GENOTYPING OF SOYSNP6K, POPULATION STRUCTURE AND RELATEDNESS OF A WHOLE COLLECTION OF TROPICAL SOYBEAN

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Soybean (Glycine max L.) is an annual, self-pollinated species, whose production in Brazil has the potential to become the largest in the world, because genetic improvements have been able to develop new varieties adapted to low latitudes and pest resistant. In fact, farmers and breeders have been selected carefully cultivars based on agronomic traits and consistency in yield through the time. However, the current Brazilian soybean germplasm pool is the result of several cycles of selection and effective recombination among a relatively small number of genotypes selected from the USA cultivars. This frequent selection, admixed population, and the crossing of a small number of cultivars in the Brazilian soybean breeding programs can lead to increase the genetic relationship and affect the patterns of population structure. For this, our goal was to estimate the levels of population structure and assess population relatedness of a whole collection of tropical soybean. Thus, we genotyped 169 cultivars of a tropical soybean collection, by using an Infinium iSelect HD Custom Genotyping BeadChip of 6k (Illumina Inc., San Diego, CA, USA). Population structure was estimated under the Markov Chain Monte Carlo (MCMC) algorithm for the generalized Bayesian clustering method implemented in InStruct software, and pairwise molecular coancestry among subpopulations was performed according to Reynolds distance by using Arlequin software. A high coverage of the tropical soybean genome was obtained with the BeadChip 6k of SNPs. In mean 247.5 SNPs markers were found by chromosome, with variation from 198 (chromosome 1) to 323 (chromosome 8). According to the posterior bayesian clustering analysis implemented in InStruct, the most probable number of subpopulations was 9. The average molecular coancestry among the pairwise subpopulation comparisons was 0.234 in the tropical soybean collection as a whole. Approximately 60% of the pairwise coancestry estimates were lowest to 0.23 (Mean=0.196), 30% ranged from 0.24 to 0.3 (Mean=0.264), and 1% was higher than 0.31 (Mean=0.332). Each subpopulation (K=9) contained admixed cultivars that come from different soybean genetic breeding programs of Brazil. In fact, this result confirms the shared genetic base among the public and private breeding programs of soybean in Brazil. In addition, the most of cultivars had moderate to strong relatedness among subpopulations of tropical soybean collection. This result was expected because previous studies indicate that the Brazilian soybean ancestors have a narrow genetic base, with only four ancestors, representing approximately 48% of the overall genetic base. In addition, these results will be relevant for the management of breeding programs of tropical soybean and to assist in the application of genome-wide association studies and high-resolution genetic linkage maps of important traits.

Keywords: Coancestry, breeding, soybean germplasm, Genotyping.