Genetic diversity and population structure assessed by SNP markers in a panel of maize inbred lines

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The study of genetic diversity and population structure provides a better understanding of the genetic relationship between individuals in a population. In plant breeding, information about the genetic distance between individuals orients the selection of parents in order to allow a better use of the genetic variability. In association studies, the correction for population structure is important to control the identification of false associations between phenotype and genotype (type I error). Thus, the aim of this study was to investigate the genetic diversity and population structure in a set of 132 maize inbred lines from the Embrapa Maize and Sorghum breeding program. Genomic DNA of these lines was extracted and genotyped with 1,250 SNPs using the KASP method, through the LGC Genomics. A total of 719 SNPs showing less than 20% of missing data, and minor allele frequency (MAF) higher than 10% was selected for this study. Clustering analysis was performed based on the UPGMA method, considering the Rogers Dissimilarity Coefficient available in the software PowerMaker. Population structure was evaluated using the software STRUCTURE, considering a burn-in period of 250,000 and 500,000 iterations with three replicates, assuming admixture model, with a number of subgroups (k) ranging from 2 to 10. An integrated analysis suggested that this maize panel was likely to be composed by four subpopulations (k = 4), one group of Flint lines related to L3, another group of Dent lines related to L228-3, a third group of recently developed materials associated to L371101-2 also behaving as Dent, and a larger group formed by the remaining lines. This grouping is highly consistent with the pedigree data. We expect that results of the present analysis can be directly used by breeding programs to better explore the genetic variability within the heterotic groups to develop new lines and between the groups to generate promising hybrids. Moreover, the information generated herein will be useful to correct type I errors in association mapping analysis. Financial Support: Generation Challenge Programme, FAPEMIG, CNPq and Embrapa