



Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2026.v26.no.2.073>

DECIPHERING GENETIC DIVERGENCE AND TRAIT RELATIONSHIPS IN SOYBEAN *Glycine max* (L.) MERRILL).

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(Date of Receiving-29-05-2026; Date of Revision-17-08-2026; Date of Acceptance-27-08-2026)

ABSTRACT

Twenty-five soybean genotypes including three checks were taken as experimental material to assess genetic divergence present among them. Data were collected on eleven quantitative traits. Analysis of variance showed significant differences among genotypes for all traits, indicating the presence of substantial genetic variability. High phenotypic coefficient of variation and genotypic coefficient of variation was observed for seed yield per plant (g), plant height (cm), number of pod bearing nodes per plant and number of pods per plant. Heritability was found higher for all the studied traits. High heritability coupled with high genetic advance as a percentage of mean was observed for plant height (cm), number of primary branches per plant, number of pod bearing nodes per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g) and seed yield per plant (g) an indication of predominance of additive gene action and direct selection of these traits will be effective. Hundred seed weight (g), number of seeds per pod and number of pods per plant showed significant positive correlation as well as positive direct effect on seed yield per plant (g) indicates these traits can be useful in selection to increase yield. Mahalanobis D^2 statistics distributed the genotypes into four clusters. Cluster I contained maximum number of genotypes. Maximum inter cluster distance observed between Cluster III and IV, suggesting good scope for developing superior recombinants through hybridization between these clusters. Among all the traits studied, plant height (cm), days to 50% flowering and Seed yield per plant (g) contributed the most to overall genetic divergence.

Key words: Soybean, Heritability, Phenotypic coefficient of variation, Genotypic coefficient of variation, Correlation analysis, Path coefficient analysis, Genetic divergence.

Introduction

Soybean crop is recognised as the most important legume- derived oilseed crop worldwide due to exceptional nutritional value and wide industrial applications. Owing to its high protein (38-24%) and oil content (18-22%) (Ogre *et al.*, 2023), soybean serves as a major source of edible oil, livestock feed and industrial products. Soybean contributes to soil fertility through biological nitrogen fixation, making it an important component of sustainable agricultural systems (Agarwal *et al.*, 2013; Talukdar and Shivakumar, 2016). Consequently, Soybean has become a strategic crop for ensuring global food, nutritional, and economic security. (Hartman *et al.*, 2011). Soybean cultivation is concentrated in a few major producing

countries; Brazil emerged as the largest producer followed by the United States, Argentina, China and India, which together account for the majority of global production. Although India ranked fourth globally in terms of soybean cultivation area, covering about 13.08 million hectares (approximately 9.55% of the global soybean area), it ranked fifth in production because of its relatively lower productivity, indicating considerable scope for enhancing yield through the development and adoption of improved cultivars and better crop management practices (Anonymous, 2025). Although India is one of the leading soybean countries in terms of cultivated area. Despite having a large area coverage, soybeans still suffer low productivity when compared to other major soybean-

growing nations due to unstable climatic conditions, biotic and abiotic stresses and restricted genetic diversity among cultivated genotypes, which continue to limit productivity (Kumawat *et al.*, 2024). Expanding the genetic base and identifying superior genotypes are therefore essential for development of high yielding, resistant and tolerant to biotic stresses and climate resilience cultivars.

Seed yield is a complex quantitative trait controlled by several interrelated component traits and influenced by environmental factors. Therefore, the success of any breeding programme depends on the availability and effective utilization of genetic variability (Jandong *et al.*, 2020). Estimation of genetic parameters such as genotypic and phenotypic coefficients of variation, heritability and genetic advance provides valuable information on the nature of gene action and the effectiveness of selection (Zafar *et al.*, 2023). Correlation analysis reveals the association among traits, whereas path coefficient analysis partitions these associations into direct and indirect effects, thereby identifying traits with the greatest contribution to seed yield. Furthermore, assessment of genetic divergence using Mahalanobis D² statistics facilitates the identification of genetically diverse parents for hybridization, increasing the likelihood of obtaining superior recombinants (Ghuge *et al.*, 2023). Therefore, the combined evaluation of genetic variability, character association, path coefficient and genetic divergence provides a sound basis for the development of high-yielding soybean cultivars. In view of the above, the present study was undertaken to estimate genetic variability, character associations, and assessment of genetic divergence among twenty-five soybean genotypes to identify promising breeding material for future varietal improvement.

Materials and Methods

The study was carried out during the *kharif* 2025 at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.), India. The experimental material comprised twenty-five genotypes of soybean, including three checks, namely RSC 10-52, RSC 11-15 and RSC 11-07. The experiment was laid out in Randomized Complete Block Design with three replications. Observations were recorded on five randomly selected plants from each genotype in each replication, and the mean values were used for statistical analysis. Data were collected for eleven quantitative traits, these observations were subjected to appropriate statistical analyses including analysis of variance (Fisher, 1918), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) suggested by Burton (1952), heritability in broad

Table 1: Analysis of variance for yield and its attributing traits in soybean genotypes.

Source of Variation	Mean sum of squares		
	R	T	E
Degree of freedom	2	24	48
Days to 50% flowering	0.05	22.28**	0.33
Days to maturity	0.49	76.23**	0.83
Plant Height (cm)	4.12	639.48**	6.50
No. of primary branches per plants	0.208	0.842**	0.088
No. of pod bearing nodes per plant	0.18	19.61**	0.48
Number of pods per plant	4.90	238.58**	5.52
Number of seeds per pod	0.026	0.219**	0.014
100 seed weight (g)	0.27	3.72**	0.33
Protein content (%)	3.46	21.86**	0.62
Oil content (%)	0.47	4.80**	0.09
Seed yield per plant (g)	0.27	9.99**	0.21

R: Replication; T: Treatment; E: Error
*5% level of significance ** 1% level of significance

sense using formula given by Hanson *et al.*, (1956), genetic advance as percentage of mean suggested by Johnson *et al.*, (1955), analysis of correlation coefficient as per formula suggested by Miller *et al.*, (1958), path coefficient analysis by Dewey and Lu (1959) and Mahalanobis D² statistics (1936) was used to estimate genetic divergence among the genotypes, for reliable interpretation of the experimental results.

Results and Discussion

The analysis of variance revealed significant differences among the tested genotypes for all the quantitative traits, indicating adequate variability. Similar findings were also reported by the previous workers

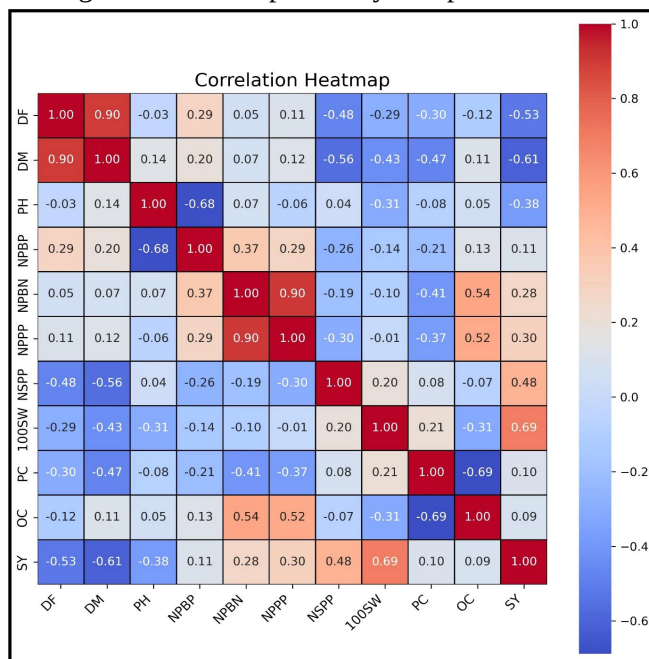


Fig. 1: Heatmap for genotypic correlation coefficient.

Table 2: Genetic variability parameters for yield and yield-attributing traits.

Characters	Mean	Range		GCV %	PCV %	h^2_{bs} %	GA as % of mean
		Min	Max				
Days to 50% flowering	47.27	41.33	50.67	5.72	5.85	95.67	11.53
Days to Maturity	106.41	95.33	113.33	4.71	4.79	96.82	9.55
Plant Height (cm)	53.62	27.27	86.87	27.09	27.51	97.01	54.97
No. of primary branches per plant	3.37	2.33	4.80	14.87	17.29	73.97	26.35
No. of pod bearing nodes per plant	12.46	8.73	17.87	20.27	21.02	93.06	40.29
Number of pods per plant	44.81	33.73	68.63	19.67	20.35	93.37	39.15
Number of seeds per pod	2.36	1.89	2.84	11.05	12.16	82.58	20.68
100 seed weight (g)	7.52	5.88	10.83	14.14	16.08	77.27	25.60
Protein content (%)	36.68	31.71	41.16	7.25	7.57	91.92	14.33
Oil content (%)	18.69	16.00	21.00	6.70	6.90	94.39	13.41
Seed Yield per plant (g)	5.23	1.73	8.67	34.49	35.61	93.82	68.83

Kalamkhede *et al.*, (2025), Kumari *et al.*, (2022), Tandekar *et al.*, (2022) and Khumukcham *et al.*, (2022).

The estimates of genetic parameters for yield and its attributing traits viz., genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent of mean along with mean and range are given in Table 2. According to Sivasubramanian and Madhavamenon (1973), genotypic coefficient of variation and phenotypic coefficient values are classified as low (<10%), moderate (10–20%), and high (>20%). In the present study, for all the characters minimum difference between phenotypic and genotypic coefficients of variation was observed indicating less environmental influence and scope of selection for these traits.

High genotypic coefficient of variation and phenotypic coefficient values were recorded for seed yield per plant (34.49% and 35.61%), plant height (27.09% and 27.51%)

and number of pod-bearing nodes per plant (20.27% and 21.02%). Number of pods per plant also exhibited high phenotypic coefficient of variation (20.35%) with a nearly high genotypic coefficient of variation (19.67%), suggesting the presence of substantial genetic variability for these traits. Moderate genotypic coefficient of variation and phenotypic coefficient of variation estimates were observed for number of primary branches per plant (14.87% and 17.29%), number of seeds per pod (11.05% and 12.16%) and 100-seed weight (14.14% and 16.08%), indicating limited genetic variability among the genotypes. Low genotypic coefficient of variation and phenotypic coefficient of variation values were recorded for days to 50% flowering (5.72% and 5.85%), days to maturity (4.71% and 4.79%), protein content (7.25% and 7.57%) and oil content (6.70% and 6.90%), reflecting comparatively less genetic variability for these traits.

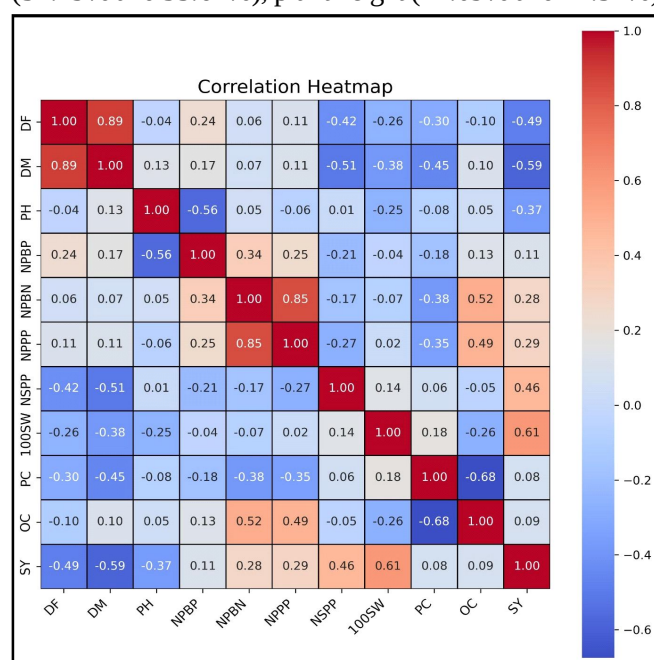
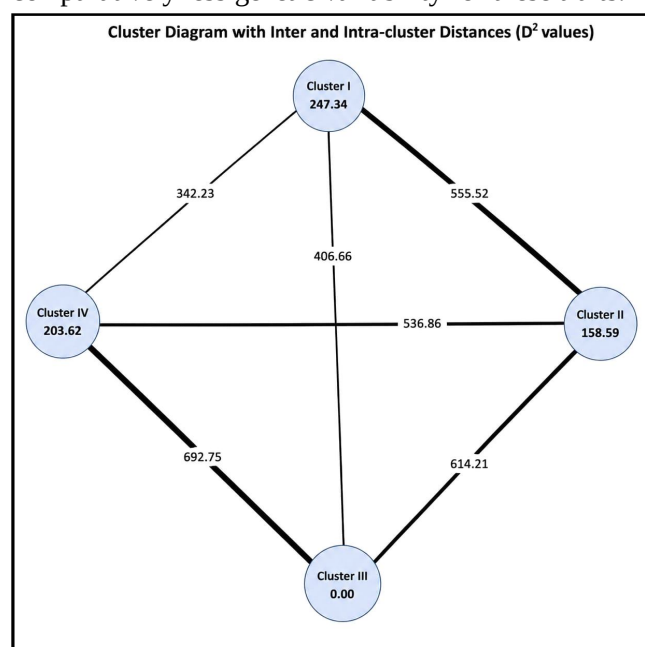
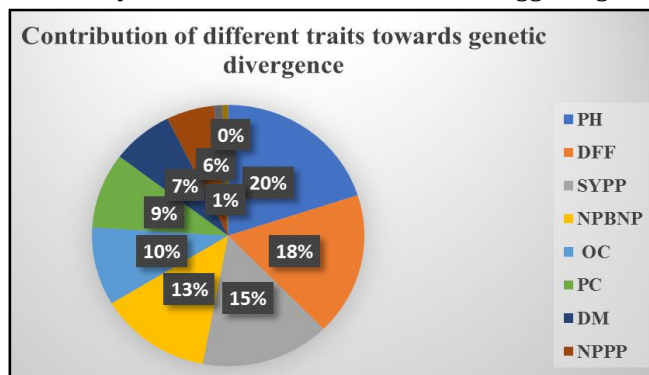
**Fig. 2:** Heatmap for phenotypic correlation coefficient.**Fig. 3:** Diagrammatic representation of inter and intra cluster distances.

Table 3: Estimates of genotypic and phenotypic correlation coefficients for seed yield and its attributing traits.

Traits		DFP	DM	PH	NPBPP	NPBNP	NPPP	NSPP	100 SW	PC	OC	SYPP
DFP	G	1	0.901**	-0.034	0.289*	0.054	0.107	-0.476**	-0.290*	-0.302**	-0.118	-0.527**
	P	1	0.892**	-0.040	0.240*	0.057	0.109	-0.426**	-0.256*	-0.298**	-0.105	-0.489**
DM	G		1	0.136	0.201	0.073	0.119	-0.560**	-0.432**	-0.473**	0.110	-0.614**
	P		1	0.132	0.166	0.070	0.111	-0.505**	-0.384**	-0.453**	0.105	-0.589**
PH	G			1	-0.680**	0.072	-0.062	0.035	-0.311**	-0.076	0.051	-0.383**
	P			1	-0.564**	0.053	-0.060	0.013	-0.250*	-0.079	0.049	-0.368**
NPBPP	G				1	0.366**	0.286*	-0.264*	-0.145	-0.209	0.128	0.107
	P				1	0.335**	0.253*	-0.217	-0.038	-0.178	0.127	0.111
NPBNP	G					1	0.902**	-0.194	-0.099	-0.408**	0.540**	0.278*
	P					1	0.855**	-0.170	-0.068	-0.381**	0.515**	0.283*
NPPP	G						1	-0.299**	-0.006	-0.373**	0.519**	0.303**
	P						1	-0.268*	0.023	-0.349**	0.488**	0.294**
NSPP	G							1	0.200	0.081	-0.073	0.483**
	P							1	0.139	0.064	-0.047	0.458**
100 SW	G								1	0.214	-0.313**	0.694**
	P								1	0.179	-0.265*	0.606**
PC	G									1	-0.688**	0.097
	P									1	-0.675**	0.083
OC	G										1	0.089
	P										1	0.087
SYPP												1

****Significance at 1% probability level, *Significance at 5% probability level**
 (DFP: Days to 50% flowering, DM: Days to maturity, PH: Plant height(cm), NPBPP: Number of primary branches per plant, NPBNP: Number of pod bearing nodes per plant, NPPP: Number of pods per plant, NSPP: Number of seeds per pod, 100 SW: 100 seed weight(g), PC: Protein content (%), OC: Oil content (%), SYPP: Seed yield per plant (g))

The present findings are consistent with the reports of Tandekar *et al.*, (2022), Kumar *et al.*, (2024), Vasanth *et al.*, (2023) and Parindiyal *et al.*, (2023), for high variability traits. Similar moderate variability for number of primary branches per plant, number of seeds per pod, and 100-seed weight was reported by Mehra *et al.*, (2020), Tandekar *et al.*, (2022), and Pawar *et al.*, (2020). Likewise, the low variability observed for days to 50% flowering, days to maturity, protein content, and oil content was supported by the findings of Pawar *et al.*, (2020), Chandel *et al.*, (2017), and Tandekar *et al.*, (2022). High heritability recorded all characters studied, suggesting that

**Fig. 4:** Contribution of different traits towards genetic divergence.

genetic factors largely control the expression of these characters and are less affected by environmental factors. The presence of high heritability indicated that the inheritance of these traits is governed by additive gene action. This result showed close resemblance with the report of Patel *et al.*, (2025) for number of pods per plant, number of primary branches per plant and number of seeds per pod, for plant height and seed yield per plant by Kalamkhede *et al.*, (2025), for 100- seed weight, oil content, number of primary branches per plant, protein content, plant height and number of seeds per pod by Tandekar *et al.*, (2023). Vasanth *et al.*, (2023) also reported high heritability for plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, days to 50% flowering, 100-seed weight, days to maturity, plant height, number of nodes per plant and number of pods per plant by Joshi *et al.*, (2018).

However, the genetic advance as percent over mean was found high in plant height(cm), number of primary branches per plant, number of pod bearing nodes per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g) and seed yield per plant (g). genotypic coefficient of variation alone is not sufficient

Table 4: Direct (bold diagonal) and indirect effects (off diagonal) of traits on the yield of soybean genotypes at genotypic level.
Residual = 0.0947

Traits	DFE	DM	PH	NPBPP	NPBNP	NPPP	NSPP	100 SW	PC	OC	SYPP
DFE	-0.4026	0.3416	-0.0039	0.1279	-0.0093	0.0533	-0.2755	-0.2100	-0.1133	-0.0353	-0.527**
DM	-0.3628	0.3790	0.0156	0.0892	-0.0127	0.0595	-0.3236	-0.3134	-0.1779	0.0330	-0.614**
PH	0.0138	0.0517	0.1147	-0.3015	-0.0125	-0.0309	0.0203	-0.2253	-0.0287	0.0152	-0.383**
NPBPP	-0.1162	0.0763	-0.0780	0.4433	-0.0633	0.1428	-0.1524	-0.1052	-0.0784	0.0382	0.107
NPBNP	-0.0217	0.0277	0.0083	0.1621	-0.1732	0.4510	-0.1124	-0.0720	-0.1535	0.1613	0.278*
NPPP	-0.0429	0.0451	-0.0071	0.1266	-0.1563	0.4999	-0.1729	-0.0047	-0.1400	0.1553	0.303**
NSPP	0.1918	-0.2121	0.0040	-0.1168	0.0337	-0.1495	0.5782	0.1449	0.0303	-0.0218	0.483**
100 SW	0.1166	-0.1638	-0.0356	-0.0643	0.0172	-0.0032	0.1155	0.7250	0.0803	-0.0937	0.694**
PC	0.1214	-0.1794	-0.0088	-0.0925	0.0708	-0.1863	0.0466	0.1549	0.3758	-0.2058	0.097
OC	0.0475	0.0418	0.0058	0.0567	-0.0935	0.2597	-0.0422	-0.2272	-0.2587	0.2989	0.089

**Significance at 1% probability level, *Significance at 5% probability level
(**DFE**: Days to 50% flowering, **DM**: Days to maturity, **PH**: Plant height(cm), **NPBPP**: Number of primary branches per plant, **NPBNP**: Number of pod bearing nodes per plant, **NPPP**: Number of pods per plant, **NSPP**: Number of seeds per pod, **100 SW**: 100 seed weight(g), **PC**: Protein content (%), **OC**: Oil content (%), **SYPP**: Seed yield per plant (g))

for determination of the extent of variation that perpetuate from one generation to the next. genotypic coefficient of variation together with heritability estimates would give a better picture of the extent of genetic advance that can be made through selection (Johnson *et al.*, 1963) for estimating genetic gain under selection. High heritability estimate coupled with high genetic advance as a percentage of mean was observed for indicates high improvement can be achieved from direct selection due to predominance of additive gene action.

High heritability coupled with moderate genetic advance as per cent of mean for days to 50% flowering, protein content, and oil content suggested limited genetic gain from selection, indicating that direct selection for these traits would be less effective. High heritability coupled with low genetic advance as per cent of mean

for days to maturity suggested the predominance of non-additive gene action, indicating a limited improvement from direct selection. Therefore, the trait may be better exploited through hybridization and heterosis breeding. Similar findings were recorded by Bairagi *et al.*, (2023) for number of pods per plant, plant height and primary branches per plant, Vasanth *et al.*, (2023) and Tandekar *et al.*, (2023) for 100 seed weight, seed yield per plant, number of seeds per pod, number of pods per plant, number of primary branches per plant and plant height.

The genotypic correlation coefficient and phenotypic correlation coefficient estimates were presented in Table 3. Number of pod bearing nodes per plant, number of pods per plant, number of seeds per pod and 100 seed weight (g) showed significant positive correlation with seed yield per plant (g) at both genotypic and phenotypic

Table 5: Direct (bold diagonal) and indirect effects (off diagonal) of traits on the yield of soybean genotypes at phenotypic level.
Residual = 0.237.

Traits	DFE	DM	PH	NPBPP	NPBNP	NPPP	NSPP	100 SW	PC	OC	SYPP
DFE	-0.2990	0.0869	0.0119	-0.0060	0.0164	0.0192	-0.1740	-0.1126	-0.0289	-0.0032	-0.489**
DM	-0.2666	0.0974	-0.0396	-0.0041	0.0199	0.0196	-0.2062	-0.1691	-0.0439	0.0032	-0.589**
PH	0.0119	0.0128	-0.3005	0.0141	0.0152	-0.0106	0.0052	-0.1101	-0.0076	0.0015	-0.368**
NPBPP	-0.0717	0.0162	0.1695	-0.0249	0.0961	0.0447	-0.0886	-0.0170	-0.0173	0.0039	0.111
NPBNP	-0.0171	0.0068	-0.0159	-0.0084	0.2865	0.1514	-0.0693	-0.0301	-0.0369	0.0158	0.283*
NPPP	-0.0324	0.0108	0.0180	-0.0063	0.2449	0.1772	-0.1093	0.0099	-0.0338	0.0150	0.294**
NSPP	0.1274	-0.0492	-0.0038	0.0054	-0.0487	-0.0474	0.4081	0.0614	0.0062	-0.0014	0.458**
100 SW	0.0764	-0.0374	0.0751	0.0010	-0.0196	0.0040	0.0568	0.4407	0.0173	-0.0081	0.606**
PC	0.0890	-0.0441	0.0236	0.0045	-0.1090	-0.0618	0.0263	0.0789	0.0969	-0.0208	0.083
OC	0.0313	0.0102	-0.0147	-0.0032	0.1474	0.0865	-0.0191	-0.1166	-0.0654	0.0308	0.087

**Significance at 1% probability level, *Significance at 5% probability level
(**DFE**: Days to 50% flowering, **DM**: Days to maturity, **PH**: Plant height(cm), **NPBPP**: Number of primary branches per plant, **NPBNP**: Number of pod bearing nodes per plant, **NPPP**: Number of pods per plant, **NSPP**: Number of seeds per pod, **100 SW**: 100 seed weight(g), **PC**: Protein content (%), **OC**: Oil content (%), **SYPP**: Seed yield per plant (g))

Table 6: Distribution of 25 soybean genotypes into different clusters using D² analysis.

Clusters	Genotypes	List of genotypes
Cluster I	15	RSC 12-05, RSC 10-52 (check), RSC 12-32, RSC 12-67, CG RSC 11-15 (check), RSC 12-25, RSC 12-95, RSC 12-54, RSC 12-63, RSC 11-07 (check), RSC 12-52, RSC 10-02, RSC 12-65, RSC 12-70, RSC 12-69.
Cluster II	5	RSC 12-50, RSC 12-51, RSC 12-53, RSC 12-62, RSC 12-55
Cluster III	1	RSC 12-56
Cluster IV	4	RSC 12-61, RSC 12-64, RSC 12-66, RSC 12-68

level indicating that increase in these traits will contribute significantly to increase in seed yield, thus can be effectively used as selection parameters to improve. While characters days to 50% flowering, days to maturity and plant height (cm) showed significant negative correlation with seed yield per plant (g) suggesting that with an increase in these traits will result in decrease in seed yield and vice versa. Similar findings were drawn by Srivastava *et al.*, (2025) and Pal *et al.*, (2024) for number of pods per plant and number of seeds per pod. Painkra *et al.*, (2018) for 100-seed weight.

In order to obtain a clear picture of the inter-relationship between different characters, the direct and indirect effects of the different characters on seed yield per plant were worked out in Table 4 and Table 5. All traits showed a positive direct effect on seed yield, except for days to 50% flowering and number of pod bearing nodes per plant. However, the positive correlation of number of pod bearing nodes per plant with seed yield was mainly due to positive indirect effects through other yield-contributing traits. The residual effect at genotypic level is (0.0947), which is very low, indicating that the independent variables included in the study explained all variation (directly or indirectly).

At phenotypic level, days to 50% flowering, plant height (cm) and number of primary branches per plant exerted negative direct effects on seed yield. While other traits exhibited positive direct effects. The residual effect at phenotypic level is low, *i.e.* 0.237, indicating that this proportion of variation in yield explained by other independent variables is not under study.

100-seed weight (g), number of seeds per pod and number of pods per plant showed high positive direct effects coupled with significant positive association with seed yield per plant at both genotypic and phenotypic

Table 7: Inter and intra (bold) cluster distances based on D² values.

Clusters	I	II	III	IV
I	247.34			
II	555.52	158.59		
III	406.66	614.21	0.00	
IV	342.23	536.86	692.75	203.62

levels. Result indicates that these traits contributed substantially towards yield improvement and direct selection will be fruitful to increase seed yield. Similar results were drawn by Patel *et al.*, (2025); Patil *et al.*, (2024); Thorat *et al.*, (2023); Berhanu *et al.*, (2021); Pawar *et al.*, (2020) and Tandekar *et al.*, (2023).

The genetic divergence among twenty-five genotypes is analysed using Mahalanobis D² statistics, which divided these genotypes into four separate clusters using Tocher's method, and their distribution across these clusters is described in Table 6.

The distribution of genotypes into four discrete clusters suggested that a moderate degree of genetic diversity was present in the evaluated material. Cluster I possesses the highest number of genotypes, which consist of 15 genotypes, viz, RSC 12-05, RSC 10-52 ©, RSC 12-32, RSC 12-67, RSC 11-15 ©, RSC 12-25, RSC 12-95, RSC 12-54, RSC 12-63, RSC 11-07 ©, RSC 12-52, RSC 10-02, RSC 12-65, RSC 12-70, RSC 12-69 followed by cluster II with 5 genotypes namely RSC 12-50, RSC 12-51, RSC 12-53, RSC 12-62, RSC 12-55, cluster IV contained 4 genotypes *i.e.*, RSC 12-61, RSC 12-64, RSC 12-66, RSC 12-68 and cluster III comprised 1 genotype RSC 12-56.

Inter and intra cluster distances based on D² were shown in Table 7. The maximum inter cluster distance was observed between cluster III and IV (692.75) followed by cluster II and III (614.21), cluster I and II (555.52), cluster II and IV (536.86), cluster I and III (406.66), whereas the minimum distance was found in cluster I and IV (342.23). This indicates that clusters with the maximum distance show considerable genetic diversity is present among the genotypes of these clusters, so for the hybridization programme, we can choose parents from the members of clusters III and IV. The maximum intra-cluster distance was observed in cluster I (247.34) followed by cluster IV (203.62), whereas the minimum was observed in cluster II (158.59). The clustering arrangement may be exploited in picking the divergent parents by determining suitable cross combinations. It will foster intense feasible variability for several attributes. Thus, the lines with high intra and inter-cluster values can be utilized in the crop improvement

Table 8: Mean cluster performance of 11 yield and yield attributing characters for 25 soybean genotypes.

Clusters				
Traits	I	II	III	IV
DF	46.47	47.73	49.67	49.08
DM	104.91	108.87	103.67	109.67
PH	48.44	79.20	46.67	42.78
NPBP	3.36	2.93	3.47	3.93
NPBNP	11.40	13.31	10.27	15.92
NPP	42.42	43.57	37.93	57.08
NSPP	2.38	2.31	2.84	2.23
100 SW	7.93	6.63	7.80	7.00
PC	37.51	35.91	39.41	33.86
OC	18.41	18.86	16.00	20.23
SYPP	5.70	3.68	5.61	5.31

(**DF**: Days to 50% flowering, **DM**: Days to maturity, **PH**: Plant height(cm), **NPBP**: Number of primary branches per plant, **NPBNP**: Number of pod bearing nodes per plant, **NPP**: Number of pods per plant, **NSPP**: Number of seeds per pod, **100 SW**: 100 seed weight(g), **PC**: Protein content (%), **OC**: Oil content (%), **SYPP**: Seed yield per plant (g))

programmes for further selection followed by hybridization. (Yasin *et al.*, 2024).

The cluster mean values for 11 yield and yield-attributing traits are presented in Table 8. Cluster I recorded the lowest mean for days to 50% flowering (46.47), Cluster III for days to maturity (103.67), and Cluster IV for plant height (42.78), indicating their suitability for selecting early-flowering, early-maturing, and dwarf genotypes, respectively. Cluster IV exhibited the highest mean values for primary branches per plant (3.93), pod-bearing nodes per plant (15.92), pods per plant (57.08), and oil content (20.23). Cluster III showed the highest mean for seeds per pod (10.27) and protein content (39.41), whereas Cluster I recorded the highest mean for 100-seed weight (7.93 g) and seed yield per plant (5.70 g), suggesting these clusters as potential sources of desirable parents in soybean breeding. Selection of genotypes for hybridization programme aiming to improve yield can be chosen from cluster I and III as these clusters show highest mean for maximum traits and lowest mean for days to 50% and days to maturity for early duration genotypes.

Contribution of the characters toward total divergence

The involvement/contribution of the characters in connection with the manifestation of the entire genetic divergence (Table 4) indicated that the greatest per cent of the contribution comes from plant height recorded the highest contribution (20 %), followed by days to 50% flowering (17.67%) and seed yield per plant (15.33%).

Table 9: Contribution of different traits towards genetic divergence.

Traits	CN	TR
Plant height (cm)	20	60
Days to 50% flowering	17.67	53
Seed yield per plant (g)	15.33	46
No. of pod bearing nodes per plant	13.33	40
Oil content (%)	9.67	29
Protein content (%)	9.33	28
Days to maturity	7.33	22
Number of pods per plant	5.67	17
Number of seeds per pod	1	3
100 seed weight (g)	0.67	2
No. of primary branches per plant	0	0

CN: Contribution (%); TR: Times Ranked 1st

All other traits contributed less than 10%, while number of primary branches per plant, 100-seed weight and number of seeds per pod showed negligible contribution. The high contribution of plant height, days to 50% flowering, and seed yield per plant indicates that these traits were the major determinants of genetic divergence among the soybean genotypes. Therefore, they should be prioritized while selecting parents for hybridization and genetic improvement programme. The characters with a maximum percent of contribution concerning the assertion of genetic divergence shall be acquired as an indicator in the selection of diverse parents from each cluster and utilized the same in the hybridization programmes for the development of desirable segregants which ultimately may result in the selection and release of new elite cultivars from the segregating population. (Yasin *et al.*, 2024).

Conclusion

The study revealed substantial genetic variability among the twenty-five soybean genotypes, indicating good scope for genetic improvement. High heritability coupled with high genetic advance for major yield-contributing traits such as plant height(cm), number of primary branches per plant, number of pod bearing nodes per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g) and seed yield per plant (g) suggested the predominance of additive gene action and the effectiveness of direct selection. Correlation and path coefficient analysis identified number of pods per plant, number of seeds per pod, and 100-seed weight as the most important traits influencing seed yield. Genetic divergence analysis further demonstrated the presence of considerable diversity among the genotypes, with plant height, days to 50% flowering, and seed yield per plant contributing most to total divergence. Therefore, these traits should be emphasized while selecting parents, and

genetically divergent genotypes may be exploited in hybridization programmes to develop high-yielding soybean varieties.

Acknowledgement

The authors sincerely acknowledge the Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India, for providing the facilities and support necessary to conduct this research.

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