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Assessment of genetic variation in soybean (*Glycine max* (L.) Merrill) using Mahalanobis D² analysis

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Abstract

The study aimed to investigate the genetic divergence and variability of yield and its contributing traits in soybean (*Glycine max* (L.) Merrill). A total of 27 soybean genotypes were evaluated in a randomized complete block design (RCBD) for important agronomic traits, including plant height, pod number per plant, seed number per pod, seed weight, and overall yield. Genetic divergence was assessed using Mahalanobis' D² statistics, which enabled the classification of genotypes into distinct groups based on their phenotypic traits. The analysis revealed significant genetic variability among the genotypes studied, with notable divergence identified for yield-related traits. High heritability in broad sense was observed in number of seeds per plant (93.89), seed yield per plant (g) (90.56), number of pods per plant (90.40), number of primary branches per plant (83.32), pod bearing length (cm) (82.44) and plant height (cm) (81.70). Multivariate analysis indicated that genotypes displayed a broad range of variability for traits, which is crucial for breeding programs focused on improving soybean yield. Genetic diversity analysis was done based on D² values, 27 genotypes were grouped into five clusters. Cluster-I had the largest group of genotypes which were 23 genotypes and Cluster-II, Cluster-III, Cluster-IV and V consisting only one genotype each. The highest inter-cluster distance was showed between cluster II and III, followed by between cluster II and V, cluster II and IV, cluster I and III, cluster I and V, cluster I and IV, cluster I and II, cluster III and V and cluster IV and V.

Keywords: Soybean, heritability, genetic advance, genetic variability, genetic diversity and clusters

Introduction

The Soybean (*Glycine max* (L.) Merrill) is one of the most important oilseed crops not only in India but in the entire world. Soybean belongs to genus *Glycine* wild, which is a family *Leguminosae*, subfamily *Papilionoideae* and tribe *Phaseoleae*. The cultivated soybean-*Glycine max* and the wild annual soybean- *G. soja*, comes under subgenus *Soja*. (Hymowitz, 2004) [5]. It has 20 chromosomes (2n = 40) and primary center of origin of soybean is China. Global soybean production for 2023-2024 is 394.71 million metric tons (United States Department of Agriculture). Brazil produced 153 million metric tons of soybean in 2023–2024, surpassing the United States as the world's largest producer. The United States of America stands second with 113.34 million metric tons, followed by Argentina (48.1 million metric tons), China (20.8 million metric tons), India (11.9 million metric tons). The total sowing area under soybean crop in India during *Kharif* 2023 was 118.547 lakh ha with production and expected yield of 118.747 lakh metric ton and 1002 kg per ha respectively. (Anonymous 2023) [1].

Genetic Divergence Analysis or Cluster Analysis

Quantification of genetic diversity existing within and between groups of germplasm is important and particularly useful in proper choice of parents for realizing higher heterosis and obtaining useful recombinants. The quantitative assessment of genetic divergence was made by adopting Mahalanobis D² statistics for yield and its contributing characters. D² statistics, a concept developed by Mahalanobis (1936) [7], is important tool to plant breeder to classify the genotypes into different groups based on genetic divergence between them. It is also useful in quantifying degree of divergence between biological populations at genotypic level and assessing the relative contribution of different component traits to the total divergence at both intra and inter- cluster level.

Rao (1952) [11] suggested the application of this technique for the assessment of genetic diversity in plant breeding. Genetic divergence was estimated for 25 finger millet germplasm lines. These genotypes were grouped following Mahalanobis D2 as described by Rao (1952) [11].

Materials and Methods

The study was conducted in *Kharif 2023* at Research cum instruction farm College of Agriculture IGKV Raipur (C.G.). The experimental material 27 genotypes were planted in Randomized Complete Block Design with three replications fulfilling all recommended agronomical requirements. Each plant entry was planted in a single row plot. The distance maintained between plant to plant and row to row was 10 and 45 following observations were recorded on five randomly selected competitive plants, from each entry and in each replication.

Results and Discussion

The values for heritability estimates were different for different traits and classified as high (>70%), moderate (50-70%) and low (<50%) (Robinson 1966). The highest heritability was recorded for the number of seeds per plant (93.89), seed yield per plant (g) (90.56), number of pods per plant (90.40), number of primary branches per plant (83.32), pod bearing length (cm) (82.44) and plant height (cm) (81.70). Similar findings had been also reported by Tigga *et al.* (2021) for seed yield per plant (g), number of pods per

plant, number of primary branches per plant, pod bearing length (cm) and plant height (cm). Banerjee *et al.* (2023) [3] for number of pods per plant. Neelima *et al.* (2018) [10] for plant height (cm) and number of pods per plant. Results was similar with Karchal *et al.* (2024) [6] for number of pods per plant and pod bearing length. Nag *et al.* (2020) [8] for number of primary branches per plant.

The highest genetic advance as percentage of mean was recorded for seed yield per plant (g) (59.90%) followed by number of seeds per plant (57.27%), number of pods per plant (45.05%), pod bearing length (cm) (28.65%), plant height (cm) (25.36%) and number of primary branches per plant (25.19%). These results were in accordance with the findings of Banerjee *et al.* (2023) [3] for seed yield per plant and number of pods per plant

High heritability coupled with high genetic advance as percentage of mean was observed for seed yield per plant (g) (90.56%) (59.90%), number of seeds per plant (93.89%) (57.27%) and number of pods per plant (90.40%) (45.05%), pod bearing length (cm) (82.44%) (28.65%), plant height (cm) (81.70%) (25.36%) and number of primary branches per plant (83.32%) (25.19%). Similar results were reported by Nag *et al.* (2007) [9] for plant height, pod bearing length, number of pods per plant, seed yield per plant and number of seeds per plant. Upadhyay *et al.* (2020) [16] for the number of seeds per plant and seed yield per plant. Satpute *et al.* (2016) [13] for plant height and Chandel *et al.* (2017) [4] for the number of primary branches per plant.

Table 1: Genetic parameters of variation for seed yield and its traits in soybean.

S.N.	Characters	Mean Range min.		Range GCV max.		PCV	h ² b (Broa Sense)	Genetic Advance	GA as % of Mean
1	Days to 50% flowering	41.79	38.00	44.67	3.41	6.56	26.98	1.52	3.65
2	Days to maturity	98.72	90.00	107.00	3.80	6.98	29.67	4.21	4.27
3	Plant height (cm)	63.73	50.33	86.33	13.62	15.07	81.70	16.16	25.36
4	Number of primary branches per plant	3.44	2.40	4.20	13.39	14.67	83.32	0.87	25.19
5	Number of pods per plant	51.63	27.80	74.40	23.00	24.19	90.40	23.26	45.05
6	Pod bearing length (cm)	38.16	29.93	53.26	15.32	16.87	82.44	10.93	28.65
7	Number of seeds per pod	2.64	2.46	2.80	3.06	5.80	27.73	0.09	3.31
8	Number of seeds per plant	108.97	36.47	164.67	28.69	29.61	93.89	62.41	57.27
9	100 seed weight (g)	11.22	8.10	14.50	11.75	14.33	67.21	2.23	19.84
10	Oil Content (%)	19.46	18.70	20.00	1.45	2.03	51.02	0.42	2.14
11	Seed yield per plant (g)	10.21	3.05	15.12	30.56	32.11	90.56	6.12	59.90
12	Protein content (%)	39.16	35.46	43.48	3.21	6.12	27.44	1.36	3.46

With a set of 27 genotypes of soybean, D2 analysis was done for 12 features. Five groups were formed using the D2 values. These demonstrated the considerable variability seen in the soybean gene pool that is available for use. The

largest Cluster-I (23 genotypes) was found using cluster analysis and Cluster-II, Cluster-III, Cluster-IV and V consisting only one genotype each.

Table 2: Soybean genotypes, includes in various clusters

S. No.	Clusters	No. of Genotypes	Name of Genotypes
1	Cluster I	23	KDSIS 1394, ASb 101, KSS 225, NRC 269, MAUS 816, MACS 1810, VLS 106, NRC 270, Pusa Sipani BS 8, Lok-Soya 03, RSC 11-95, DS 1547, TS 101, JS 25-08, NRC 271, AMS 22-16, RSC 10-46 (C), NRC 268, THPS 6, SL 1315, NRC 128 (C), NRC 142 (C), DS 1589,
2	Cluster II	1	RSC 11-07 (C)
3	Cluster III	1	KBSL 23-36
4	Cluster IV	1	BAUS (M) 6
5	Cluster V	1	DLSb 5

The highest inter-cluster distance was measured between cluster II and III (200.33), followed by between cluster II and V (198.01), cluster II and IV (121.99), cluster I and III (98.47), cluster I and V (93.45), cluster I and IV (68.16), cluster I and II (62.72), cluster III and V (37.14), and cluster

IV and V (31.79). The lowest inter cluster distance was noticed between cluster III and IV (27.69). The maximum intra cluster distances was observed in cluster I (35.76) and remaining cluster is (0.00) because of these cluster contained single genotype.

Table 3: Inter and Intra cluster distance of genotypes in soybean

Cluster Distances					
Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	35.76	62.72	98.47	68.16	93.45
Cluster II	62.72	0.00	200.33	121.99	198.01
Cluster III	98.47	200.33	0.00	27.69	37.14
Cluster IV	68.16	121.99	27.69	0.00	31.79
Cluster V	93.45	198.01	37.14	31.79	0.00

Figure given in diagonals bold is intra-cluster D2 values and figure in parenthesis is $\sqrt{D2}$ values

The cluster mean for the days to maturity was the highest in Cluster IV (106.67) and lowest in the Cluster III (90.00). High cluster mean is found by Thakur *et al.* (2015) for days to maturity in cluster IV. Cluster V has had the highest cluster mean for the plant height (86.33), while Cluster II had the lowest (52.33). The cluster mean for the number of primary branches per plant was the highest in Cluster II with (4.13) and lowest in the Cluster III (3.33). Cluster II had the highest cluster mean for the number of pods per plant (63.47) whereas Cluster III had the lowest (36.13). Cluster V has had the highest cluster mean for the pod bearing length (53.26), while Cluster II had the lowest (34.13). Cluster V has had the highest cluster mean for the number

of seeds per pod (2.80), while Cluster III and IV had the lowest (2.53). Cluster II showed the highest mean value for the number of seeds per plant (164.67), while Cluster III showed the lowest (36.47). Cluster V has had the highest cluster mean for the 100 seed weight (12.77), while Cluster II had the lowest (8.10). Cluster III showed the highest mean value for the oil content % (19.83), while Cluster V had the lowest (19.07). Cluster II showed the highest mean value for the seed yield per plant (12.01), while Cluster III showed the lowest (3.05). Cluster V has had the highest cluster mean for the protein content % (40.22), while Cluster II had the lowest (37.93).

Table 4: Mean performance of genotypes in individual cluster for seed yield and its components

Clusters	1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.
Cluster I	41.58	98.68	61.80	3.39	52.23	36.99	2.64	111.57	11.25	19.45	10.65	39.17
Cluster II	43.33	95.00	52.33	4.13	63.47	34.13	2.70	164.67	8.10	19.37	12.01	37.93
Cluster III	42.67	90.00	83.67	3.33	36.13	43.00	2.53	36.47	11.30	19.83	3.05	38.67
Cluster IV	43.00	106.67	77.00	3.86	42.87	49.13	2.53	88.33	11.90	19.66	6.19	39.60
Cluster V	43.00	104.00	86.33	3.60	50.13	53.26	2.80	86.60	12.77	19.07	9.50	40.22

1. Days to 50% flowering	4. Number of primary branches per plant	7. Number of seeds per pod	10. Oil Content (%)
2. Days to maturity	5. Number of pods per plant	8. Number of seeds per plant	11. Seed yield per plant (g)
3. Plant height (cm)	6. Pod bearing length (cm)	9. 100 seed weight (g)	12. Protein content (%)

Conclusion

Overall, high heritability coupled with high GA as % of mean was observed for seed yield per plant (g), number of seeds per plant, number of pods per plant, pod bearing length (cm), plant height (cm) and number of primary branches per plant. Suggesting that these traits are governed by additive gene effects, which is fixable, in such situation direct selection for seed yield may be effective.

Cluster II and III have the highest inter cluster distance (200.33), followed by cluster II and V (198.01), cluster II and IV (121.99), cluster I and III (98.47), cluster I and V (93.45), cluster I and IV (68.16). Indicating the presence of greater diversity between genotypes of these groups. Hence, crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement.

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Reference

1. Anonymous. All India state wise soybean area, production & productivity. SOPA Databank. 2023.
2. Anonymous. Production trends – Soybeans. USDA Foreign Agricultural Service; 2023.

3. Banerjee J, Shrivastava MK, Singh Y, Amrate PK. Estimation of genetic divergence and proximate composition in advanced breeding lines of soybean (*Glycine max* (L.) Merrill). *Environ Ecol.* 2023;41(3C):1960-1968.
4. Chandel K, Patel N, Sharma L, Gali S. Genetic variability, correlation coefficient and path analysis for yield and yield attributing characters in soybean (*Glycine max* L. Merrill). *Green Farming.* 2017;8(3):547-551.
5. Hymowitz T. Diversity within the perennial *Glycine* spp. 2004.
6. Karchal G, Patel JK, Nag SK, Tandekar K. Agromorphological characterization, genetic variability, association and divergence analysis in recombinant inbred lines (RIL's) population in soybean [*Glycine max* (L.) Merrill]; 2024.
7. Mahalanobis PC. On the generalized distance in statistics. *Proc Natl Acad Sci India.* 1936;12:49-55.
8. Nag SK, Painkra C, Tiwari A. Genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. *Int J Curr Sci.* 2020;8(1):3124-3126.
9. Nag SK, Yadav RK, Sahu L, Salam JL, Soni DK, Ranjan SK. Study of correlation and path coefficient analysis for yield and its attributes in soybean (*Glycine max* L.). *Plant Archives.* 2007;7(1):175-178.

10. Neelima G, Mehtre SP, Narkhede GW. Genetic variability, heritability and genetic advance in soybean. *Int J Pure Appl Biosci.* 2018;6(2):1011-1017.
11. Rao CR. *Advanced statistical methods in biometrical research.* New York: John Wiley & Sons; 1952. p. 357-363.
12. Robinson HF. Quantitative genetics in relation to breeding on centennial of Mendelism. *Indian J Genet.* 1966;26:171-187.
13. Satpute GK, Gireesh C, Shivakumar M, Arya GK, Patel RK, Gupta R, Husain S. Genetic variability and association studies in new soybean germplasm accessions. *Soybean Res.* 2016;14(2):77-83.
14. Thakur DK, Nag SK, Sharma A, Chandrakar S. Analysis of genetic divergence in soybean (*Glycine max* (L.) Merrill). *Trends Biosci.* 2015;8(6):1480-1483.
15. Tigga A, Nag SK. Determination of significant characters for improving seed yield in soybean (*Glycine max* L. Merrill) via correlation and path coefficient analysis. *Int J Agric Environ Biotechnol.* 2021;14(3):299-305.
16. Upadhyay P, Shrivastava MK, Amrate PK, Yadav RB. Yield determining traits, genetic variability and character association in exotic lines of soybean [*Glycine max* (L.) Merrill]. *Soybean Res.* 2020;18(2):95-102.