the genetic diversity among the evaluated genotypes and provide evidence for heterotic groups in popcorn. Furthermore, the functional genetic diversity indicates that there are informative genetic markers for popcorn.

Key words: EST-SSR; Topcross; *Zea mays* L. var. Everta