

## Genetic diversity studies in soybean [*Glycine max* (L.) Merrill] based on morphological characters

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(Received: October, 2010; Accepted : November, 2010)

From the genetic diversity studies based on 12 morphological characters of 50 soybean genotypes it could be inferred that, the traits seeds per plant and seed yield per plant contributed maximum to the genetic diversity. The clustering pattern revealed that there was no correlation between the geographical diversity and genetic diversity. The clusters IX (JS 90-29 and IC18277) and X (IC93656) were the distant clusters and clusters III (IC 39873 and IC 93751) and VIII (IC 34057 and IC 18736) were the nearest clusters. The clusters IX and I possessed the high mean values for many of the traits studied. With respect to seed yield per plant the clusters IX, VI and I were the superior clusters. The entries viz., JS 90-29 and IC18277 of IX cluster and IC93656 of X cluster can be used in crossing programme for development of good recombinants for seed yield.

Key words : Soybean, Diversity, Cluster, Dendrogram

Shadakhari, T.V., Kalaimagal, T., Senthil, N., Boranayaka, M.B., Kambe Gowda, R. and Rajesh, G. A. (2011). Genetic diversity studies in soybean [*Glycine max* (L.) Merrill] based on morphological characters. *Asian J. Bio. Sci.*, **6** (1) : 7-11.

### INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] with its varied uses is known as a wonder crop among the legumes. It is cultivated primarily for oil and protein. The yield of soybean is higher than that of other pulse crops. Because of its richness in oil, protein and therapeutic components, soybean becomes the raw material for various industries. The information on genetic diversity, which helps in choosing parents for generation of new varieties, needs continuous evaluation of germplasm for useful characters, which in earlier days was solely based on the available morphological data. Morphological traits/markers reflect not only on the genetic composition of the cultivar, but also the interaction of the genotype with the environment in which it is expressed. Therefore, under present investigation, effort was made to understand the quantum and nature of genetic variability present in a set of 50

elite soybean accessions.

### RESEARCH METHODOLOGY

The experiment was conducted during *Rabi* 2009-10. Fifty soybean genotypes were maintained in the Department of Pulses, Millet Breeding Station, Centre for Plant Breeding and Genetics, Tamil Nadu Agriculture University, Coimbatore were utilized for analysing morphological diversity. The list of accessions taken for study is appended in Table 1. Morphological characters viz., days to 50% flowering, plant height, number of primary branches per plant, number of pod clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, number of seeds per plant, hundred seed weight, seed yield per plant, days to maturity and harvest index were recorded on five randomly selected plants for different characters on each genotype

**Table 1: List of soybean accessions taken for genetic diversity study**

Sr. No.	ACC. NO	Sr. No.	ACC. NO
1.	IC2574	26	NRC 51
2.	PK 731	27	IC25166
3.	NRC 21	28	HIMS0 1565
4.	IC 9311	29	JS 92-22-A
5.	IC 18596	30	IC7361
6.	IC 110399	31	PK 258
7.	TNAU 20049	32	IC 2048
8.	SL 525	33	JS(SH)93-37
9.	JS 92-22	34	VLS 53
10.	JS 335	35	JS (SH) 91-93
11.	RKS -18	36	IC 216380
12.	AMSS 34-A	37	JS 90-29
13.	IC14467-A	38	MACS 715
14.	JS 148	39	JS 95-98
15.	UGM-73	40	IC18277
16.	PLSO 90	41	IC 62376-A
17.	JS99-02	42	JS (SH) 89-49
18.	PK257	43	IC 39873
19.	IC2572-A	44	IC16040
20.	IC25167	45	IC34057
21.	IC100790	46	IC15969
22.	TNAU 20037	47	IC18736
23.	JS (SH) 99-02	48	IC93751
24.	JS 89-24	49	IC93752
25.	IC 1024	50	IC93656

in all the three replications. The replicated data were subjected to genetic divergence analysis using Mahalanobis's  $D^2$  - statistic (Mahalanobis 1936) as suggested by Rao (1952). All the soybean accessions were grouped into respective clusters on the basis of

values following Tochers method.

## RESULTS AND ANALYSIS

$D^2$  analysis was carried out using all the twelve characters and generalized distance ( $D^2$ ) was calculated for each pair of genotypes among 1225 possible combinations. A method suggested by Tocher (Rao, 1952) was used to group the genotypes into different clusters based on the  $D^2$  values. 50 germplasm accessions were grouped into 10 clusters. Among 10 clusters, cluster II was the largest with 16 genotypes followed by cluster I with 12 genotypes. Cluster V and VII had 8 and 3 genotypes, respectively. Cluster III, IV, VI, VIII and IX had 2 genotypes each. Cluster X was solitary. The clustering composition and the distribution of genotypes into different clusters are presented in Table 2. Fifty soybean accessions were used to construct dendrogram based on Jaccard's coefficient and the results are presented in Fig 1.

$D^2$  values of intra and inter cluster D square values are given in Table 3. Maximum difference among the genotypes within the same cluster (intra cluster) was shown by cluster I (925.545) followed by cluster V (919.925), cluster VII (753.203), cluster IX (691.223), cluster II (591.154), cluster VI (59.739), cluster IV (48.332) and cluster III (45.186). Diversity among the clusters varied with inter cluster D square values of 266.431 to 3424.063. The cluster IX and X (3424.063) showed maximum inter cluster values followed by IX and IV (2110.150), X and VII (2094.742), V and X (1827.459), I and X (1635.125), and VII and IX (1625.492). The lowest inter cluster distance was noticed between cluster III and VIII (266.431).

Intra and inter cluster distance values are given in

**Table 2: Cluster composition of soybean genotypes based on D square analysis of morphological traits**

Cluster No.	No. of accessions	List of accessions included
I	12	IC2574, PK731, NRC21, IC9311, IC18596, IC110399, TNAU20049, SL525, JS92-22, JS335, RKS-18, IC7361
II	16	AMSS34-A, IC14467-A, JS148, UGM-73, PLSO90, JS99-02, PK257, IC2571-A, IC25167, IC1000790, TNAU20037, JS(SH)99-02, JS89-24, IC1024, NRC51, IC62376-A
III	2	IC39873, IC93751
IV	2	JS (SH)93-37, IC93752
V	8	IC25166, HIMS0 1564, JS92-22-A, PK258, IC2048, VLS53, JS (SH)91-93, MACS715
VI	2	JS95-98, IC16040
VII	3	IC216380, JS (SH)89-49, IC15969
VIII	2	IC34057, IC18736
IX	2	JS90-29, IC18277
X	1	IC93656

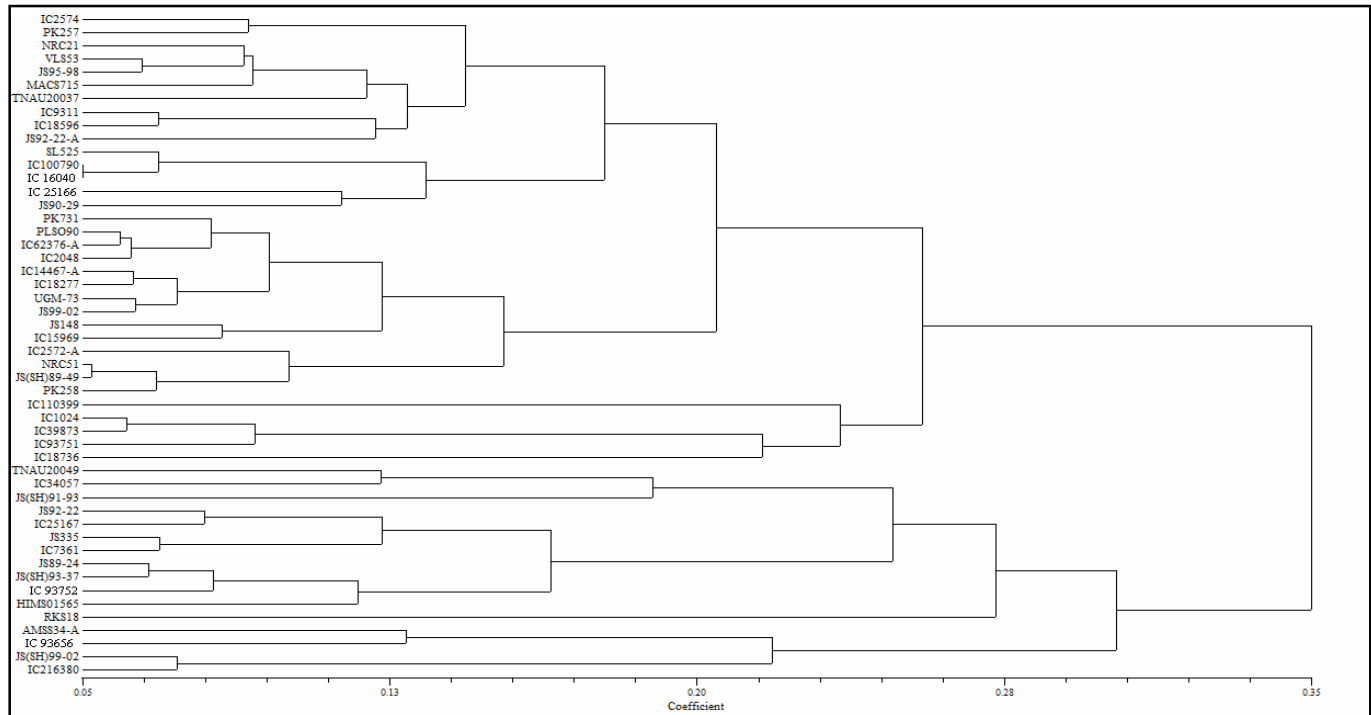


Fig. 1: Dendrogram of soybean genotypes based on 12 morphological traits

**Table 3 : Inter and Intra cluster D-square values**

Clusters	1	2	3	4	5	6	7	8	9	10
1.	925.545	757.209	548.881	999.375	867.069	628.097	963.142	768.579	1158.476	1635.125
2.		591.154	484.030	593.068	748.445	558.590	623.558	807.019	1213.802	1156.978
3.			45.186	768.088	621.165	496.668	762.446	266.431	1076.649	1140.967
4.				48.332	1062.610	1066.505	376.726	1069.708	2110.150	283.680
5.					919.925	500.636	931.044	963.670	961.997	1827.459
6.						59.739	801.508	882.702	354.488	2094.747
7.							753.203	1163.59	1625.492	884.784
8.								324.936	1442.743	1438.013
9.									691.223	3424.063
10.										0.000

**Table 4: Inter and Intra cluster distances**

Clusters	1	2	3	4	5	6	7	8	9	10
1.	30.423	27.517	23.428	31.613	29.446	25.062	31.035	27.723	34.036	40.437
2.		24.314	22.001	24.353	27.358	23.635	24.971	28.408	34.840	34.014
3.			6.722	27.713	24.923	22.286	27.612	16.323	32.812	33.778
4.				6.952	32.598	32.657	19.409	32.706	45.936	16.843
5.					30.330	22.375	30.513	31.043	31.016	42.749
6.						7.729	28.311	29.710	18.828	45.768
7.							27.445	34.112	40.317	29.745
8.								18.026	37.983	37.855
9.									26.291	58.515
10.										0.000

Table 4. Maximum difference among the genotypes within the same cluster (intra cluster) was shown by cluster I (30.423) followed by cluster V (30.330), cluster VII (27.445), cluster IX (26.291), cluster II (24.314), cluster VIII (18.026), cluster VI (7.729) and cluster IV (6.952). Diversity among the clusters varied with inter cluster distance 58.515 to 16.323. The cluster IX and X (58.515) showed maximum inter cluster distance followed by IV and IX (45.936), VI and X (45.768), V and X (42.74732.657), I and X (40.437), and VII and IX (40.317). The lowest inter cluster distance was noticed between cluster III and VIII (16.323).

The per cent contribution of each character towards divergence is presented in Table 5. It was observed that number of seeds per plant contributed maximum (40.24) towards diversity followed by seed yield per plant (20.12), harvest index (9.63), pods per cluster (9.06), pods per plant (8.85), number of seeds per pod (4.57) and pod clusters per plant (3.51). The remaining characters *viz.*, plant height, 100 seed weight, days to 50% flowering days to maturity and number of primary branches did not contribute to the total divergence.

**Table 5: Contribution of morphological characters to divergence**

Sr. No.	Characters	No. of first ranks	% Contribution
1.	Days to flowering	7	0.5714
2.	Plant height	24	1.9592
3.	No. of primary branches	1	0.0800
4.	No. of pod clusters per plant	43	3.5102
5.	No. of pods per cluster	111	9.0612
6.	No. of pods per plant	109	8.8568
7.	No. of seeds per pod	56	4.5714
8.	No. of seeds per plant	493	40.2449
9.	100 seed weight	15	1.2245
10.	Seed yield per plant	246	20.1256
11.	Days to maturity	2	0.1600
12.	Harvest index	118	9.6327

The hierarchical cluster analysis of quantitative traits with 50 selected accessions formed ten clusters which indicated the existence of high level of genetic diversity among the genotypes. Cluster II consisted of 16 accessions of different geographical origins. Cluster I also consisted of 12 genotypes with different geographical origins. It was observed that the genotypes of different geographical origin were grouped together and the genotypes with same origin were included in different

clusters. The clustering pattern of the accessions showed that geographical diversity was not related with genetic diversity. Gawande *et al.* (2002), Ganesamoorthy and Sheshadri (2002) and Sharma (2000) reported that there exists no association between genetic diversity and geographical diversity. Murthy and Arunachalm (1966) pointed out that there exists no close correspondence between the ecogeographic diversity and genetic diversity in a number of crop plants. They have described such diversity to genetic drift and selection in different environment.

Intra cluster distance was highest in cluster I (925.545) followed by cluster V (919.925) when compared with other clusters. The high intra cluster distance values revealed the presence of genetic diversity between the genotypes which were grouped together in those clusters. Hence, there is a lot of scope for exchange of genes among genotypes within these clusters. Mishra *et al.* (1987) recorded the maximum intracluster distance of 346.56, Ramgiry (1999) got the maximum intracluster distance of 1338.7. The accessions in cluster III *viz.*, IC 39873 and IC 93751 recorded very low intra cluster distance (45.186) thus showing that those genotypes were very closely related to each other. With regard to inter cluster distance the cluster IX with two genotypes *viz.*, JS 90-29 and the cluster X with IC93656 recorded the highest value. It can be inferred that crossing between these genotypes may result in good recombinants for successful breeding programme.

The clusters IX (JS (SH) 93-37) and IV (JS (SH) 93-37) and cluster X (IC93752) and VI (IC93752) recorded higher inter cluster distance values. Therefore, inter crossing between these genotypes would yield better recombinants. Several authors have suggested that the crossing between the genotypes of clusters with high inter cluster would yield good segregants for selection. (Ramgiry, 1999, Sharma, 2000, Gawande *et al.*, 2002). The lowest inter cluster distance was noticed between cluster III and VIII (266.431) which revealed that those genotypes are not very distant but could not be grouped together based on these traits.

Per cent contribution of characters towards divergence was analysed and it was found that seeds per plant and seed yield per plant contributed for maximum genetic diversity among the 50 genotypes. The traits *viz.*, plant height, number of primary branches per plant, 100 seed weight, days to 50% flowering, days to maturity and number of seeds per pod contributed very less to the genetic diversity which showed that the genotypes possessed unique features for most of the traits studied.

The present study revealed that the cluster IX and cluster I possessed high mean values for most of the desirable traits. While the cluster X with IC93656 possessed very low values for many of the traits studied and it was a poor cluster. It is inferred that with respect to seed yield and number of seeds per plant (the characters which contributed more to genetic diversity among 50 genotypes), cluster IX (JS90-29 and IC18277) was the superior cluster. These genotypes could be widely used in crossing programme for generation of large variability for seed yield. The VIII cluster with genotypes IC 34057 and IC 18736 was the best cluster for number of pods per plant followed by the III cluster with IC 39873 and IC 93751. These entries may be used in breeding programme to improve number of pods per plant and in turn yield.

From the genetic diversity studies of 12 morphological characters of 50 soybean genotypes, it could be concluded that the traits seeds per plant and seed yield per plant contributed maximum to the genetic diversity. The clustering pattern revealed that there existed no correlation between the geographical diversity and genetic diversity. The clusters IX (JS 90-29 and IC18277) and X (IC93656) were the distant clusters and clusters III (IC 39873 and IC 93751) and VIII (IC 34057 and IC 18736) were the nearest clusters. The clusters IX and I possessed the high mean values for many of the traits studied. With respect to seed yield per plant the clusters IX, VI and I appeared to be the superior clusters. The entries *viz.*, JS 90-29 and IC18277 of IX cluster and IC93656 of X cluster can be used in crossing programme for development of good

recombinants for seed yield as diverse parents could generate good amount genetic variability.

### LITERATURE CITED

- Ganesamoorthy, K. and Sheshadri, P. (2002).** Genetic divergence in soybean [*Glycine max* (L.) Merrill]. *Madras Agric. J.*, **89**(1-3): 18-21.
- Gawande, P.P., Patil, S., Maya Kumari and Bailkiwad, V.J. (2002).** Selection of superior germplasm lines of soybean [*Glycine max* (L.) Merrill] for breeding. *J. Soils & crops.*, **12**(2): 236-240.
- Mahalanobis, P.C. (1936).** On the generalized distance in statistics. *Proc. National Acad. Sci., India*, **2**: 49-55.
- Mishra, R.M., Koutu, G., Kand, Bilaiya, S.K. (1987).** D<sup>2</sup> and metrograph analysis of soybean. *J. Oilseeds Res.*, **4** (1): 103-107.
- Murthy, B.R. and Arunachalam, V. (1966).** The nature of divergence in some varieties of *linum usitatissium*. *Indian J. Genet.*, **26**:21-36.
- Ramgiry, S.R. (1999).** Genetic divergence in Soybean. *Madras Agric. J.*, **85** (3&4): 167-170.
- Rao, C.R. (1952).** *Advanced statistical methods in biometrical research*. John Wiley and Sons. Inc., New York, pp. 357-363.
- Sharma, S.R. (2000).** Genetic divergence in soybean. *J. Oilseed Res.*, **17**(1):17-19.

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