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SNP discovery, mapping and utilization for soybean genome sequencing

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Genome duplication is a common phenomenon in studying evolution of plants. The objectives in this study were to achieve a comprehensive understanding of the effects of gene duplication with single nucleotide polymorphisms (SNPs) using primers designed from soybean tentative consensus (TC) sequences. After direct sequencing of PCR products amplified with genomic DNA of 'Pureunkong' and 'Jinpumkong 2', sequences from four out of eight primer sets could not determine nucleotide sequences at the specific positions because of noisy peaks, although they appeared to be a single PCR product. The rest of primer sets produced two PCR fragments. After TA cloning with excised individual bands from each primer set, ten independent clones were chosen randomly for sequencing. With seven primer sets, sequences were separated into two or three groups in each genotype, even though they were produced from the same primer. However, one kind of partial sequence from TC144678 was present in Pureunkong, whereas Jinpumkong 2 had two different sequences. Producing multiple products leaded to poor sequencing results in direct sequencing, indicating the amplification of members of a gene family. A comparison of the paralogous sequences revealed that the sequence similarities between duplicated regions were conserved. With previously detected SNPs, the construction of a genetic map using RILs derived from the cross of Pureunkong × Jinpumkong 2 is in progress to confirm the presence and location of duplicated regions on specific linkage groups. In soybean genome sequencing by BAC clones, homologous BAC clone rather than the targeted region could be selected because soybean genome is duplicated. So, BAC clone selection by SNP markers is needed for increasing the accuracy. An understanding of gene duplication in a species should provide valuable insights into its evolutionary history and genome structure.