



Genetic diversity of popcorn genotypes using molecular analysis

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ABSTRACT. In this study, we analyzed dominant molecular markers to estimate the genetic divergence of 26 popcorn genotypes and evaluate whether using various dissimilarity coefficients with these dominant markers influences the results of cluster analysis. Fifteen random amplification of polymorphic DNA primers produced 157 amplified fragments, of which 65 were monomorphic and 92 were polymorphic. To calculate the genetic distances among the 26 genotypes, the complements of the Jaccard, Dice, and Rogers and Tanimoto similarity coefficients were used. A matrix of D_{ij} values (dissimilarity matrix) was constructed, from which the genetic distances among genotypes were represented in a more simplified manner as a dendrogram generated using the unweighted pair-group method with arithmetic average.

Clusters determined by molecular analysis generally did not group material from the same parental origin together. The largest genetic distance was between varieties 17 (UNB-2) and 18 (PA-091). In the identification of genotypes with the smallest genetic distance, the 3 coefficients showed no agreement. The 3 dissimilarity coefficients showed no major differences among their grouping patterns because agreement in determining the genotypes with large, medium, and small genetic distances was high. The largest genetic distances were observed for the Rogers and Tanimoto dissimilarity coefficient (0.74), followed by the Jaccard coefficient (0.65) and the Dice coefficient (0.48). The 3 coefficients showed similar estimations for the cophenetic correlation coefficient. Correlations among the matrices generated using the 3 coefficients were positive and had high magnitudes, reflecting strong agreement among the results obtained using the 3 evaluated dissimilarity coefficients.

Key words: Genetic diversity; Random amplification of polymorphic DNA; *Zea mays*