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MOLECULAR CHARACTERIZATION OF A SET OF TROPICAL MAIZE INBRED LINES FROM A PUBLIC BREEDING PROGRAM IN BRAZIL

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RESUMO

The characterization of genetic diversity and population differentiation for maize inbred lines from breeding programs is of great value in assisting breeders in maintaining and potentially increasing the rate of genetic gain. In our study, we characterized a set of 187 tropical maize inbred lines from the public breeding program of the Universidade Federal de Viçosa (UFV) in Brazil based on 3,083 single nucleotide polymorphisms (SNP) markers to evaluate whether this set of inbred lines represents a panel of tropical maize inbred lines for association mapping analysis and investigate the population structure and patterns of relationships among the inbred lines from UFV for better exploitation in our maize breeding program. Our results showed that there was large genotypic variation in the set of tropical maize inbred lines from the UFV maize breeding program. We also found high genetic diversity ($GD=0.34$) and low pairwise kinship coefficients among the maize inbred lines (only approximately 4.00% of the pairwise relative kinship was above 0.50) in the set of inbred lines. The LD decay distance over all ten chromosomes in the entire set of maize lines with $r^2=0.1$ was 276,237 kb. Concerning the population structure, our results from the model-based STRUCTURE and principal component analysis methods distinguished the inbred lines into three subpopulations, with high consistency maintained between both results. Additionally, the clustering analysis based on molecular data grouped the inbred lines into 22 genetic divergence clusters. Our results indicate that the set of tropical maize inbred lines from UFV maize breeding programs can comprise a panel of tropical maize inbred lines suitable for a genome-wide association study to dissect the variation of complex quantitative traits in maize, mainly in tropical environments. In addition, our results will be very useful for assisting us in the assignment of heterotic groups and the selection of the best parental combinations for new breeding crosses, mapping populations, mapping synthetic populations, guiding crosses that target highly heterotic and yielding hybrids, and predicting untested hybrids in the public breeding program UFV.

PALAVRAS-CHAVE: Zea mays L, Genetic relationships, Genetic diversity, Population structure, Linkage disequilibrium, Heterotic groups, Commercial hybrids

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