GENETIC DIVERSITY AND ASSOCIATION MAPPING IN SOYBEAN

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The recent advances in DNA sequencing have allowed a wide access to genomic variation in several plant species. The soybean reference genome was published few years ago, and several efforts of genome re-sequencing have led to the identification of a large number of allelic variations, as Single Nucleotide Polymorphism (SNP). However, re-sequencing of a large number of samples is still a costly approach. Recently, one of the approaches being used to identify these genomic variations is Genotyping by Sequencing (GBS) technique, which is a system that allows the partial sequencing of a large number of samples in a multiplex fashion. With the objective of identifying SNPs in the soybean genome, we have analyzed 239 Brazilian cultivars and 180 soybean access by GBS. In order to validate this method as a mapping tool, we have mapped qualitative and quantitative traits in soybean, such flower and pubescence color and Root Knot Nematode (*Meloidogyne incognita*) resistance. This study allowed the identification of a large number of high confidence SNPs in both population sets. By using an association mapping approach, the flower color and pubescence color were mapped on the same regions as previously published (chromosomes 13 and 06 respectively). This study also confirmed the presence of a major locus associated to nematode resistance on chromosome 10. In addition, this study allowed the evaluation of soybean Brazilian germplasm diversity at genomic level, proving to be very useful for breeding programs.