



Assessment of Genetic Diversity using D² Analysis in Soybean [*Glycine max* (L.) Merrill] Genotypes under Humid South Eastern Plain Zone V of Rajasthan

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(Received: 03 April 2024; Revised: 25 April 2024; Accepted: 17 May 2024; Published: 15 June 2024)

(Published by Research Trend)

ABSTRACT: The present study entitled “Assessment of genetic diversity using D² analysis in Soybean [*Glycine max* (L.) Merrill] genotypes” was conducted during Kharif-2023 with 40 soybean genotypes including 4 checks viz., RVSM 2011-35, NRC-138, JS 20-34, and RKS-113 in randomized block design (RBD) to assess the nature and extent of genetic diversity in soybean genotypes. Genotypes were grouped into nine distinct non-overlapping clusters using Tocher’s method and observations were recorded for 14 traits that were used in the study. The maximum intra-cluster distance was recorded by cluster VII, followed by cluster IV, while the highest inter-cluster distance was observed between cluster VII and IX, followed by cluster VI and IX and cluster VII and VIII, indicating wide diversity among the genotypes. Cluster VIII had high values for plant height, number of primary branches per plant and oil content. Cluster IX had high values for number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index (%) and seed yield per plant. Taking into account the intra-cluster distance, inter-cluster distance and cluster means, these genotypes may be used in future breeding programmes to create a broad spectrum of variability for various yield contributing characters, allowing for the development of superior genotypes for multiple characters.

Keywords: D² analysis, intra-cluster, inter-cluster, diversity and Tocher’s method.

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill.] is a very important leguminous seed crop known for its highly valued protein and oil owing to its use in food, feed and industrial applications. Soybean is sometimes referred to as the "Golden Bean" and the "Miracle Crop" of the twenty-first century because of its numerous applications. It has a high percentage of high-quality protein (42 per cent) and oil (20 per cent). Along with vitamins A, B, and E, it is abundant in minerals including calcium, phosphorus, and iron. It provides a variety of essential amino acids (EAA), including lysine, which is typically lacking in sources of plant-based protein. In terms of taxonomy, soybean originates from North-East China and is a member of the order Fabales, family Fabaceae, subfamily Faboidae and genus *Glycine*. The genus *Glycine* may be divided into two subgenera, *Glycine* and *Soja*. It is an autogamous,

diploid (2n=40) plant. Soybean improves soil productivity by fixing atmospheric nitrogen at a rate of 65-100 kg per hectare through symbiosis with the bacteria *Rhizobium japonicum*, which renews and maintains soil fertility (Patil *et al.*, 2014).

Soybean oil is beneficial to human health since it is plentiful in vitamin E and is high in vital fatty acids while being low in saturated fat. Soybean oil has 15 per cent saturated fatty acids, whereas 85 per cent are unsaturated (Balasubramanian and Palaniappan 2001). In India, soybean is cultivated over an area of 124 lakh hectares with a production of 139.7 lakh tonnes and the productivity is 1130 kg per hectare. In Rajasthan, soybean is cultivated over an area of 10.3 lakh hectares and it produces 9.9 lakh tonnes of grain with a productivity of 953 kg per hectare. In Kota division, soybean is produced over an area of 6.45 lakh hectares with a production of 6.001 lakh tonnes, with a productivity of 931 kg per hectare (Anonymous 2022-

23). Development of high yielding cultivars with appropriate plant architecture and duration is of paramount importance. For this purpose selection of genotypes with suitable plant types to be used as parents in hybridization program is the need of the hour. The genetic diversity between the genotypes is important as the genetically diverse parents are able to produce high heterotic effects (Mian and Bahl 1989). A successful hybridization strategy between genetically diverse parents will lead to significant amount of heterotic response in F_1 hybrids and wide range of variability in segregating generations. Keeping in view of the above information the present study was carried out to study the nature and extent of genetic diversity among the forty genotypes of soybean and identification of potential combinations for further improvement. Genetic diversity was estimated as per Mahalanobis D^2 statistics (1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952).

MATERIAL AND METHODS

The experiment was carried out with forty genotypes of soybean along with four checks in Randomized Block

Design (RBD) with three replications at AICRP on soybean, Agricultural Research Station, Umedganj, Kota, Rajasthan, during *Kharif* 2023. The plot size for each genotype was 3m × 1.8m with spacing 45cm × 10cm. The observations were recorded on five randomly selected plants per plot for fourteen characters *viz.*, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed yield per plant (g), 100-seed weight (g), biological yield per plant (g), harvest index (%), protein content (%) and oil content (%) whereas, the observations for days to 50 percent flowering and days to maturity were recorded on a whole plot basis. Using Mahalanobis D^2 statistics (1936), which are based on multivariate analysis, the collected data of different characters was subjected to an analysis of genetic divergence. The genotypes were then grouped into different intra- and inter-cluster groups using Tocher's method, as described by Rao (1952). It calculates the relative contributions of each character to the overall divergence and quantifies the variation in intra- and inter-cluster distance.

Table 1: List of forty soybean genotypes used in the study

Sr. No.	Name of genotypes	Source of genotypes	Sr. No.	Name of genotypes	Source of genotypes
1.	AUKS 23-1	AICRP, ARS, AU, Kota	21.	AUKS 23-21	AICRP, ARS, AU, Kota
2.	AUKS 23-2	AICRP, ARS, AU, Kota	22.	AUKS 23-22	AICRP, ARS, AU, Kota
3.	AUKS 23-3	AICRP, ARS, AU, Kota	23.	AUKS 23-23	AICRP, ARS, AU, Kota
4.	AUKS 23-4	AICRP, ARS, AU, Kota	24.	AUKS 23-24	AICRP, ARS, AU, Kota
5.	AUKS 23-5	AICRP, ARS, AU, Kota	25.	AUKS 23-25	AICRP, ARS, AU, Kota
6.	AUKS 23-6	AICRP, ARS, AU, Kota	26.	AUKS 23-26	AICRP, ARS, AU, Kota
7.	AUKS 23-7	AICRP, ARS, AU, Kota	27.	AUKS 23-27	AICRP, ARS, AU, Kota
8.	AUKS 23-8	AICRP, ARS, AU, Kota	28.	AUKS 23-28	AICRP, ARS, AU, Kota
9.	AUKS 23-9	AICRP, ARS, AU, Kota	29.	AUKS 23-29	AICRP, ARS, AU, Kota
10.	AUKS 23-10	AICRP, ARS, AU, Kota	30.	AUKS 23-30	AICRP, ARS, AU, Kota
11.	AUKS 23-11	AICRP, ARS, AU, Kota	31.	AUKS 23-31	AICRP, ARS, AU, Kota
12.	AUKS 23-12	AICRP, ARS, AU, Kota	32.	AUKS 23-32	AICRP, ARS, AU, Kota
13.	AUKS 23-13	AICRP, ARS, AU, Kota	33.	AUKS 23-33	AICRP, ARS, AU, Kota
14.	AUKS 23-14	AICRP, ARS, AU, Kota	34.	AUKS 23-34	AICRP, ARS, AU, Kota
15.	AUKS 23-15	AICRP, ARS, AU, Kota	35.	AUKS 23-35	AICRP, ARS, AU, Kota
16.	AUKS 23-16	AICRP, ARS, AU, Kota	36.	AUKS 23-36	AICRP, ARS, AU, Kota
17.	AUKS 23-17	AICRP, ARS, AU, Kota	37.	RVSM 2011-35 (C)	RVSKVV, Gwalior
18.	AUKS 23-18	AICRP, ARS, AU, Kota	38.	NRC 138 (C)	IISR, Indore, Madhya Pradesh
19.	AUKS 23-19	AICRP, ARS, AU, Kota	39.	JS-20-34 (C)	JNKVV, Jabalpur Madhya Pradesh
20.	AUKS 23-20	AICRP, ARS, AU, Kota	40.	RKS-113 (C)	AICRP, ARS, AU, Kota, Rajasthan

RESULTS AND DISCUSSION

In culmination to genetic relationship, based on the relative magnitude of D^2 , forty soybean genotypes were grouped into nine distinct, non-overlapping clusters as shown in Table 2. The discrimination of genotypes into discrete clusters suggested the presence of a high degree of genetic diversity in the material evaluated. Among nine clusters, cluster I was the biggest with 25 genotypes *viz.*, AUKS 23-1, AUKS 23-3, AUKS 23-4, AUKS 23-5, AUKS 23-8, AUKS 23-9, AUKS 23-10, AUKS 23-11, AUKS 23-12, AUKS 23-15, AUKS 23-16, AUKS 23-17, AUKS 23-18, AUKS 23-19, AUKS 23-20, AUKS 23-21, AUKS 23-23, AUKS 23-25,

AUKS 23-26, AUKS 23-29, AUKS 23-30, AUKS 23-31, AUKS 23-32, AUKS 23-33, AUKS 23-34; cluster VII contained 5 genotypes *i.e.*, AUKS 23-14, AUKS 23-24, AUKS 23-28, NRC-138 (C), JS 20-34 (C) and cluster IV contained 4 genotypes *i.e.*, AUKS 23-27, AUKS 23-35, AUKS 23-36 and RVSM 2011-35 (C) while, rest of the clusters contained a single genotype only. Cluster II contained genotypes AUKS 23-22, cluster III (AUKS 23-13), cluster V (AUKS 23-6), cluster VI (RKS-113 (C)), cluster VIII (AUKS 23-7) and cluster IX (AUKS 23-2). This suggests that the genotypes being studied are diverse.

The average D^2 values of intra and inter-cluster distances as well as the closest and farthest clusters

from one another based on D^2 values are displayed in Table 3. The intra-cluster distance ranged from 29.87 to 49.97. The maximum intra-cluster distance was recorded by cluster VII (49.97), followed by cluster IV (40.52) and cluster I (29.87). Cluster II, cluster III, cluster V, cluster VI, cluster VIII and cluster IX recorded (0.00) intra-cluster distance because these clusters contained a single genotype. The genotypes allocated to each cluster exhibit greater diversity, as shown by the maximum intra-cluster distance, while the minimum intra-cluster distance suggests a strong relationship between the genotypes inside the cluster. Similarly, the inter-cluster distances ranged from 21.71 to 209.27. The highest inter-cluster distance was observed between cluster VII and IX (209.27) followed by cluster VI and IX (173.19), cluster VII and VIII (161.66), cluster IV and VI (152.37), cluster IV and VII (147.84), cluster III and VII (143.71) and Cluster II and IX (128.17). The lowest inter-cluster distance was noticed between cluster II and VI (21.71) followed by

cluster III and V (31.06), cluster III and VIII (33.41), cluster V and VI (37.73), cluster V and VIII (38.53), cluster II and V (41.33) and cluster III and VI (42.29). The greater the distance between two clusters, wider is the expected genetic diversity between them.

The mean values of fourteen characters for 9 clusters are presented in Table 4. Cluster VIII and IX had genotypes with a higher mean value for days to 50 per cent flowering and days to maturity. Cluster VIII had high values for plant height, number of primary branches per plant and oil content. Cluster IX had high values for number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index % and seed yield per plant. Cluster III had high cluster mean values for protein content. Similar results were also reported by Promin *et al.* (2014); Dubey *et al.* (2018); Joshi *et al.* (2018); Sareo *et al.* (2018); Darai *et al.* (2020); Beyene and Jalata (2022).

Table 2: Distribution of soybean genotypes into different clusters.

Cluster	Number of genotypes	Genotypes
Cluster I	25	AUKS 23-1, AUKS 23-3, AUKS 23-4, AUKS 23-5, AUKS 23-8, AUKS 23-9, AUKS 23-10, AUKS 23-11, AUKS 23-12, AUKS 23-15, AUKS 23-16, AUKS 23-17, AUKS 23-18, AUKS 23-19, AUKS 23-20, AUKS 23-21, AUKS 23-23, AUKS 23-25, AUKS 23-26, AUKS 23-29, AUKS 23-30, AUKS 23-31, AUKS 23-32, AUKS 23-33, AUKS 23-34
Cluster II	1	AUKS 23-22
Cluster III	1	AUKS 23-13
Cluster IV	4	AUKS 23-27, AUKS 23-35, AUKS 23-36 and RVSM 2011-35 (C)
Cluster V	1	AUKS 23-6
Cluster VI	1	RKS-113 (C)
Cluster VII	5	AUKS 23-14, AUKS 23-24, AUKS 23-28, NRC-138 (C) and JS 20-34 (C)
Cluster VIII	1	AUKS 23-7
Cluster IX	1	AUKS 23-2

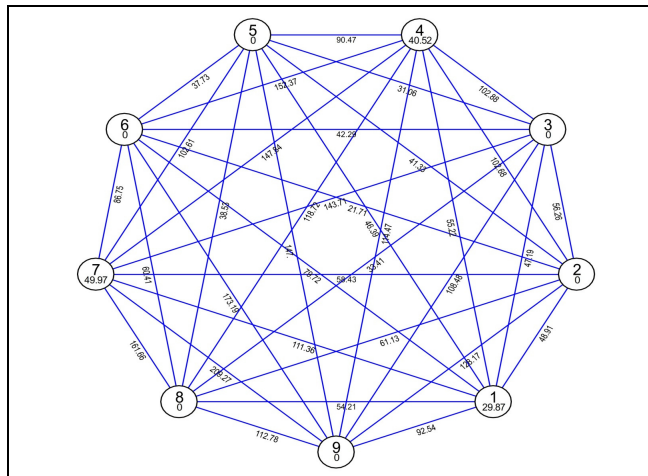
Table 3: Average intra and inter-cluster distance based on corresponding D^2 values.

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	29.87	48.91	47.19	55.22	46.39	79.72	111.36	54.21	92.54
Cluster II		0.00	56.26	102.68	41.33	21.71	58.43	61.13	128.17
Cluster III			0.00	102.88	31.06	42.29	143.71	33.41	108.48
Cluster IV				40.52	90.47	152.37	147.84	118.72	114.47
Cluster V					0.00	37.73	102.61	38.53	147.00
Cluster VI						0.00	86.75	60.41	173.19
Cluster VII							49.97	161.66	209.27
Cluster VIII								0.00	112.78
Cluster IX									0.00

Table 4: Mean values of different characters for 40 genotypes of soybean grouped in different clusters.

Clusters	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Protein content (%)	Oil content (%)	Seed yield per plant (g)
Cluster I	42.83	99.75	80.38	6.91	12.24	65.05	3.35	2.78	9.11	22.90	24.98	35.19	16.02	5.68
Cluster II	38.00	97.00	73.53	5.28	13.97	67.60	3.19	2.60	8.80	22.51	25.36	34.26	17.22	5.71
Cluster III	44.00	100.67	82.80	7.60	15.38	72.93	3.53	2.93	11.35	25.75	28.21	37.45	19.60	7.28
Cluster IV	44.17	100.67	71.95	7.01	10.45	67.87	3.50	2.75	8.50	19.95	19.43	36.26	13.55	3.86
Cluster V	42.33	99.00	77.80	8.47	9.07	60.20	3.06	2.33	8.07	18.29	21.66	35.94	19.00	3.95
Cluster VI	38.00	96.67	69.47	7.40	15.17	72.27	3.25	2.73	8.76	24.10	24.36	37.10	19.71	5.87
Cluster VII	32.40	90.47	57.76	5.79	10.12	53.17	3.46	2.75	9.03	22.29	22.42	36.68	15.10	4.88
Cluster VIII	44.67	101.33	85.40	9.07	13.13	83.67	3.45	2.93	9.07	28.48	20.29	33.30	20.40	5.77
Cluster IX	44.67	101.33	73.07	7.20	15.63	94.87	3.61	3.00	12.70	31.53	34.53	30.36	16.28	10.84

TOCHER'S METHOD



Mahalanobis Euclidean Distance (Not to the Scale)

Fig. 1. Diagrammatic representation of intra and inter-cluster distance.

CONCLUSIONS

From the results of the present investigation, it can be suggested that genotypes from cluster VII should be selected for developing early maturity varieties of soybean, while genotypes from cluster IX, VIII and III should be selected for selection as parents in hybridization programmes for improving grain yield in soybean and cluster VI should be selected for enhancing nutritional value of soybean. Maximum intra-cluster distances was recorded by cluster VII, followed by cluster IV and cluster I, indicates that there was greater diversity present among these genotypes. Highest inter-cluster distance was observed between cluster VII and IX, followed by cluster VI and IX, cluster VII and VIII which indicates greater genetic diversity between clusters. Thus, the genotypes of these clusters are employed in hybridization programmes to produce better and more acceptable recombinants, which in turn increase soybean grain production.

FUTURE SCOPE

Based on Mahalanobis D^2 statistics, the current study contributes to the discovery of a diversified germplasm line and gene stock, which is necessary for any successful breeding plan to improve yield and its contributing attributes.

Acknowledgement. We really appreciate the significant assistance in conducting the research that the Agriculture Research Station and the College of Agriculture, Ummedganj, Kota, provided.

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How to cite this article: Govind Tikiani, B.L. Meena, S.C. Sharma, Yamini Tak, L.K. Meena and Kamal Kumar Sharma (2024). Assessment of Genetic Diversity using D^2 Analysis in Soybean [*Glycine max* (L.) Merrill] Genotypes under Humid South Eastern Plain Zone V of Rajasthan. *Biological Forum – An International Journal*, 16(6): 131-134.