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Genetic Diversity Studies in Soybean [*Glycine max* (L.)Merrill] Genotypes

K. Soniasabanam[1], Ashna Akbar[1] and H P Chaturvedi[1]

[1]Department of Genetics and Plant Breeding, Nagaland University, SASRD- Medziphema- 797106

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Abstract:

Genetic diversity among 20 soybean genotypes was worked out using Mahalanobis D^2 statistic. On the basis of genetic distance, the twenty genotypes were grouped into 5 clusters. Out of the 20 genotypes cluster II has the highest genotypes (9) followed by cluster III (4), cluster I and cluster IV (3 each) and cluster V had 1 genotype. The inter cluster divergence was observed to be highest between Cluster I and Cluster IV indicating that these two clusters were genetically diverse. Hence, the genotypes of Cluster I and Cluster IV could be utilized in hybridization program to achieve greater variability in the segregating generations. Among the different characters studied test weight followed by plant height, number of pods per plant and days to 50% flowering contributed maximum towards divergence.

Key words: Cluster, D^2 values, Genetic divergence, Soybean

Introduction:

Soybean is a miracle crop containing about 40% protein and 20% oil and plays an important role in the world food system. It also contains a good amount of minerals, salts and vitamins and its sprouting grains contains a considerable amount of vitamin C. Vitamin A is present in the form of precursor carotene which is converted into vitamin A in the intestine. It has become the major source of edible vegetable oils and of high protein feed and food supplements in the world. In fact, it is one of the nature's most efficient protein producers. It produced about three times more than rice, wheat or maize on per hectare production basis. Soybean is also called as "*Wonder crop*" and "*Meat for poor*". It is the richest, cheapest and easiest source of best quality protein and fats. It is also an excellent source of good quality unsaturated oil. Soybean provides a cheaper and high protein rich alternative substitute to animal protein. It is an important crop in the world and has been the dominant oilseed since the 1960s (Smith and Huyser, 1987). In any crop, germplasm is a valuable source of base population and provides the scope for wider adaptability. However, to understand the useable variability, grouping or classification of genetic stocks based on minimum divergence or resemblance between them is quite imperative. The nature and magnitude of genetic divergence helps the plant breeder in choosing the right type of parents for higher amount of heterotic expression in F_1 and broad spectrum of variability in subsequent segregation generations (Maurya and Singh, 1977). Therefore, the present study was carried out to analyze the genetic diversity among soybean

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esponding author's e-mail:hpchaturvedi68@gmail.com

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genotypes in order to select the potential parents for breeding program.

Materials and Methods:

The present investigation was carried out in the experimental farm of Nagaland University, School of Agricultural and Rural Development, Medziphema Campus, Nagaland. The period of crop growth cycle was for seven months *i.e*. from June to December 2016. The experiment was laid out in Randomized Block Design with twenty genotypes in three replication. All the seeds of twenty genotypes were collected from North Eastern Region of India including commercial one. Recommended Standard agronomic practices and plant protection measures were undertaken. Observations were recorded on five randomly sampled plants in each replication on Days to 50% flowering, Days to 80% maturity, plant height, Number of primary branches, Pod length, Number of pods per plant, Number of seeds per pod, 100 seed weight and Seed yield per plant.The genetic divergence was estimated using Mahalanobis's D^2 statistics (Mahalanobis, 1936). All the genotypes were grouped into clusters on the basis of D^2 values, by using Tocher's method (Rao, 1952).

Result and Discussion:

Analysis of variance revealed significant variation among the 20 genotypes for all the characters. The genetic divergence was estimated by utilizing D^2 statistic proposed by Mahalanobis (1936). Using this technique, all the genotypes were grouped into 5 clusters. Out of the 20 genotypes cluster II has the highest genotypes (9) followed by cluster III (4), cluster I and cluster IV (3 each) and cluster V had 1 genotype

Table-1 Clustering pattern of 20 genotypes of soybean on the basis of genetic divergence

Cluster Number	No. of Genotypes	Genotypes
I	3	Manipur local (small), CAU-SLC-3 (small), Arunachal Pradesh (Jia-Olivia)
II	9	Manipur local (medium), Okhra-1, NRC 67, RNS-2001-04, JS2029, CAU-SLC-1W, Dimapur, CAU-SLC-1, Mungshvur (Mimi village- KiphireDist)
III	4	Arunachal Pradesh (West Siang- Ado), Assam, Longphea (Mon Dist), CAU-SLC=2
IV	3	Manipur local (large), Himso 1685, CAU-SLC-1/P (Bold)
V	1	JS 9305

The inter cluster distance were greater than intra cluster distance revealing considerable amount of genetic diversity among the genotypes studied as shown in Table: 2.The results indicated that the genotypes from the same geographical locations were grouped in different clusters as revealed by Cluster I, II, III, IV and V. The collections which originated from different places were in the same cluster and distribution of the genotypes from the same place into different clusters, suggested that the pattern of grouping of genotypes was independent of their geographical distribution. The clustering pattern of the genotypes indicated that geographical diversity had no significant impact on genetic diversity. This was in agreement with the findings of Govanakoppa et al. (2002) and Chaturvedi et al. (2011). The inter cluster divergence was observed to be highest between Cluster I and Cluster IV (90.2) indicating that these two clusters were genetically diverse. Hence, the genotypes of Cluster I and Cluster IV could be utilized in hybridization program to achieve greater variability in the segregating generations. The inter cluster divergence was minimum between Cluster I and Cluster III (10.86) indicating close relationship between the genotypes belonging to these clusters.

Table-2 Average intra and inter cluster distance

Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	5.2	35.73	10.86	90.2	44.22
Cluster 2		6.96	18.68	25.86	15.23
Cluster 3			2.31	50.87	31.59
Cluster 4				6.45	35.96
Cluster 5					0

The cluster mean shown in Table- 3 revealed that there is a considerable difference between the clusters for all the characters studied. Cluster I recorded highest cluster mean for days to 50% flowering, days to 80% maturity and pod length. Cluster III recorded highest cluster mean for plant height, number of pods per plant and yield per plant. Cluster IV recorded highest cluster mean for test weight. Cluster V recorded highest cluster mean for number of primary branches and number of seeds per pod. The percent contributions by each character to total genetic divergence are presented in Table- 4. Among the different characters studied test weight followed by plant height, number of pods per plant and days to 50% flowering contributed maximum towards divergence.

Table- 3 Cluster wise mean value of 9 parameters in soybean.

Clusters	Days to 50% flowering	Days to 80% maturity	Plant height (cm)	Number of primary branches	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Test weight	Yield per plant
Cluster 1	92.02	160.8	81.98	3.71	90.62	3.84	2.36	4.48	45.07
Cluster 2	62.56	105.32	39.66	4.25	82.7	3.37	2.33	13.62	53.61
Cluster 3	87.13	152.43	91.92	4.24	98.75	3.78	2.35	9.44	91.13
Cluster 4	63.2	103.64	54.78	3.98	68.6	3.82	2.36	22.15	56.01
Cluster 5	55.73	84.83	23.73	10.8	22.1	3.1	2.93	15.26	23.94

Table- 4 Contribution of different characters towards divergence

Characters	Percentage contribution.
Days to 50% flowering	4.21%
Days to 80 maturity	0.53%
Plant height (cm)	14.21%
Number of primary branches	1.58%
Number of pods per plant	6.32%
Pod length(cm)	1.05%
Number of seeds per pod	3.68%
Test weight	65.26%
Yield per plant	3.16%

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