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Genetic variability, character association and path coefficient analysis for seed yield and its contributing traits in soybean (*Glycine max* (L.) Merrill)

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Abstract

The present investigation was undertaken to assess the magnitude of genetic variability, character association and direct and indirect effects of yield-contributing traits on seed yield in 50 soybeans (*Glycine max* (L.) Merrill) genotypes during the *Kharif* - 2025. The experiment was conducted in a randomized complete block design with two replications at the Research-cum-Instructional Farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. Analysis of variance revealed significant differences among genotypes for all twelve traits studied, indicating the presence of substantial genetic variability. High heritability coupled with high genetic advance as percentage of mean was observed for seed yield per plant, number of seeds per plant, 100-seed weight, pod-bearing length, number of pods per plant, plant height, and number of primary branches per plant, suggesting considerable scope for effective selection. Seed yield per plant exhibited significant positive genotypic and phenotypic correlations with number of pods per plant, number of seeds per plant, and 100-seed weight. Genotypic path coefficient analysis revealed that number of seeds per plant exerted the highest positive direct effect on seed yield, followed by 100-seed weight, days to maturity, and pod-bearing length. Although number of pods per plant exhibited a negative direct effect, its strong positive indirect effect through number of seeds per plant resulted in a significant positive correlation with seed yield. Therefore, number of seeds per plant and 100-seed weight may be considered important selection criteria for improving seed yield in soybean, while number of pods per plant may also be emphasized because of its strong association with number of seeds per plant and seed yield.

Keywords: Genetic variability, heritability, genetic advance, correlation, path coefficient analysis, seed yield, soybean

Introduction

Soybean (*Glycine max* (L.) Merrill) is one of the world's most important oilseed and protein-rich crops and has considerable nutritional, economic, and industrial significance. The crop originated in East Asia, particularly China, and is believed to have been domesticated from its wild progenitor, *Glycine soja* (Zafar *et al.*, 2023). Because of its diverse nutritional and industrial applications, soybean is commonly referred to as the "Golden Bean," "Miracle Legume," or "Wonder Crop." Soybean seeds contain approximately 40% protein and 20% oil, in addition to appreciable quantities of unsaturated fatty acids, minerals such as calcium and phosphorus, and several vitamins, making the crop nutritionally valuable (Kumar *et al.*, 2020). Its high-quality protein and edible oil also make soybean an economical and readily available source of protein and dietary fat (Patel *et al.*, 2025).

In India, soybean is predominantly cultivated during the *Kharif* season, largely under rainfed conditions. During 2023-24, soybean occupied approximately 13.25 million hectares and produced about 13.06 million tons, with an average productivity of 985 kg ha⁻¹. Madhya Pradesh, Maharashtra, and Rajasthan are the major soybean-producing states of the country. In Chhattisgarh, soybean was cultivated on approximately 0.03 million hectares, with an average productivity of 949 kg ha⁻¹ (Anonymous, 2024) [34, 25, 5].

Seed yield is a complex quantitative trait controlled by several genes and substantially influenced by environmental conditions. Consequently, direct selection for yield alone may be less effective, particularly when environmental variation masks genetic differences.

The identification of genetically variable and heritable yield-contributing traits is therefore essential for developing effective selection strategies. Estimates of genotypic and phenotypic coefficients of variation, heritability, genetic advance, and genetic advance as percentage of mean provide useful information regarding the magnitude and nature of genetic variability and the expected response to selection (Hamawaki *et al.*, 2012) [14]. Correlation analysis provides information about the strength and direction of association between seed yield and its component traits. However, correlation coefficients alone do not distinguish between direct and indirect contributions of individual traits. Path coefficient analysis, originally developed to partition correlations into direct and indirect effects, provides a more meaningful understanding of the relative contribution of component traits to yield (Dewey and Lu, 1959). Such information is particularly useful for identifying reliable selection criteria in soybean breeding programmes [10]. Therefore, the present study was undertaken to estimate the extent of genetic variability, heritability, genetic advance, genotypic and phenotypic associations, and direct and indirect effects of yield-contributing traits on seed yield in soybean genotypes.

Materials and methods

The field experiment was conducted during the Kharif season of 2025 at the Research-cum-Instructional Farm of Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India. A total of 50 soybean (*Glycine max* (L.) Merrill) genotypes, comprising 48 test genotypes and two check varieties, were evaluated under field conditions to assess genetic variability and the association of yield with its component traits. The experiment was laid out in a Randomized Complete Block Design (RCBD) with two replications. Sowing was carried out on 28 June 2025, and all genotypes were grown under uniform field conditions following the recommended agronomic practices for soybean. Observations were recorded on five randomly selected plants from each genotype in each replication for the following traits: days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, pod-bearing length (cm), number of pods per plant, number of seeds per pod, number of seeds per plant, 100-seed weight (g), and seed yield per plant (g). Oil and protein contents were also determined for each genotype. Oil content was estimated by Soxhlet extraction using petroleum ether as the solvent following the procedure prescribed by AOAC (1990). Protein content was estimated using the Micro-Kjeldahl method according to AOAC

(1975), with a conversion factor of 6.25 used to calculate protein content from the nitrogen concentration. The mean values obtained from the selected plants were subjected to statistical analysis. Analysis of variance (ANOVA) was performed separately for each trait following the procedure described by Panse and Sukhatme (1985) to determine the significance of differences among the soybean genotypes. Genotypic and phenotypic variance components were estimated from the ANOVA, and genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated following Burton (1952) [24, 8]. The magnitude of GCV and PCV was classified according to the criteria proposed by Sivasubramanian and Madhava Menon (1973). Broad-sense heritability was estimated according to Allard (1960) and categorized following Robinson (1966). Genetic advance (GA) and genetic advance as percentage of mean (GAM) were estimated following Johnson *et al.*, (1955) [28, 15], assuming a selection intensity of 5%. Genotypic and phenotypic correlation coefficients were estimated from the corresponding genotypic and phenotypic variance and covariance components following Miller *et al.*, (1958). The significance of correlation coefficients was assessed using the appropriate standard errors. Path coefficient analysis was performed separately at the genotypic and phenotypic levels following the method of Dewey and Lu (1959), with seed yield per plant considered as the dependent variable and the remaining traits as independent variables. The analysis was used to partition the correlation coefficients into direct and indirect effects of the component traits on seed yield. The residual effect was estimated to quantify the proportion of variation in seed yield not accounted for by the traits included in the path analysis. The magnitude of direct and indirect effects was interpreted according to the scale proposed by Lenka and Mishra (1973) [22, 20].

Results and discussion

Analysis of variance revealed significant differences among the soybean genotypes for all the traits evaluated (Table 1). Genotypic mean squares were highly significant at the 1% level for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, pod bearing length, number of pods per plant, number of seeds per pod, number of seeds per plant, hundred-seed weight, protein content and seed yield per plant. In contrast, oil content exhibited significant variation at the 5% level. The significant genotypic differences observed for the traits indicated the presence of considerable genetic variability among the genotypes in soybean. The present findings were in agreement with Bhangare *et al.* (2024), Dutta *et al.* (2021) [7, 11].

Table 1: Analysis of variance for yield and its contributing traits

S.No.	Source	Mean Sum of Squares (MSS)		
		Replication	Treatment	Error
	Degrees of freedom	1	49	49
1	Days to 50% flowering	23.04	11.71**	2.8
2	Days to maturity	19.36	18.68**	3.3
3	Plant height (cm)	585.16	430.21**	46.7
4	No. of primary branches per plant	0.02	0.61**	0.13
5	Pod bearing length(cm)	877.35	365.24**	28.04
6	No. of pods per plant	435.06	338.3**	51.32
7	No. of seeds per pod	0.45	0.09**	0.04
8	Number of seeds per plant	559.61	2381.02**	12.53
9	Hundred seed weight (g)	1.05	9.46**	0.35

10	Oil content (%)	0.22	3.03*	1.61
11	Protein content (%)	9.22	7.12**	2.13
12	Seed yield per plant (g)	2.92	18.64**	0.33

**Significance at 1% probability level, *Significance at 5% probability level

Genetic Variability Parameters

The mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance (GA), and genetic advance as percentage of mean (GAM) were estimated for the twelve traits evaluated in soybean, and the results are presented in Table 2.

Coefficient of variation: In all the traits, PCV values were slightly higher than the corresponding GCV values, suggesting a certain degree of environmental influence on their expression. The highest GCV was recorded for seed yield per plant (36.06%), followed by number of seeds per plant (30.85%) and number of pods per plant, while the lowest was observed for days to maturity (2.26%). Likewise, seed yield per plant exhibited the highest PCV (36.39%), followed by number of seeds per plant (31.70%), number of pods per plant (24.17%), hundred-seed weight (23.54%) and pod bearing length (23.02%). Relatively low GCV and PCV were observed for days to maturity, days to 50% flowering, oil content and protein content. The comparatively high GCV and PCV for seed yield and its associated traits indicated substantial variability and greater scope for selection. Similar findings were reported by Aditya *et al.*, (2011), Rakhonde *et al.* (2025) and Gadhiya *et al.* (2025) for seed yield and related traits. The lower variability observed for days to 50% flowering and days to maturity was consistent with the findings of Chandrawat *et al.* (2017) and Agarwal *et al.* (2000) [1, 27, 13].

Heritability: High heritability was observed for ten traits, ranging from 70.10% for protein content to 98.24% for seed yield per plant. The highest estimates were recorded for seed yield per plant (98.24%), hundred-seed weight (96.34%) and number of seeds per plant (94.74%), indicating a strong genetic contribution and good scope for selection. Moderate heritability was recorded for number of seeds per pod (56.41%), whereas oil content showed low heritability (46.92%), suggesting a relatively greater influence of environmental factors on its expression.

Genetic Advance

The estimates of genetic advance showed considerable variation among the traits. The highest genetic advance was

observed for number of seeds per plant (54.99), followed by plant height (22.00), pod bearing length (20.99) and number of pods per plant (18.56). Seed yield per plant recorded a genetic advance of 5.05, while moderate values were observed for days to maturity (4.24), hundred-seed weight (3.53), days to 50% flowering (3.10) and protein content (2.23). The lowest genetic advance was recorded for number of seeds per pod (0.20), followed by number of primary branches per plant (0.74) and oil content (0.98).

Genetic Advance as Percentage of Mean

Genetic advance as percentage of mean (GAM) was classified according to Johnson *et al.*, (1955) as low (<10%), moderate (10-20%) and high (>20%). The highest GAM was recorded for seed yield per plant (73.72%), followed by number of seeds per plant (61.88%), hundred-seed weight (46.75%), pod bearing length (43.78%), number of pods per plant (42.24%), plant height (35.89%) and number of primary branches per plant (22.91%). Low GAM was observed for number of seeds per pod (8.84%), days to 50% flowering (7.55%), protein content (5.79%), oil content (5.15%) and days to maturity (4.23%).

High heritability coupled with high GAM was observed for seed yield per plant, number of seeds per plant, hundred-seed weight, pod bearing length, number of pods per plant, plant height and number of primary branches per plant, indicating a greater contribution of additive genetic effects and good prospects for selection. In contrast, high heritability with low GAM for days to maturity, days to 50% flowering and protein content suggested greater influence of non-additive effects. Oil content showed low heritability and low GAM, indicating greater environmental influence. The present findings were consistent with Amit Kumar *et al.* (2010) and Kalamkhede *et al.* (2025), who reported high heritability coupled with high genetic advance for major yield-contributing traits in soybean. Similar results were reported by Fufa and Nepir (2025) for seed yield, plant height, number of seeds per plant and number of pods per plant. High heritability with low genetic advance for days to maturity was also reported by Karishma *et al.* (2025) and Fufa and Nepir (2025) [16, 12].

Table 2: Estimation of Genetic Variability Parameters for yield and its contributing traits

Traits	GCV (%)	PCV (%)	$h^2(bs)$ (%)	GA	GAM%
Days to 50% flowering	4.20	4.82	76.13	3.10	7.55
Days to maturity	2.26	2.49	82.34	4.24	4.23
Plant height (cm)	18.45	19.54	89.15	22.00	35.89
Number of primary branches per plant	12.45	13.96	79.54	0.74	22.91
Pod bearing length (cm)	22.12	23.02	92.33	20.99	43.78
Number of pods per plant	22.27	24.17	84.84	18.56	42.24
Number of seeds per pod	5.72	7.61	56.41	0.20	9.13
Number of seeds per plant	30.85	31.70	94.74	54.99	61.88
100-seed weight (g)	23.10	23.54	96.34	3.53	46.75
Oil content (%)	3.62	5.29	46.92	0.98	5.15
Protein content (%)	3.35	4.00	70.10	2.23	5.79
Seed yield per plant (g)	36.06	36.39	98.24	5.05	73.72

Correlation Coefficient Analysis

Genotypic and phenotypic correlation coefficients among yield and its component traits are presented in Table 3. Seed yield per plant exhibited positive and significant associations with number of pods per plant ($r_g = 0.550^{**}$, $r_p = 0.533^{**}$), number of seeds per plant ($r_g = 0.809^{**}$, $r_p = 0.807^{**}$) and 100-seed weight ($r_g = 0.421^{**}$, $r_p = 0.414^{**}$), indicating their potential as important selection criteria for improving soybean yield. In contrast, plant height, oil content and protein content showed negative and non-significant associations with seed yield at both levels.

Among the component traits, days to 50% flowering was positively and significantly associated with days to maturity ($r_g = 0.879^{**}$, $r_p = 0.891^{*}$), while plant height showed a strong positive association with pod bearing length ($r_g = 0.927^{**}$, $r_p = 0.903^{*}$). Number of primary branches per plant was positively associated with number of pods per plant ($r_g = 0.490^{**}$, $r_p = 0.465^{**}$) and number of seeds per pod ($r_g = 0.393^{**}$, $r_p = 0.354^{**}$). Pod bearing length was positively associated with number of pods per plant ($r_g = 0.446^{**}$, $r_p = 0.364^{**}$). Number of pods per plant showed a strong positive association with number of seeds per plant ($r_g = 0.738^{**}$, $r_p = 0.712^{**}$), while number of seeds per pod was positively associated with number of seeds per plant ($r_g = 0.393^{**}$, $r_p = 0.346^{**}$).

The positive association of yield with number of pods per plant, number of seeds per plant and 100-seed weight was consistent with Thakur *et al.*, (2015), Tigga and Nag (2021), Aditya *et al.* (2011), Khonde (2025) and Patel *et al.* (2025). The negative association of protein content with seed yield agreed with Pawar *et al.* (2020), while Painkra *et al.* (2018) reported similar negative associations for oil and protein contents [32, 33, 18, 26, 23].

Path Coefficient Analysis: The genotypic path coefficient analysis showing the direct and indirect contributions of the

component traits towards seed yield per plant is presented in Table 4. Genotypic path analysis revealed that number of seeds per plant (0.9842) had the highest positive direct effect on seed yield, followed by hundred-seed weight (0.4759), days to maturity (0.1593) and pod bearing length (0.1280). Positive but low direct effects were observed for protein content (0.0517) and primary branches per plant (0.0372), whereas number of pods per plant (-0.2089), plant height (-0.1240), oil content (-0.0497) and seeds per pod (-0.0052) showed negative direct effects. The residual effect was 0.3270. The positive direct effects of hundred-seed weight, days to maturity and pod bearing length were comparable with the findings of Pawar *et al.* (2020), Berhanu *et al.* (2021), Shekar *et al.* (2018), Malek *et al.* (2014) and Thakur *et al.* (2015). Similar results for number of seeds per plant and hundred-seed weight were reported by Akram *et al.* (2016) and Tandekar *et al.* (2020) [29, 21, 3, 31, 6].

Overall, number of seeds per plant and hundred-seed weight emerged as the major traits contributing directly to seed yield. Although number of pods per plant showed a negative direct effect, its positive indirect effect through number of seeds per plant (0.7265) resulted in a favourable association with yield. Thus, these traits may be emphasized in selection for improving seed yield in soybean.

Conclusion

For developing high-yielding soybean varieties, number of pods per plant and 100-seed weight can serve as important selection criteria due to their high heritability, high genetic advance, significant positive association with seed yield, and favourable direct effects. Therefore, greater emphasis on these traits during selection could improve the efficiency of breeding programmes aimed at enhancing seed yield in soybean.

Table 3: Genotypic correlation coefficient and Phenotypic correlation coefficient

Traits	DFF	DTM	PH	NPB	PBL	NPPP	NSPP	NSP	HSW	OC	PC	SYPP
DFF (rg)	1.000	0.879**	-0.016	0.216	0.039	0.048	-0.060	0.076	0.040	-0.063	-0.134	0.076
(rp)	1.000	0.891*	0.004	0.212*	0.058	0.029	-0.075	0.055	0.022	-0.108	-0.163	0.055
DTM (rg)		1.000	-0.091	0.171	-0.043	-0.092	-0.052	-0.092	0.065	-0.070	-0.212	0.001
(rp)		1.000	-0.079	0.155	-0.026	-0.091	-0.076	-0.093	0.059	-0.094	-0.227*	-0.012
PH (rg)			1.000	0.248	0.927**	0.330*	0.323*	0.249	-0.387**	0.191	0.021	-0.027
(rp)			1.000	0.223*	0.903*	0.260**	0.196	0.220**	-0.374**	0.154	-0.033*	-0.029
NPB (rg)				1.000	0.258	0.490**	0.393**	0.239	0.021	0.043	0.171	0.185
(rp)				1.000	0.237*	0.465**	0.354**	0.223*	0.009	0.034	0.132	0.173
PBL (rg)					1.000	0.446**	0.225	0.313*	-0.339*	0.092	0.073	0.062
(rp)					1.000	0.364**	0.129	0.282**	-0.324**	0.078	0.001*	0.051
NPPP (rg)						1.000	0.325*	0.738**	0.043	0.027	0.043	0.550**
(rp)						1.000	0.342**	0.712**	0.047	0.022	0.079	0.533**
NSPP (rg)							1.000	0.393**	-0.074	0.149	0.010	0.275
(rp)							1.000	0.346**	-0.064	0.153	0.081	0.246*
NSP (rg)								1.000	-0.043	-0.165	-0.091	0.809**
(rp)								1.000	-0.039	-0.131	-0.064	0.807**
HSW (rg)									1.000	0.066	-0.102	0.421**
(rp)									1.000	0.020	-0.060	0.414**
OC (rg)										1.000	-0.140	-0.207
(rp)										1.000	-0.095	-0.167
PC (rg)											1.000	-0.090
(rp)											1.000	-0.069
SYPP (rg)												1.000
(rp)												1.000

**Significance at 1% probability level, *Significance at 5% probability level (Note: DFF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height (cm), NPB: Number of primary branches per plant, PBL: Pod bearing length, NPPP: Number of pods per plant, NSPP: Number of seeds per pod,

NSP: Number of seeds per plant, HSW: Hundred seed weight (g), OC: Oil content (%), PC: Protein content (%), SYPP: Seed yield per plant (g), rg: genotypic correlation, rp: phenotypic correlation)

Table 4: Genotypic path coefficient for yield and its contributing traits

Trait	DFF	DTM	PH	NPB	PBL	NPPP	NSPP	NSP	HSW	OC	PC	rx _y
DFF	-0.1401	0.1399	0.0019	0.0081	0.0049	-0.0101	0.0004	0.0391	0.0356	0.0032	-0.0069	0.076
DTM	-0.1232	0.1593	0.0113	0.0064	-0.0055	0.0192	0.0003	-0.0906	0.0315	0.0035	-0.0109	0.0010
PH	0.0023	-0.0145	-0.1243	0.0093	0.1186	-0.0686	-0.0017	0.2447	-0.1841	-0.0095	0.0011	-0.0270
NPB	-0.0302	0.0273	-0.0308	0.0372	0.0331	-0.1025	-0.0021	0.2357	0.0102	-0.0022	0.0089	0.1850
PBL	-0.0055	-0.0069	-0.1152	0.0096	0.1279	-0.0932	-0.0012	0.3079	-0.1612	-0.0046	0.0038	0.0620
NPPP	-0.0068	-0.0147	-0.0411	0.0183	0.0571	-0.2089	-0.0017	0.7265	0.0204	-0.0014	0.0023	0.550**
NSPP	0.0084	-0.0083	-0.0402	0.0147	0.0288	-0.0679	-0.0052	0.3865	-0.0353	-0.0075	0.0006	0.2750
NSP	-0.0056	-0.0147	-0.0309	0.0089	0.0401	-0.1542	-0.0021	0.9842	-0.0207	0.0082	-0.0048	0.809**
HSW	-0.0105	0.0104	0.0481	0.0008	-0.0434	-0.0089	0.0004	-0.0428	0.4759	-0.0033	-0.0053	0.421**
OC	0.0089	-0.0112	-0.0237	0.0017	0.0118	-0.0057	-0.0008	-0.1624	0.0316	-0.0497	-0.0073	-0.2070
PC	0.0188	-0.0339	-0.0027	0.0064	0.0094	-0.0089	-0.0005	-0.0898	-0.0484	0.0069	0.0517	-0.0900

Residual effect =0.327 Diagonal values (bolded) are direct effect values and the remaining values are indirect effect values

(Note: DFF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height (cm), NPB: Number of primary branches per plant, PBL: Pod bearing length, NPPP: Number of pods per plant, NSPP: Number of seeds per pod, NSP: Number of seeds per plant, HSW: Hundred seed weight (g), OC: Oil content (%), PC: Protein content (%), SYPP: Seed yield per plant (g))

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