

## Genetic Diversity Analysis in Soybean [*Glycine max* (L.) Merr.] Genotypes

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**ABSTRACT:** The present investigation was carried out at the experimental farm area of Agriculture Research Station, Agriculture University, Kota during *rabi* 2023. Out of 52 soybean genotypes, 12 lines, 3 testers and 36 F<sub>1</sub>s including one checks were evaluated in randomized block design with three replications. Among 10 clusters, cluster I was biggest with 41 genotypes followed by cluster II and III with 2-2 genotypes. Cluster IV-X was solitary containing single genotype. The intra cluster distances ranged from 0 (cluster VI-X), which is solitary cluster to 8.84 (cluster III) indicating high diversity. The inter cluster D<sup>2</sup> values exhibited a highest value of 18.82 (cluster V and X) and lowest value of 9.23 (cluster I and X) suggesting large amount of diversity among genotypes.

**Keywords:** soybean, intra cluster, inter cluster.

### INTRODUCTION

Soybean [*Glycine max* (L.) Merr.] have long been recognized as a plant food product that is relatively high in protein, when compared with other crop plants, hence called as 'meat of the field'. It has been originated in North Eastern China (Vavilov, 1951). All of the essential amino acids are found in soybean protein, which also contains heart-healthy oil that meets 30% of the global need for vegetable oil and a variety of health benefits, including lactose-free fatty acids, antioxidants, folic acid, and vitamin B complex. This crop's versatility has led to a notable increase in its contribution to the industrial, agricultural, and medicinal sectors. In India and other Asian nations, the rapid population growth combined with the steady decline in arable land has created more health risks for people. Because soybeans have a high protein content and a reasonable amount of oil that can be used as a source of energy, they could be considered the perfect food crop for the people living in poor and developing nations. In a short amount of time, soybeans, which only occupied a tiny 0.03 million hectares in 1970, have grown to become the main oilseed crop in India. With an estimated production of 11.40 million hectares and a productivity of 10.1 q/ha, the crop has grown at an unprecedented rate, reaching an area of 11.40 million hectares (Anonymous, 2017).

It is commonly known that genetic diversity is essential for improving self-pollinated and cross-pollinated crops (Murty and Anand 1966; Gaur *et al.* 1978). The degree of diversity found in the germplasm that is currently available is indicated by estimates of genetic

divergence. Additionally, assessing genetic diversity is crucial in order to identify the gene sources responsible for a given trait. Any crop improvement program must start with the selection of genetically diverse parents because it increases the likelihood of choosing better segregants for different characters. Plant breeders can identify the diverse parents for upcoming hybridization programs and obtain desired recombinants with a higher degree of heterosis with the assistance of precise information regarding the nature and degree of genetic diversity. In light of this, the current study was conducted to evaluate the type and extent of genetic diversity found in soybean germplasm, which will aid in the selection of effective genotypes with desired traits for use in the hybridization program.

Keeping these aspects in view, the present study in soybean was conducted with the objectives to study the genetic diversity for various morphological traits in 52 experimental materials which include varieties and crosses (F<sub>1</sub>) of soybean.

### MATERIAL AND METHOD

The present investigation was carried out at the experimental farm area of Agriculture Research Station, Agriculture University, Kota during *rabi* 2023. Out of 52 genotypes, 12 lines, 3 testers and 36 F<sub>1</sub>s including one checks were evaluated in randomized block design with three replications. Each genotype was raised in a plot consisting of 3 rows each of 1.5m length with spacings of 45cm between rows and 15cm between the plants. Five plants per genotype per replication were randomly selected for recording the observations at appropriate stages of crop growth on characters such as

plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g), biological yield per plant (g), seed yield per plant (g), protein content (%), oil content (%) and harvest index (%).

The observations on days to 50 per cent flowering and days to maturity were recorded on plot basis. The mean data over randomly selected plants from all the replications were subjected to the statistical analysis. Genetic diversity was studied using  $D^2$  statistic as per Mahalanobis, 1936. Intra- and inter-cluster distances and cluster means for different characters were also computed.

## RESULT AND DISCUSSION

Improvement of genetically diverse parents in breeding programs is credited with improving soybean yield, oil content, and protein content. On the other hand, Indian soybean varieties have been found to have a limited genetic base, possibly as a result of using the same parents to evolve new varieties. Presumably because one of the biggest issues facing soybean farmers in tropical and sub-tropical regions like India is seed longevity. Knowing the genetic divergence among the cultivars that are currently available is therefore crucial for choosing the parents to use in a hybridization program in order to achieve the desired genetic recombination for yield.

**Clustering pattern of entries.** Clustering pattern of 52 genotypes were grouped into ten clusters. Among eight clusters, cluster I was biggest with forty-one genotypes followed by cluster II and III with two-two genotypes. Cluster IV-X was solitary containing single genotype.

**Intra and inter cluster  $D^2$  values.** The intra cluster distances ranged from 0 (cluster VI-X), which is solitary cluster to 8.84 (cluster III) indicating high diversity. The inter cluster  $D^2$  values exhibited a highest value of 18.82 (cluster V and X) and lowest value of 9.23 (cluster I and X) suggesting large amount of diversity among genotypes (Table 2). Thus considerable variability prevailed among the genotypes within these clusters may be helpful to realize heterosis

or improvement of traits through simple selection Patil *et al.* (2011); Chavan *et al.* (2014).

Based on inter cluster  $D^2$  values, the genotypes belonging to cluster V and X appeared to be more diverse (18.82) followed by cluster III and V (18.02), cluster IV and VII (17.91), cluster IV and VIII (17.34) and cluster II and V (16.54) suggesting that selection of genotypes from these divergent groups would yield higher magnitude of heterosis for the characters concerned. Among the clusters, Cluster X has been the most diverse as measured from it inter cluster distances with other clusters which was maximum, while, the cluster IX found to be the nearest with number of other clusters. Selection of genotypes with short inter cluster distance would not be desirable to reap higher yield benefits and this is attributed to smaller allelic frequency difference between these genotypes, which results in lower heterotic progenies.

**Cluster mean analysis.** Analysis of cluster means indicates diversity demonstrated by different clusters for a character. Based on the means, it is possible to know the character influencing divergence and the variation observed in cluster mean also points to the degree of variability (Table 3).

There was no much difference for the mean value of character days to 50 per cent flowering. However, genotypes included in the cluster VII showed minimum days to maturity (89.00) followed by VIII and IX. Genotypes in cluster V comprised of late flowering types. The genotypes of cluster VIII were tall followed by cluster III and VII, while those of cluster V were dwarf, while remaining clusters had intermediate height. Number of branches per plant was highest for the cluster V (7.64) followed by cluster V and IV. The cluster II included high test weight (12.07g) followed by IX and III. The cluster IV includes highest seed yield per plant genotypes with highest number of pods per plant, biological yield per plant and high protein containing genotypes. And the remaining clusters showed more or less intermediate mean value for the above said characters. Cluster VII include the genotypes having high oil content (20.65%) as well as minimum days to maturity genotypes (89.00).

**Table 1: Distribution of soybean genotypes into different clusters.**

Sr. No.	Cluster	Genotypes
1	Cluster I	JS 20-34, NRC 138, RKS 18 RKS 113, AUKS 200 , AUKS 212, JS 20-98, AUKS 202, AUKS 208, AUKS 218, JS 21-72, RKS 18 x JS 20-34, RKS 113 x JS 20-34, AUKS 199 x JS 20-34, AUKS 200 x JS 20-34, AUKS 212 x JS 20-34, RVSM 11-35 X JS 20-34, JS 20-98 x JS 20-34, AUKS 202 x JS 20-34, AUKS 218 x JS 20-34, JS 21-72 x JS 20-34, RKS 18 x NRC 138, RKS 113 x NRC 138, AUKS 199 x NRC 138, AUKS 212 x NRC 138, RVSM 11-35 x NRC 138, JS 20-98 x NRC 138, AUKS 202 x NRC 138, AUKS 208 x NRC 138, AUKS 218 x NRC 138, JS 21-72 x NRC 138, RKS 18 x SL 958, AUKS 199 x SL 958, AUKS 200 x SL 958, AUKS 212 x SL 958, RVSM 11-35 x SL 958, AUKS 202 x SL 958, AUKS 208 x SL 958, AUKS 218 x SL 958, JS 21-72 x SL 958, NRC 165 x SL 958
2	Cluster II	AUKS 208 x JS 20-34, JS 95 -60
3	Cluster III	RVSM 2011-35, NRC 165 x JS 20-34
4	Cluster IV	RKS 113 x SL 958
5	Cluster V	SL 958
6	Cluster VI	JS 20-98 x SL 958
7	Cluster VII	NRC 165
8	Cluster VIII	NRC 165 x NRC 138
9	Cluster IX	AUKS 200 x NRC 138
10	Cluster X	AUKS 199

**Table 2: Average intra and inter cluster D<sup>2</sup> values of 52 soybean genotypes.**

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	7.37	10.10	10.26	12.46	12.41	9.87	10.21	9.41	9.92	9.23
II		<b>6.45</b>	11.77	13.90	16.54	12.09	14.37	11.90	11.71	11.58
III			<b>8.84</b>	13.78	18.02	11.80	12.65	11.26	11.55	13.65
IV				0.00	10.19	14.48	17.91	17.34	14.69	13.90
V					0.00	11.98	16.23	15.45	16.76	18.82
VI						0.00	10.38	10.57	15.64	14.78
VII							0.00	11.92	11.05	14.42
VIII								0.00	12.27	14.38
IX									0.00	14.98
X										0.00

**Table 3: The mean values of twelve characters in 10 clusters of 52 soybean genotypes.**

	DDF	DM	PH (cm)	PL (cm)	NSPP	100-SW	BYPP(g)	GYPP(g)	NBPP	NPPP	PC (%)	OC (%)	HI (%)
Cluster-I	37.83	96.20	59.97	3.59	2.76	10.79	58.28	18.29	5.53	92.81	39.81	20.37	31.26
Cluster-II	32.17	92.00	51.29	3.48	2.60	12.07	45.44	13.13	5.56	68.36	38.58	20.07	29.06
Cluster-III	36.67	94.33	60.85	3.96	3.47	10.80	57.76	17.64	4.18	88.38	39.44	19.70	30.50
Cluster-IV	50.67	116.33	71.95	3.67	3.02	10.23	73.64	26.84	7.14	113.63	39.75	20.03	36.44
Cluster-V	52.33	121.67	76.85	3.80	2.72	9.90	57.74	18.51	7.41	103.80	40.32	19.87	32.14
Cluster-VI	51.67	109.33	74.58	3.50	2.53	9.93	55.62	13.55	4.03	86.93	38.70	20.22	24.38
Cluster-VII	30.67	89.00	56.20	3.85	2.74	9.85	50.71	14.47	3.67	95.32	39.70	20.65	28.56
Cluster-VIII	30.33	89.33	62.23	4.05	2.65	9.62	56.56	13.79	4.25	66.20	40.25	20.00	24.37
Cluster-IX	31.00	89.33	46.90	3.60	2.67	11.73	65.99	20.86	2.34	98.90	39.48	18.95	31.61
Cluster-X	36.33	90.33	46.13	3.25	2.53	10.45	54.97	16.09	7.64	90.45	38.71	20.23	29.42

## CONCLUSIONS

The findings of the research revealed a high genetic variation among genotypes, the genotypes AUKS 199 (Cluster X) were substantially more divergent from the genotypes JS 20-34, NRC 138, RKS 18 RKS 113, AUKS 200, AUKS 212, JS 20-98, AUKS 202, AUKS 208, AUKS 218 and JS 21-72 (cluster I) than the other genotypes. Hence, these genotypes could be used for commercial cultivation and in genetic improvement programs. Furthermore, they could be used in diverse parental crosses, which are likely to create heterotic hybrids, to help the production of even more strongly diverse lines.

## REFERENCES

- Anonymous (2017). World Agricultural Production. United States Department of Agriculture. *Foreign Agricultural Service*, 2017.
- Chavan, R. B., Pulate, S. C. and Thakare, D. S. (2014). Assessment of existing genetic variability and diversity in soybean [*Glycine max* (L) Merrill]. *An International Quarterly Journal of Biology & Life Sciences*, 2, 949-955.
- Gaur, P. C., Gupta, P. K. and Kishore, H. (1978). Studies on genetic divergence in potato. *Euphytica*, 27, 361-368.
- Murty, B. R. and Anand, I. J. (1966). Combining ability and genetic diversity in some varieties of *Linum usitatissimum*. *Indian Journal of Genetics and Plant Breeding*, 26, 21-36.
- Patil, S. S., Naik, M. R., Patil, P. P. and Shinde, D. A. (2011). Genetic variability, correlation and path analysis in soybean. *Legume Research*, 34, 36-40.
- Vavilov, N. I. (1951). The origin, variation, immunity and breeding of cultivated plants. Tr. From Russian by K.S. Chester. *Chronica Botanica*, 1(6), 364.

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