

**RESEARCH ARTICLE :**

Genetic divergence in soybean [*Glycine max* (L.) Merrill] during *Rabi* season

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SUMMARY : Genetic diversity studies are a prerequisite for any breeding programme as it helps in selection of diverse parents which is essential for a successful hybridization programme. The present investigation was carried out using twenty four genotypes of soybean to identify the diversity of soybean genotypes for morpho-agronomic traits. The analysis of variance studies were highly significant for all the characters studied except number of branches per plant and number of pods per plant. The genotypes were grouped in 5 five clusters and genotypes in cluster IV can be used for direct adoption or in the hybridization programme to develop superior genotypes. Among the various morpho-agronomic traits days to 50% flowering, seed yield and 100 seed weight has contributed maximum for genetic diversity for the characters studied.

KEY WORDS :

Soybean, Morpho-agronomic characters, Cluster analysis, Genetic diversity

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BACKGROUND AND OBJECTIVES

Genetic diversity plays a key role in selection of parents as hybrids between lines of diverse origin produce greater heterosis and desirable segregants. The main aim of cluster analysis is to maximize the homogeneity within groups and the heterogeneity between groups (Hair *et al.*, 2005). D² analysis aims at selection of genetically diverse parents and evaluation of a large number of germplasm lines at a time. The genetic diversity on yield related traits was evaluated in genotypes of soybean (Malik *et al.*, 2006 and 2007 and Ngon *et al.*, 2006).

RESOURCES AND METHODS

Twenty four genotypes of soybean were evaluated in a Randomized Block Design with two replications during *Rabi* 2013-14. Each entry was grown in four rows of four meters length with a spacing of 30 x 10 cm. All the recommended package of practices were followed for raising a healthy crop. Data was recorded for eight morpho-agronomic characters *viz.*, days to 50% flowering, plant height, number of branches per plant, number of nodes per plant, number of clusters per plant, number of pods per plant, 100 seed weight and seed yield. Observations on days to 50% flowering and seed yield were recorded on per plot basis. The D² analysis

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was carried out for these characters to access genetic divergence using Mahalanobis's D^2 statistics (Mahalanobis, 1936). The genotypes were grouped on the basis of minimum generalized distance using the Tocher's method (Rao, 1952).

OBSERVATIONS AND ANALYSIS

Analysis of variance was found to be significant for all the characters studied except number of branches per plant and number of pods per plant. Based on D^2 statistics the 24 genotypes were grouped in 5 clusters and the distribution of genotypes into different clusters is given in Table 1. The genotypes within the clusters have smaller D^2 values among themselves than between

the clusters. Cluster II comprised of 14 genotypes; followed by cluster I with 7 genotypes and cluster III, IV and V had single genotypes each. Genotypes of different origins were included in one cluster indicating that there is no relationship between genetic diversity and geographical distribution of the genotypes. Murthy and Arunachalam (1966) stated that genetic drift and selection in different environments could cause greater genetic diversity than geographic distance.

The average intra and intercluster distance (D) between two populations varied from 0.00 to 6.8 and 6.18 to 14.4, respectively (Table 2). The maximum inter cluster distance was found between cluster I and II (D=14.4) followed by clusters II and IV (D=14.38) and clusters II and V (D=13.51). The last three clusters are

Table 1 : Distribution of twenty four soybean genotypes into various clusters

Clusters numbers	Number of genotypes	Genotype details
I	7	NRC 2007 2-19,RKS 18, AYT II RI, AMS MB 5-18, AMS MB 5-19, BASAR, GP 13
II	14	KDS 344,BHEEM, JS 335, DSB 21, NRC 2007 A-3-1, NRC 2008 B-26, LSB 23, DS 2614, AMS 243, NRC 2007 A-2-3, JS 93-05
III	1	KS 103
IV	1	NRC 2011 F-1-15
V	1	GP 18

Table 2 : Average inter and intra cluster (diagonal) distance values in twenty four soybean genotypes

Clusters	I	II	III	IV	V
I	5.85	14.4	8.83	12.04	10.02
II		6.8	10.41	14.38	13.51
III			0.00	6.18	9.22
IV				0.00	11.69
V					0.00

Table 3 : Cluster means for morpho- agronomic characters in twenty four soybean genotypes

Clusters	Days to 50 % flowering	Plant height (cm)	Number of branches/plant	Number of nodes/plant	Number of clusters/plant	Number of pods/plant	100 seed weight (g)	Seed yield (q/ha)
I	55.86	33.90	3.83	8.03	7.14	22.89	12.64	14.73
II	50.18	28.80	3.58	7.33	7.61	31.35	10.07	12.44
III	54.00	43.30	4.60	10.80	11.4	34.70	9.60	27.08
IV	55.50	30.10	4.10	9.20	13.6	53.40	9.48	38.96
V	53.00	27.50	3.30	7.70	11.7	38.70	11.17	9.19
Mean	52.33	30.94	3.70	9.77	8.05	30.25	10.82	14.688
S.E.±	0.2918	2.861	0.7190	1.182	0.988	4.553	0.588	2.266
C.V %	0.7885	13.077	27.450	21.516	17.346	21.291	7.684	21.820
Percentage contribution of characters towards total divergence								
Number of times appearing first	14.9	6	1	3	5	8	20	44
% contribution	53.99	2.17	0.36	1.09	1.81	2.9	7.25	15.94

solitary which had only single genotype with their intra cluster distance zero. Arunachalam (1981) established that more genetically diverse the parents used in a hybridization programme, the greater will be the chance of obtaining high heterotic hybrids and broad spectrum variability. Therefore in the present study based upon large cluster distances it is advisable to attempt crossing of genotypes of cluster I,IV and V with genotypes of cluster II having large number of genotypes is the cluster which may lead to favorable genetic variability for seed yield improvement in soybean.

Variation for several characters among single as well as multi genotypic clusters was observed (Table 3). The results revealed that days to 50% flowering contributed maximum (53.99%) towards divergence and was responsible for differentiating the genotypes. Seed yield (q/ha) (15.94) and 100 seed weight (7.25) were also important traits contributing to total divergence. These three characters contributed 77.1 % of total diversity in the material studied. On the other hand rest of the traits had lower contribution (below 5%) towards the total genetic divergence. Hence selection for divergent parents based on these characters would be useful for heterosis breeding in soybean. Malik *et al.* (2006) reported that pods per plant (29.47%), branches per plant (31.72%), 100-seed weight (39.01%) and grain yield per plant (46.55%) contributed to a high level of diversity among the soybean accessions. Moe and Girdthai (2013) reported that number of filled pods per hill (39.40%), yield per hill (45.6%) and harvest index (32.2%) showed a high level of diversity among the soybean genotypes.

The cluster IV got desirable rating in respect of seed yield (q/ha), number of pods per plant, number of clusters per plant, while cluster III had desirable rating for number of branches per plant, number of nodes per plant and plant height. Cluster I had desirable rating for 100 seed weight. The genotypes with high mean values of characters in any cluster as well as high D^2 values between clusters can be used either for direct adoption or for hybridization programme in order to breed for better genotypes of soybean.

Conclusion :

The various morpho-agronomic characters studied

was found to be significant except number of branches per plant and number of pods per plant. The characters *viz* days to 50% flowering, seed yield and 100 seed weight has contributed maximum for genetic diversity for the characters studied. The genotypes in cluster IV can be used for direct adoption or in the hybridization programme to develop superior genotypes.

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