

Efficiency of RAPD versus SSR markers for determining genetic diversity among popcorn lines

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ABSTRACT. Using only one type of marker to quantify genetic diversity generates results that have been questioned in terms of reliability, when compared to the combined use of different markers. To compare the efficiency of the use of single versus multiple markers, we quantified genetic diversity among 10 S₇ inbred popcorn lines using both RAPD and SSR markers, and we evaluated how well these two types of markers discriminated the popcorn genotypes. These popcorn genotypes: "Yellow Pearl Popcorn" (P1-1 and P1-5), "Zélia" (P1-2 and P1-4), "Curagua" (P1-3), "IAC 112" (P9-1 and P9-2), "Avati Pichinga" (P9-3 and P9-5), and "Pisankalla" (P9-4) have different soil and climate adaptations. Using RAPD marker analysis, each primer yielded bands of variable intensities that were easily detected, as well as non-specific bands, which were discarded from the analysis. The nine primers used yielded 126 bands, of which 104 were classified as polymorphic, giving an average of 11.6 polymorphisms per primer. Using SSR procedures, the number of alleles per locus ranged from two to five, giving a total of 47 alleles for the 14 SSR loci. When comparing the groups formed using SSR and RAPD markers, there were similarities in the combinations of genotypes from the same genealogy. Correlation between genetic distances obtained through RAPD and SSR markers was relatively high (0.5453), indicating that both techniques are efficient for evaluating genetic diversity in the genotypes of popcorn that we evaluated, though RAPDs yielded more polymorphisms.

Key words: *Zea mays*; DNA markers; RAPD and *SSR* loci; Microsatellites; Comparative analysis of molecular groups