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## Assessment of genetic diversity and inheritance studies for pre-harvest sprouting resistance in soybean (*Glycine max* L. Merr.)

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A set of 43 diverse soybean genotypes consisting of improved varieties, breeding lines and some indigenous genotypes of North East India were subjected to analysis of genetic diversity along with screening and inheritance study of resistance to Pre-Harvest Sprouting (PHS).

Genetic diversity was studied based on eighteen morpho-physiological attributes and 28 polymorphic SSR markers. Variability parameters estimated for the eighteen traits displayed significant variation for all the traits. Per cent seed germination in pods (SGP) was considered as a measure of PHS tolerance. Both genotypic (GCV= 293.6) and phenotypic level (PCV= 45.08), the highest coefficient of variation was exhibited by SGP followed by seed germination and pods per plant. Character association studies revealed significant and positive association of PHS with seed germination per cent and number of branches. Highest positive direct effect on PHS was observed for number of clusters followed by seed germination (%) and pods per cluster.

D2 analysis followed by grouping of genotypes by Tocher's method resulted into grouping of the genotypes into seven distinct clusters. Highest contribution to diversity was exhibited by pod diameter (33%) followed by seed weight (22%) and pod length (15%).

The set of genotypes were also subjected to analysis of diversity with a set of 28 polymorphic Simple Sequence Repeat (SSR) markers. A total of 190 scorable bands in the 43 genotypes were studied. The number of alleles per primer varied from 2 to 12 with an average of 3.2 alleles per locus and the percentage of polymorphism varied from 14.29% to 100%. The PIC values ranged from 0.2688 (Sat\_211) to 0.8562 (Sat\_356) with an average of 0.6692. Most of the SSR markers had PIC value greater than 0.3 and hence these can be reported as the most informative markers. The diversity detected by the markers were evaluated by parameters Shanon -Weaver Diversity index and Gene Diversity.

Principal component analysis performed for the 43 soybean genotypes using 190 alleles of the twenty-eight SSR markers revealed clear diversity among the genotypes under study. The pairwise genetic similarity ranged from 0.21 to 0.81. Cluster analysis based on the SSR markers grouped 43 genotypes into eleven diverse clusters at 35% similarity level.

Pre-harvest sprouting is a major setback to soybean production under high rainfall condition of the North East Part of the country including Assam. This causes major yield loss to the crop and results in the degradation of seed quality. In order to expand soy cultivation in this nonconventional part of the country, it is very important to study the genetics and inheritance pattern of PHS. In the present investigation, soybean genotypes under study were screened for incidence of Pre-Harvest Sprouting (PHS) and scored on a scale of 0-9. Twenty-two entries showed significant susceptibility to PHS while the rest 21 entries were resistant to PHS sprouting under the same environmental conditions. This study revealed the presence of resistance to PHS paving the way for an attempt to study the inheritance pattern of PHS resistance in soybean. Nine cross combinations between highly resistant and susceptible exhibited complete resistance in F1 with score zero (0). The F2 populations exhibited segregation for PHS resistance in a definite 3 (Resistance): 1(Susceptible) ratio which was confirmed by Chi-square ( $\chi^2$ ) test. This confirmed that the resistance to PHS was governed by a single dominant gene.

### Speaker Biography

M K Sarma is the Plant Breeding and Genetics Coordinator of the Advanced Level Biotech Hub, and also the Professor in the Assam Agricultural University. He has been performing research in the field of Plant Breeding and Genetics for 23 years. He was also the visiting scientist to the Molecular Genetics and Genomics Laboratory, Chungnam National University, South Korea. He has published 65 Research Papers and 10 Chapters.

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