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Assessment of genetic diversity among soybean (*Glycine max* L.) genotypes during *kharif* season

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Abstract
Genetic diversity studies for soybean genotypes were conducted at ZARS, Ganeshkhind, Pune during *kharif* 2024 season. Total 40 genotypes were evaluated for 12 different characters during the investigation in Randomized Block Design (RBD) with three replications using D^2 Statistics. The Mahalanobis D^2 analysis revealed considerable genetic variability among the evaluated genotypes. The forty genotypes were analysed and divided into seven clusters. Cluster I was the largest cluster with 27 genotypes, followed by Cluster III which had 8 genotypes. Remaining Clusters II, IV, V, VI, VII had contain only one genotype each indicating wide divergence from other clusters. Cluster III showed the maximum intra-cluster distance (8.56). The maximum inter-cluster distance was observed in between the Cluster IV and cluster VI (20.79) indicated the heterogenous behaviour. The minimum inter-cluster distance was noticed in between Cluster II and Cluster V (5.58) indicated proximity among the genotype with each other. The character secondary branches per plant contributed maximum to the genetic divergence. According to the D^2 statistics genotype JS-SH-93-01 was top ranking for five characters out of twelve characters. Similarly, genotypes JS-72-44, MACS-1340, MACS-124, MACS-450, DS-228, AUKS-212, RSC-1172, KDS-344 and JS-SH-93-01 can be employed for future breeding programs based on the examination of divergence classes and mean performance.

Keywords: Soybean, genetic divergence, cluster, genotypes

Introduction

Soybean (*Glycine max* L.) is a vital legume crop cultivated worldwide for its high-quality protein and oil content, contributing significantly to food, feed, and industrial applications. Despite its significance, soybean productivity in India remains considerably lower than that in major soybean-producing countries such as the USA and Brazil (Tiwari *et al.* 2019) [4]. It is also known as ‘Golden bean’ or ‘Miracle bean’ (Sureshrao *et al.* 2014) [17]. Soybean contains high quality protein (40%) and oil (20%) (Karr-Lilienthal *et al.* 2005) [18]. In India, it is primarily grown as a kharif crop under rainfed conditions and plays an important role in enhancing farmers income and ensuring nutritional security. In India soybean is mostly grown in Maharashtra, Rajasthan, Gujarat, Karnataka, Telangana, Chhattisgarh. India ranks 5th in soybean production while Maharashtra ranks first in India. In Maharashtra soybean is grown as *kharif* crop with 52.69 lakh tonnes (2023-2024) production and 946 kg/ha productivity. The major soybean growing districts in Maharashtra are Akola, Washim, Amravati, Nagpur, Satara, Sangali, Kolhapur, Solapur, Pune, Ahmednagar districts. The crop’s productivity depends not only on agronomic management but also on the genetic potential of the varieties grown. Therefore, identifying and utilizing genetically diverse germplasm is essential for developing superior and high-yielding cultivars. In plant breeding, a higher degree of genetic divergence among parental lines often increases the likelihood of obtaining transgressive segregants and heterotic combinations.

Materials and Methods

The soybean genotypes were evaluated for 12 different characters viz. days to 50 percent flowering, days to maturity, plant height, plant spread, primary branches per plant, secondary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, protein content, oil content and seed yield per plant.

Total 40 genotypes were sown at ZARS, Ganeshkhind, Pune in Randomized Block Design with three replications during *kharif* 2024 season. All the recommended agronomic and cultural practices were followed for raising the crop. Data of five plants were collected for statistical analysis. Degree of genetic divergence is measured by the D^2 statistics given by Mahalanobis (1936) [1] between the groups and multivariate data. Genetic diversity of forty genotypes were assessed for twelve different characters. Arunachalam and Bandopadhyay (1984) [2] developed a technique to categorize parental divergence into four classes of divergence (DC). The mean (M) and standard deviation (S) of the intra and inter-cluster divergence (D) values were computed to account for the varying amount of variation in parental divergence.

Result and Discussion

The results of genetic diversity based on twelve traits are summarized in table 1. It was observed that the pair of comparison between these genotypes ranged from 31.14 to 432.22 of D^2 values indicated the presence of genetic diversity. Mahbub *et al.* (2016) [3], Joshi *et al.* (2018) [5], Banerjee *et al.* (2023) [6] and Zafar *et al.* (2023) [7] also recorded the adequate genetic diversity among the soybean genotypes. The highest D^2 value was observed between the genotypes JS-93-05 and RSC-1172 (432.22). The lowest D^2 value was noticed between the genotypes JS-72-280 and MDS-5001 (31.14).

Cluster analysis is responsible for determining intra and inter-cluster diversity, which is used for selection of parents for crop improvement programme. Cluster analysis is the method by which different genotypes are grouped into various clusters, indicating similarities between them with the help of different characters under consideration. The more difference between two clusters, greater the genetic diversity between genotypes.

Total forty genotypes were analysed and divided into seven clusters in Table 2. Cluster I was the largest cluster with 27 genotypes, followed by Cluster III which had 8 genotypes. Remaining Clusters II, IV, V, VI, VII had contain only one genotype each indicating wide divergence from other clusters. Sharma *et al.* (2005) formed 15 Clusters from 62 genotypes, out of which 9 were mono-genotypic. Shinde *et al.* (2013) [9] grouped 40 genotypes into 12 Clusters. Cluster I were the largest with 20 genotypes followed by Cluster II and IV each with 5 genotypes, while Cluster VI had 2 genotypes and remaining were solitary. Six Clusters were formed from 40 genotypes by Thakur *et al.* (2015) with Cluster III containing maximum 12 genotypes and Cluster VI, IV, I comprised 8, 5 and 3 genotypes respectively. 9 Clusters were formed from 120 genotypes and 5 checks by Joshi *et al.* (2018) [5]. Cluster IX was the largest Cluster containing 40 genotypes, followed by Cluster V with 34 genotypes, Cluster III with 13 genotypes, Cluster VII with 12 genotypes, Cluster VI with 11 genotypes, Cluster IV and VIII 5 genotypes each and Cluster II with one genotype. Mishra *et al.* (2018) [11] divided the 60 soybean genotypes into 16 clusters. Cluster I were the largest cluster containing 14 genotypes followed by Cluster III with 12 genotypes, Cluster V with 8 genotypes, Cluster VIII with 7 genotypes, Cluster XV with 8 genotypes and remaining11 Clusters contain one genotype each respectively. Banerjee *et al.* (2023) [6] grouped 60 genotypes into 8 clusters in which Cluster I contained 53 genotypes and remaining Clusters contained one genotype each. Table 1. represented the genetic divergence analysis of intra-cluster and inter-cluster D^2 and D values.

Cluster III showed the maximum intra-cluster distance (8.56) followed by Cluster I (7.87). The remaining mono-genotypic Clusters II, IV, V, VI and VII recorded 0.00 intra cluster value.

The maximum inter-cluster distance was observed in between the Cluster IV and cluster VI (20.79) followed by Cluster IV and Cluster VII (20.64), Cluster III and IV (20.40) indicated the heterogenous behaviour. More the difference between the clusters more the genetic variability indicated different genetic constitution among the genotypes. Similar results were obtained by Jain *et al.* (2016) [12], Mahbub *et al.* (2016) [3], Arora *et al.* (2018) [13], Shete *et al.* (2023) [14] and Bhangare *et al.* (2025) [15]. The minimum inter-cluster distance was noticed in between Cluster II and Cluster V (5.58), followed by Cluster VI and Cluster VII (9.48), Cluster I and Cluster IV (9.65), Cluster I and Cluster II (10.49) indicated proximity among the genotype with each other. The more distance present in the clusters more diverse genotypes in cluster which can be easily exploited for crop improvement programme. The lower distance between clusters represented similarities in genotypes in the clusters.

Cluster I was recorded the maximum inter cluster distance with Cluster III (15.28), followed by Cluster VII (14.80), Cluster VI (14.64), Cluster V (10.95), Cluster II (10.49), Cluster IV (9.65), Cluster I (7, 87). Whereas, Cluster II showed the highest inter cluster distance from Cluster VII (16.62) followed by Cluster VI (14.65), Cluster IV (13.06), Cluster III (10.48), Cluster
V (5.58). Cluster III was more distant from Cluster IV (20.40) followed by Cluster VII (14.42), Cluster VI (11.64), Cluster V (11.58), Cluster III (8.56). Cluster IV recorded the maximum distance from Cluster VI (20.79) followed by Cluster VII (20.64), Cluster V (13.68). Cluster V recorded the maximum distance from Cluster VII (16.88) followed by Cluster VI (15.40). Cluster VI was more distant from Cluster VII (9.48).

Genotypes having similar characteristic features are grouped into same cluster even though they belong from different geographical regions, while the genotypes from different clusters varies from each other due to adequate amount of variation present between them even if they are from same geographical regions. Similar results were reported by Shadakshari *et al.* (2011) [16]

Table 1: Average intra and inter cluster D^2 and D values of 7 clusters formed from 40 soybean genotypes.

Clusters	I	II	III	IV	V	VI	VII
I	61.94 (7.87)	110.04 (10.49)	233.48 (15.28)	93.12 (9.65)	119.90 (10.95)	214.33 (14.64)	219.04 (14.80)
II		0.00 (0.00)	109.83 (10.48)	170.56 (13.06)	31.14 (5.58)	214.62 (14.65)	276.22 (16.62)
III			73.27 (8.56)	416.16 (20.40)	134.10 (11.58)	135.49 (11.64)	207.94 (14.42)
IV				0.00 (0.00)	187.14 (13.68)	432.22 (20.79)	426.01 (20.64)
V					0.00 (0.00)	237.16 (15.40)	284.93 (16.88)
VI						0.00 (0.00)	89.87 (9.48)
VII							0.00 (0.00)

Note: Figure in parenthesis indicate D values.

Table 2: Distribution of 40 genotypes into different cluster

Cluster no.	Number of genotypes included	Genotypes
I	27	MACS-57, JS-71-05, NRC-259, MACS-1281, MACS-1340, MACS-1407, KDS-992, DS-228, KDS-726, KDS-726, JS-SH-93-37, MACS-450, MACS-124, JS-72-246, KDS-753, NRC-37, MACS-1037, JS-335, DS-1529, AS-55, MACS-1188, JS-97-52, JS-80-21, KDS-344, AUKS-212, JS-72-44, NRC-12.
II	1	JS-72-280
III	8	MACS-13, NRC-25, MACS-1259, PK-416, NRC-1, DS-1510, JS-2425, Monetta.
IV	1	JS-93-05
V	1	MDS-5001
VI	1	RSC-1172
VII	1	JS-SH-93-01

Cluster means showed wide range of genetic variation for most of characters represented in Table 3.

The cluster mean for days to 50 percent flowering ranged from 43.67 to 51.67. The genotype in Cluster IV (43.67) was early for days to 50 percent flowering followed by Cluster III (47.67), Cluster VII (48.67). The genotype from Cluster V (51.67) was late for days to 50 percent flowering.

The maximum cluster mean for days to maturity was recorded by Cluster VI (110.00) followed by Cluster I (104.27), Cluster III (104.25) and the minimum cluster mean was obtained by Cluster V, Cluster VI (98.67) respectively.

Cluster mean for plant height ranged from 54.00 to 108.47. The minimum cluster mean for plant height was noticed by Cluster V (54.00) followed by Cluster II (58.80), Cluster III (73.79). Whereas, the maximum cluster mean for plant height was noticed by Cluster VII (108.47) followed by Cluster I (83.48) and Cluster VI (77.27).

Cluster mean for plant spread ranged in between 29.13 and 61.00. The maximum cluster mean for plant spread was noticed by Cluster VII (61.00) followed by Cluster VI (48.53), Cluster I (43.82). However, the minimum cluster mean for plant spread was observed by Cluster II (29.13) followed by Cluster IV (33.00) and Cluster III (39.20).

Cluster mean for primary branches per plant was ranged in between 3.00 to 4.53. The minimum cluster mean for primary branches per plant was observed in Cluster II (3.00) followed by Cluster III (3.03) and Cluster VI (3.40). The maximum cluster mean was recorded by Cluster VII (4.53) followed by Cluster IV (4.20) and Cluster V (3.73).

The maximum cluster mean for secondary branches per plant recorded by Cluster VII (7.80) followed by Cluster VI (6.40), Cluster V (6.00). The minimum cluster mean for secondary branches per plant was observed in Cluster II (5.00) and Cluster IV (5.00) followed by Cluster I (5.54) and Cluster V (6.00). The cluster mean ranges from 5.00 to 7.80.

The cluster mean for number of pods per plant ranged between 57.00 to 167.36. Cluster VI (167.36) had the highest cluster mean for number of pods per plant followed by Cluster VII (160.81), Cluster I (91.94). The lowest mean for this trait was observed in Cluster V (57.00) followed by Cluster II (57.14) and Cluster IV (69.55).

Cluster mean for number of seeds per pod was ranged from 2.40 to 2.73. The highest mean for number of seeds per pod was showed by Cluster V (2.73) followed by Cluster I (2.63), Cluster VI (2.60). Whereas, the lowest cluster mean was observed in Cluster IV (2.40) followed by Cluster II (2.47).

Table 3: Cluster means for 12 traits in soybean.

Clusters	Days to 50 percent flowering (no.)	Days to maturity (no.)	Plant height (cm)	Plant spread (cm)	No. of primary branches/plant	No. of secondary branches/plant	No. of pods/plant	No. of seeds/pod	100-seed weight (g)	Protein content (%)	Oil content (%)	Seed yield/plant (g)
I	49.22	104.27	83.48	43.82	3.94	5.54	91.94	2.63	14.68	43.19	16.65	33.21
II	50.33	102.33	58.80	29.13	3.00	5.00	57.14	2.47	12.17	48.95	17.33	16.26
III	47.67	104.25	73.79	39.20	3.03	6.03	77.27	2.54	14.66	46.38	16.77	26.93
IV	43.67	98.67	75.40	33.00	4.20	5.00	69.55	2.40	15.33	45.76	16.58	24.46
V	51.67	98.67	54.00	41.00	3.73	6.00	57.00	2.73	15.55	38.35	16.73	23.06
VI	50.67	110.00	77.27	48.53	3.40	6.40	167.36	2.60	11.61	37.13	14.25	47.94
VII	48.67	102.67	108.47	61.00	4.53	7.80	160.81	2.53	9.97	48.06	18.89	38.97

The highest cluster mean for 100-seed weight was recorded by Cluster V (15.55) followed by Cluster IV (15.33), Cluster I (14.68). While, the lowest cluster mean was recorded in Cluster VII (9.97) followed by Cluster VI (11.61) and Cluster II (12.17).

Cluster means for protein content was ranged between 37.13 to 48.95. The maximum cluster mean was recorded by Cluster II (48.95) followed by Cluster VII (48.06), Cluster III (46.38) and minimum cluster mean was observed by Cluster VI (37.13) followed by Cluster V (38.35).

Cluster means for oil content was ranged from 14.25 to 18.89. The maximum cluster mean for oil content was recorded by Cluster VII (18.89) followed by Cluster II (17.33) and Cluster V (16.73). The minimum cluster mean was recorded by Cluster VI (14.25) followed by Cluster IV (16.58) and Cluster I (16.65).

The maximum cluster mean was recorded by Cluster VI (47.94) followed by Cluster VII (38.97) and Cluster I (33.21). The minimum cluster mean was recorded by Cluster II (16.26) followed by Cluster V (23.06) and Cluster IV (24.46). The range of cluster mean was ranged between 16.26 to 47.94.

Table 4. represented the contribution of twelve characters in total divergence. In genetic divergence the character secondary branches per plant contributed highest (63.97%) followed by number of pods per plant (15.51%), days to maturity (6.92%), plant height (3.46%), primary branches per plant (3.21%), protein content (2.44%), plant spread

(2.31%) and 100-seed weight (0.90%) contributed major portion in genetic divergence. Thorat *et al.* (2023) observed that the seed yield per plant contributed (36.82%) followed by 100-seed weight (33.33%), plant height (10.69%), protein content (8.13%) and oil content (5.57%) in genetic divergence. Upadhyay *et al.* (2022) recorded that the number of seed per plant contributed maximum (32.73%) followed by days to maturity (27.84%), days to flower initiation (11.92%), biological yield (11.76%), pods per plant (10.04%), 100-seed weight (4.49%) etc. Naik *et al.* (2016) recorded the maximum contribution of yield per hectare (23.6%) in genetic divergence followed by seed longevity and plant height. Days to 50 percent flowering contributed least (4.12%). Characters like protein content (4.74%), seed yield per plant (4.10%), days to 50 percent flowering (3.21%), plant spread (0.90%), primary branches per plant (0.90%), number of seeds per pod (0.77%) contributed less in genetic divergence. Whereas, secondary branches per plant had no contribution in genetic divergence.

Table 4: Percent share of various characters to divergence.

Sr. No.	Characters	Times ranked 1st	Contribution%
1.	Days to 50 percent flowering (No.)	2	0.26
2.	Days to maturity (No.)	54	6.92
3.	Plant height (cm)	27	3.46
4.	Plant spread (cm)	18	2.31
5.	Primary branches per plant (No.)	25	3.21
6.	Secondary branches per plant (No.)	499	63.97
7.	Number of pods per plant	121	15.51
8.	Number of seeds per pod	1	0.13
9.	100-Seed weight (g)	7	0.90
10.	Protein content (%)	19	2.44
11.	Oil content (%)	3	0.38
12.	Seed yield per plant (g)	4	0.51
	Total	780	100

Conclusions

Cluster III showed the maximum intra-cluster distance followed by Cluster I. The maximum inter-cluster distance was observed in between the Cluster IV and cluster VI followed by Cluster IV and Cluster VII, Cluster III and IV indicated the heterogenous behaviour. The characteristics that contributed most to overall divergence were secondary branches per plant, no. of pods per plant, days to maturity, plant height, primary branches per plant, protein content and plant spread. Genotypes JS-72-44, MACS-1340, MACS-124, MACS-450, DS-228, AUKS-212, RSC-1172, KDS-344 and JS-SH-93-01 can be employed for next breeding programs based on the examination of divergence classes and mean performance.

References

1. Mahalanobis PC. On generalized distance in statistics. Proceedings of the National Institute of Sciences of India. 1936;2:49-55.
2. Arunachalam V, Bandopadhyay A. Limits to genetic divergence for occurrence of heterosis: experimental evidence from crop plants. Indian Journal of Genetics and Plant Breeding. 1984;44(3):548-554.
3. Mahbub MM, Shirazy BJ. Evaluation of genetic diversity in different genotypes of soybean (*Glycine max* (L.) Merrill). American Journal of Plant Biology. 2016;1(1):24-29.
4. Tiwari S, Tripathi N, Tsuji K, Tantwai K. Genetic diversity and population structure of Indian soybean (*Glycine max* (L.) Merr.) as revealed by microsatellite markers. Physiology and Molecular Biology of Plants. 2019;25(4):953-964.
5. Joshi D, Pendra P, Kamendra, Singh K, Adhikari S. Study of genetic divergence in soybean germplasm. Chemical Science Review and Letters. 2018;7(26):533-539.
6. 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). Environment and Ecology. 2023;41(3C):1960-1968.
7. Zafar SA, Aslam M, Khan HZ, Sarwar S, Rehman RS, Hassan M, El Sabagh A. Estimation of genetic divergence and character association studies in local and exotic diversity panels of soybean (*Glycine max* L.) genotypes. Phyton-International Journal of Experimental Botany. 2023;92:1887-1906.
8. Sharma B, Singh BV, Singh KS, Pusphendra P, Gupta AK, Gupta MK. Genetic divergence in Indian varieties of soybean (*Glycine max* (L.) Merrill). Indian Journal of Pulses Research. 2005;18(1):84-86.
9. Shinde SR, Chavan RB, Pawar RM. Genetic divergence in soybean (*Glycine max* (L.) Merrill). Asian Journal of Bio Science. 2013;8(2):225-228.
10. Thakur DK, Nag SK, Sharma A, Chandrakar SC. Analysis of genetic divergence in soybean (*Glycine max* (L.) Merrill). [Journal name/details missing-needs completion]. 2015.
11. Mishra S, Jha A, Panchshwar DK, Shrivastava AN. Study of genetic divergence in advance breeding lines of soybean (*Glycine max* (L.) Merrill) for yield attributing traits. International Journal of Bio-Resource and Stress Management. 2018;9(1):103-107.
12. Jain S, Chacharia M, Singh J, Srivastava SC, Tomar SS. Genetic diversity in soybean (*Glycine max* (L.) Merrill). Environment and Ecology. 2016;34(1A):285-287.
13. Arora RN. Assessment of genetic diversity for yield and seedling traits in soybean (*Glycine max* L. Merrill). Electronic Journal of Plant Breeding. 2018;9(1):355-360.
14. Shete RR. Identifying promising genotypes for genetic divergence and path analysis in soybean (*Glycine max* (L.) Merr.). International Journal of Agricultural Sciences. 2023;[volume/issue missing]:[pages missing].
15. Bhangare VR, Deshmukh MP, Kale SD, Kamble MS, Patil PB. Assessment of genetic diversity in 35 soybean

genotypes (*Glycine max* (L.) Merrill). Plant Archives. 2025;25(1):1265-1271.
16. Shadakshari TV, Kalaimagal T, Senthil N, Boranayaka MB, Kambe Gowda R, Rajesha G. Genetic diversity studies in soybean (*Glycine max* (L.) Merrill) based on morphological characters. Asian Journal of Biological Sciences. 2011;6(1):7-11.
17. Sureshrao SS, Singh VJ, Gampala S, Rangare NR. Assessment of genetic variability of the main yield related characters in soybean. International Journal of Food, Agriculture and Veterinary Sciences. 2014;4(2):69-74.
18. Karr-Lilienthal LK, Grieshop CM, Merchen NR, Mahan DC, Fahey GC. Chemical composition and protein quality comparisons of soybeans and soybean meals from five leading soybean-producing countries. Journal of Agricultural and Food Chemistry. 2005;53(2):219-225.