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Genetic diversity analysis in soybean [*Glycine max* (L.) Merrill] using simple sequence repeat (SSR) markers

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SUMMARY

The genetic diversity studies using SSR markers revealed that among the primers used, Satt207 and Satt135 produced a maximum of four alleles. PIC was highest for the SSR primer Satt207 which indicated that the primer Satt 207 might be an effective and useful tool to determine the genetic differences among the soybean accessions and to study the phylogenetic relationship. The SSR marker profiles resulted in fifteen clusters at nearly 77 per cent similarity. Cluster V consisted of 15 accessions followed by VIII cluster with six genotypes. The formation of 15 clusters through SSR data revealed that the presence of genetic diversity at molecular level was high among the selected germplasm.

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Soybean [*Glycine max* (L.) Merrill] is a marvellous world's leading economic oilseed crop and ranks first among the oilseeds in the world. It is unique in being a legume-cum-oilseed crop. Soybean is the world's foremost provider of vegetable proteins (42%) and oil (20%), Hence it is called miracle golden bean of the 21st Century. A rapid advancement in DNA based marker techniques has proven to be powerful in genetic diversity estimation. These markers are highly heritable, available in high numbers and often exhibit enough polymorphism to discriminate even closely related genotypes. The DNA based markers have largely overcome the problems encountered with morphological and biochemical markers. Among the DNA markers, PCR based DNA marker like SSR share a number of general advantages over other markers. The major advantages are the speed with which results are generated, low amounts of genomic DNA required and the ability to share the information on primer sequences without the need to exchange DNA. Microsatellites or simple sequence repeats (SSRs) that consist of tandemly repeated core sequences which often vary in repeat number and are flanked by conserved DNA sequences. (Maughan *et al.*, 1995).Therefore, under present investigation, effort was made to understand molecular diversity present in a set of 50 elite soybean accessions.

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MATERIALS AND METHODS

The Experiment was conducted during *Rabi* 2009-10. Fifty accessions of soybean germplasm maintained in the Department of Pulses, Centre for Plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University (TNAU), Coimbatore were utilized. The list of accessions taken for study is presented in Table 1.

SSR primers screening:

Eleven SSR primers from first base (Mumbai) were initially screened for their repeatable amplification with five accessions. Primers were selected for further analysis