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Genetic diversity studies in soybean (*Glycine Max* (L.) Miller)

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Abstract
The present investigation was conducted during Kharif 2024 to assess genetic diversity and identify promising parents for future breeding programs. A total of 100 soybean genotypes, along with five checks, were evaluated using an augmented block design comprising four blocks. In this study, genetic divergence among the genotypes was evaluated using D^2 analysis. The 100 genotypes were grouped into eight clusters based on the D^2 values. Cluster I was the largest, consisting of 63 genotypes, followed by Cluster II with 21 genotypes and Cluster IV with 10 genotypes. Clusters III, V, VI, and VIII each contained a single genotype. Plant height (31.67%) and pods per plant (29.05%) contributed the most toward total genetic diversity. The highest intra-cluster distance was observed in Cluster VII, while the greatest inter-cluster distance was recorded between Clusters IV and VII.

Keywords: Chhani, consumption, fuel-wood, households, Lanchaan

1. Introduction
Soybean (*Glycine max* L. Merrill) belongs to the Febaceae family and the subfamily Faboideae. It is short day and self-pollinated crop. It is also known as "Wonder crop" due to its ease of cultivation, multiple uses, and significant nutritional value. Soybean contains approximately 40 per cent of protein and 20 per cent oil making them an important source of both plant based protein and edible oil. India is fifth largest producer of soybean in world, with Madhya Pradesh, Maharashtra, and Uttar Pradesh being the leading soybean producing states. Given the steady rise in the global population, the demand for improved crop varieties with higher yield potential is becoming increasingly critical. Therefore the present study was undertaken to assess the genetic diversity among soybean genotypes, which will help in identifying superior parental combinations for the development of improved, high yielding commercial varieties.

2. Materials and Methods
The study was conducted on 100 soybean genotypes and 5 checks using augmented block design to assess genetic diversity at Regional Research centre, Amravati during kharif season 2024. The data was recorded for ten characters *viz* days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods clusters per plant, number of pods per plant, number of seeds per pod, seed weight (g), seed yield per plant (g) and oil content (%). In this study, genotypes were grouped into different clusters using Tocher's method (Rao 1952) [7] and genetic diversity was evaluated using D^2 analysis (1936).

3. Results and Discussion
3.1 Contribution of each character towards genetic divergence
The contribution to the total divergence was maximum by plant height (31.67%). This was followed by number of pods per plant (29.05%), days to maturity (13.90%), days to 50% flowering (13.83%) and 100 seed weight (3.23%), seed yield per plant (2.16%), number of pod clusters per plant (2.07%) and number of branches per plant (1.76%), oil content (1.27%) and number of seed per pod (1.06).

3.2 Grouping of genotypes into different clusters

In the present study, all 100 genotypes along with 5 checks were grouped into eight distinct clusters. The largest number of genotypes was grouped into cluster I accounting for 63 genotypes, followed by cluster II with 21 genotypes, clusters IV with 10 genotypes and cluster VII with 7 genotypes, while clusters III, V, VI and VIII each had only 1 genotype.

3.3 Average intra and inter cluster distance

The result presented in table show that inter cluster distances were more than the intra cluster distances which indicated the presence of narrow genetic variation within a cluster. As cluster V, cluster VI and cluster VIII has only one genotype, the intra-cluster value is zero. While the maximum intra cluster distances as observed for cluster VlI (15.85) followed by cluster II (12.00). The average inter cluster distance was maximum between cluster IV and VII (29.84), followed by cluster IV and V (29.16) and cluster II and IV (27.09). The high values of inter-cluster distance revealed substantial genetic divergence among the groups (Singh and Chaudhury, 1985) [8].

3.4 Cluster mean analysis

The highest cluster means for each character were observed as follows: for days to 50% flowering, cluster VI recorded the highest mean (46.90 days) for days to maturity, cluster VI also showed the highest mean (103.50 days) plant height was highest in cluster V (58.94 cm); number of branches per plant was maximum in cluster V (4.35); number of pod clusters per plant was highest in cluster VI (7.30) number of pods per plant was maximum in cluster VIII (40.75); number of seeds per pod was highest in cluster VI (2.39); 100 seed weight was also highest in cluster VI (12.03 g); seed yield per plant was maximum in cluster VI (7.40 g); and oil content was highest in cluster VI (19.99%).

Table 1: Contribution of each character towards genetic divergence

Source	Times rank first	% Contribution
Days to 50% flowering	755	13.83
Days to maturity	759	13.90
Plant height (cm)	1729	31.67
No of branches/plant	96	1.76
No of pod cluster	113	2.07
No of pod per plant	1586	29.05
No of seed per pods	58	1.06
100 seed weight (g)	176	3.23
Seed yield/plant (g)	118	2.16
Oil Content (%)	69	1.27

Table 2: Average intra and inter cluster distance in soybean genotypes

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	10.77	18.66	14.03	15.35	20.23	13.60	20.63	16.23
Cluster II		12.00	24.15	27.09	16.12	17.14	17.05	21.30
Cluster III			0.00	18.78	22.60	16.56	21.21	23.80
Cluster IV				11.16	29.16	19.29	29.84	16.85
Cluster V					0.00	24.43	13.43	22.14
Cluster VI						0.00	21.35	22.39
Cluster VII							15.85	26.27
Cluster VIII								0.00

Table 3: Cluster mean values of ten characters in eight clusters in soybean

	Days to 50% flowering	Days to maturity	Plant height	Number of branches/ plant	Number of pod cluster / plant	Number of pods /plant	Number of seeds / pod	100 seed weight (g)	Seed yield / plant (g)	Oil content
Cluster I	41.49	94.65	42.87	2.51	5.18	29.42	2.01	9.92	4.83	18.26
Cluster II	46.71	99.77	50.55	3.23	6.76	39.61	1.85	8.92	6.22	18.73
Cluster III	36.90	96.50	47.78	1.95	3.90	20.11	2.24	11.29	4.35	17.84
Cluster IV	38.79	90.81	33.33	2.32	5.26	26.96	2.19	11.33	5.72	18.87
Cluster V	41.10	90.70	58.94	4.35	5.50	37.95	1.80	8.63	5.21	18.27
Cluster VI	46.90	103.50	42.18	2.75	7.30	28.31	2.39	12.03	7.40	19.99
Cluster VII	44.10	97.01	58.10	3.29	5.56	33.32	1.86	9.36	5.05	18.14
Cluster VIII	35.90	90.30	37.86	2.35	4.34	40.75	2.36	10.08	3.78	17.35

4. Conclusion

Based on the values of D^2 analysis, all 100 genotypes along with five checks were grouped into eight distinct clusters. The largest number of genotypes was grouped into cluster I accounting for 63 genotypes, followed by cluster II with 21 genotypes and Cluster IV with 10 genotypes. Cluster VII contained 7 genotypes, while clusters III, V, VI and VIII each had only single genotype. Among all clusters, the highest intra cluster distance was recorded for Cluster VII (15.85), followed by Cluster II (12.00), suggesting considerable genetic variation among genotypes within these clusters. In contrast, minimum intra cluster distances were found in Clusters III, V, VI, and VIII due to the presence of a single genotype in each cluster**.** The highest average inter cluster distance was observed between Cluster IV and Cluster VII (29.84), followed by Cluster IV and Cluster V (29.16). Selection of parents from these genetically divergent cluster would result in higher level of heterosis for the respective traits. On the basis of cluster mean and inter-cluster distance values, it can be concluded that hybridization between the genotypes of cluster IV and VII, IV and V, II and IV, VI and VII, I and VII would be promising for developing high yielding soybean varieties.

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