Population structure and genetic diversity of maize inbreds derived from tropical hybrids

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ABSTRACT. The objectives of this study were to identify the population structure and to assess the genetic diversity of maize inbreds. We genotyped 81 microsatellite loci of 90 maize inbreds that were derived from tropical hybrids and populations. The population structure analysis was based on a Bayesian approach. Each subpopulation was characterized for the effective number of alleles, gene diversity, and number of private alleles. We also performed an analysis of molecular variance and computed a measure of population differentiation ($F_{ST}$). The genetic distances were computed from the similarity index of Lynch and the dissimilarity measures proposed by Smouse and Peakall. The cluster analyses were based on the unweighted pair-group method using arithmetic averages and Tocher method. The clustering efficiency was assessed by the error rate of the discriminant analysis. We also performed a principal coordinates analysis. The population structure analysis revealed three tropical heterotic pools, which have
been used by worldwide and Brazilian maize seed companies. The degree of genetic differentiation and of intra- and inter-population genetic diversity for these tropical heterotic pools are comparable to that observed for temperate and subtropical heterotic pools. The higher allelic frequency variation within each tropical heterotic pool and the high genetic diversity between the inbreds were evidence of heterotic groups within the main tropical heterotic pools.

**Key words:** Heterotic pools; Genetic diversity; Clustering; Microsatellites