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GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN SOYBEAN: UNRAVELLING THE CONTRIBUTION OF YIELD COMPONENTS TO CROP PERFORMANCE

Kumari Alka[1], Nutan Verma[1*], Supriya Supal Surin[1], Manigopa Chakraborty[1], Shivam Mishra[2], Sumit Kumar Mishra[1] and Aakanksha Modi[2]
[1]Department of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Ranchi – 834 006, India
[2]Department of Agricultural Statistics and Computer Application, Birsa Agricultural University, Kanke, Ranchi– 834 006, India
*Corresponding author E-mail: nvbau2012@gmail.com

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ABSTRACT

A field experiment was conducted during *kharif* 2024 at Birsa Agricultural University, Ranchi, to assess the extent of genetic variability in 30 soybean genotypes for yield and yield-contributing traits. Analysis of variance revealed highly significant differences among genotypes for all characters, indicating ample genetic variability. High genotypic and phenotypic coefficients of variation (GCV and PCV) were observed for grain yield per plant, grain yield per plot, branches per plant, and pods per plant, suggesting wide variability and good prospects for improvement. High heritability coupled with high genetic advance was recorded for plant height, branches per plant, pods per plant, grain yield per plant, grain yield per plot, and 100-seed weight, indicating additive gene action and effectiveness of direct selection. Protein and oil content, despite moderate to high heritability showed low genetic advance, suggesting non-additive gene effects and environmental influence. Grain yield was strongly and positively associated with plant height, branches, 100-seed weight, pods per plant, and grain yield per plant, while days to 50% flowering had a negative correlation and effect on yield. Path coefficient analysis showed strong direct effects of number of branches per plant, 100 seed weight, plant height, and grain yield per plant as major determinants of productivity.

***Keywords* :** Soybean, variability, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic variability, heritability, genetic advance, correlation, path analysis, direct effect, indirect effect.

Introduction

Soybean (*Glycine max* L. Merrill), often called the “Golden Bean,” “Yellow Jewel,” and “Miracle Crop,” is one of the world’s most important oilseed and protein-rich legumes. Belonging to the family Fabaceae, soybean is a self-pollinated diploid species (2n = 40) valued for its dual role as a source of edible oil and high-quality protein. Originating in Northeast China, it has been cultivated for more than 4,000 years (Hymowitz, 1970) and today plays a critical role in food, feed, and industrial sectors. Globally, soybean is a major supplier of vegetable oil, while its de-oiled cake serves as an essential component in livestock feed and food processing (Fasoula & Boerma, 2007). Its nutritional richness about 40% protein and 20% oil, along with isoflavones, essential amino acids, and minerals makes it indispensable for human health and animal nutrition (Dukariya *et al.,* 2020). Additionally, soybean enhances soil fertility through biological nitrogen fixation, contributing to sustainable agriculture.

In India, soybean ranks fifth in production (15.18 million tons) and fourth in area globally, with a productivity of 1,172 kg/ha in 2024 -25 (Anonymous, 2025). Madhya Pradesh, Maharashtra, and Rajasthan dominate soybean cultivation, contributing nearly 93%

of national output, while states like Jharkhand are emerging as new production hubs. Despite its importance, average productivity in India remains below the global mean, necessitating genetic improvement for yield stability and quality enhancement.

Improving soybean productivity requires a thorough understanding of the genetic variability present within breeding materials, as this variability underpins the potential for selecting superior parents and combining desirable alleles. Because the expression of genetic variation is often influenced by environmental conditions, assessing its extent and nature is crucial before initiating any crop improvement program. Effective breeding depends not only on sufficient genetic diversity but also on insights into heritability and expected genetic advance, which together inform selection strategies. Evaluating relationships among yield and its component traits further enhances this process; while correlation analysis helps identify traits associated with yield, such associations may be direct or indirectly mediated by other traits. Therefore, integrating correlation and path coefficient analyses allows breeders to distinguish direct and indirect effects, offering a clearer understanding of trait contributions to yield and improving the efficiency of selecting high-performing soybean genotypes suited to specific agro-ecological conditions.

Materials and Methods

The experiment was carried out during the *kharif* season of 2024 at the Western Research Plot, Department of Genetics and Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand. The experimental material comprised 30 soybean genotypes (*Glycine max* (L.) Merrill), including three checks: National Check (NC), Zonal Check (ZC) and Local Check (LC), as listed in Table 1. The trial was arranged in a Randomized Block Design (RBD) with three replications. Each genotype was planted in four rows of 3 m length, with row spacing of 45 cm and plant spacing of 10 cm. A basal fertilizer dose of 20:40:40:40 kg ha^{-1} (N:P:K:S) was applied at sowing. Observations were recorded on five randomly selected plants from each plot for nine quantitative traits viz, days to 50 % flowering, days to maturity, plant height (cm), number of branches per plant, 100-seed weight (g), number of seeds per pod, number of pods per plant, grain yield per plant (g), and grain yield per plot (kg/plot) along with two quality traits, oil content (%) and protein content (%).

The mean data recorded for all traits were subjected to analysis of variance (ANOVA) following the standard procedure for RBD to determine the significance of differences among genotypes. Estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated according to Burton (1952). Heritability in the broad sense and genetic advance as a percentage of the mean were estimated using the methods proposed by Johnson *et al*. (1955) to assess the extent of genetic variability and predict the expected genetic gain from selection and to assess the interrelationships between seed yield per plant and its component traits, correlation coefficients were calculated. Additionally, path analysis was analysed to estimate the direct and indirect effects of these yield-contributing characters. Correlation coefficient was estimated by Johanson and path analysis was calculated as suggested by Dewey and Lu (1959).

Result and Discussion

The analysis of variance for the 30 soybean genotypes demonstrated highly significant differences across all evaluated traits, including yield components and quality attributes (Table 2). The mean sum of squares for genotypes exhibited highly significant differences across all traits, demonstrating considerable genetic variation among the genotypes studied. Similarly, Baraskar *et al.* (2014) found significant genotypic differences.

The characters grain yield per plant, grain yield per plot, pods/plant and number of branches per plant exhibited high GCV and PCV estimates suggesting ample genetic diversity and strong potential for effective selection. The relatively small difference between PCV and GCV for these traits further implies minimal environmental influence, thereby enhancing selection efficiency. Similar trends were reported by Maranna *et al.* (2021) in soybean. Traits like protein content and days to maturity exhibited low GCV and PCV, indicating limited variability and potential environmental influence, implying limited scope for improvement through direct selection.

High heritability was observed for traits such as days to maturity, grain yield per plot, and 100-seed weight, indicating strong genetic control, while moderate heritability for pods per plant and seeds per pod suggests greater environmental influence. Grain yield per plant and per plot, along with branches per plant, showed both high heritability and high genetic advance, reflecting additive gene action and high potential for improvement through selection. In contrast, protein and oil content, despite moderate to high heritability, had low genetic advance, indicating non-additive gene effects and stronger environmental influence. These results suggest that yield-related traits are most responsive to selection, whereas quality traits may require hybridization or recurrent selection, consistent with observations by Mofokeng (2021).

Correlation analysis revealed that days to 50% flowering was strongly positively correlated with days to maturity and moderately with plant height, indicating that early flowering is generally associated with early maturity, consistent with Patil *et al.* (2006). However, it showed a negative correlation with number of pods per plant at the genotypic level, suggesting delayed flowering may reduce pod formation, as also reported by Gohil *et al.* (2003). Grain yield-related traits, including number of branches per plant, 100-seed weight, number of pods per plant, and grain yield per plant, exhibited strong positive correlations among themselves and with grain yield per plot, highlighting their importance as primary yield determinants, in agreement with Malek *et al.* (2014), and Jain *et al.* (2015). Protein content correlated positively with maturity, plant height, and seeds per pod, while oil content correlated positively with grain yield and pod number but negatively with protein, aligning with Dukariya *et al.* (2020) and Oliveira *et al.* (2017).

Path coefficient analysis clarified the cause-and-effect relationships underlying these correlations. Grain yield per plot was strongly influenced directly by grain yield per plant, number of branches, 100-seed weight, and plant height, whereas days to 50% flowering, days to maturity, number of pods per plant, and number of seeds per pod had negative or negligible direct effects but contributed positively via indirect pathways through other traits. This emphasizes the greater importance of traits with strong direct effects for selection, such as branching and seed weight, over phenological traits like flowering and maturity, consistent with findings by Dewey and Lu (1959), Kang *et al.* (1983), Board and Tan (1995), and Bhuva *et al.* (2020).

Overall, the study confirms that number of branches per plant, 100-seed weight, number of pods per plant, and grain yield per plant are the most critical traits for improving soybean yield, and selection should focus primarily on these traits while considering indirect contributions of phenological and seed traits.

Conclusion

Overall, the results highlight that traits such as grain yield per plant, grain yield per plot, plant height, branches per plant, and pods per plant possess high genetic variability, heritability, and genetic advance, signifying additive gene effects and responsiveness to selection. Genotypes like BAUS-102 (yield), MACS-1140 (protein), and BAUS-103 (oil) stand out as promising parents for developing improved soybean varieties with enhanced productivity and seed quality.

The combination of high heritability and high genetic advance in several yield components underscores the potential for direct selection, while traits with low genetic advance despite high heritability (e.g., protein and oil content) may benefit from recombination breeding or marker-assisted strategies. These findings provide a solid foundation for soybean improvement programs targeting high yield, early maturity, and enhanced nutritional quality. The study also indicates that grain yield in soybean is primarily governed by number of branches per plant, 100-seed weight, plant height, and number of pods per plant, which exhibited high heritability, strong genetic advance, and significant direct effects on yield. In contrast, traits like days to 50% flowering negatively impacted yield directly but contributed indirectly via other traits. Therefore, selection for branching, seed weight, plant height, and pod number should be prioritized in breeding programs, while quality traits such as protein and oil content may require alternative strategies due to their lower genetic advance and environmental sensitivity.

Table 1: List of thirty soybean genotypes used in present investigation.

S. No.	Name of genotypes	Pedigree	Source of genotypes/varieties
1	**BS – 4**	Monetta x EC34500	BAU, Ranchi
2	**BS – 3 (LC)**	Bragg x JS 75-05	BAU, Ranchi
3	**RKS – 18**	MALS -450 x Monetta	IGAU, Raipur
4	**RSC 10-46**	Bragg x JS-335	IGAU, Raipur
5	**BSS -2**	JSS-335 x MACS-58	BAU, Ranchi
6	**RSC 11-42**	JS 97-52 x JS 93-05	IGAU, Raipur
7	**BS -1**	Mutant of sipaya black	BAU, Ranchi
8	**JS 20-116 (Z C)**	JS 97-52 x JSM 120 A	JNKVV, Jabalpur
9	**RSC 11-35**	JS 97-52 x MAUS 504	IGAU, Raipur

10	**BAUS (M) -5**	Mutant of B.S.S-2	BAU, Ranchi
11	**AMS 2014 -1**	AMS 99-33 x H6P5	PDKV, RRC, Amravati
12	**BAUS (M) -1**	Mutant of B.S.S-2	BAU, Ranchi
13	**JS-335**	JS 78-77 x JS 71-05	IGAU, Raipur
14	**BAUS (M) -11**	Mutant of RKS -18	BAU, Ranchi
15	**JS 97-52**	PK 327 x L129	IGAU, Raipur
16	**BAUS (M) -15**	Mutant of RKS -18	BAU, Ranchi
17	**NRC -128 (NC)**	JS 97-52 x (EC 389148 xPS1042)	ICAR- DOSR, Indore
18	**MACS 1140**	JS20-98 x JS 20-34	ARI, Pune
19	**RAUS -5**	PUSA 16 x JS 335	RAU, Kota
20	**MACS -1407**	JS97-52 x AG525	ARI, Pune
21	**BAUS -100**	JS 20-37 x JS 335	BAU, Ranchi
22	**BAUS -134**	JS 20-98 x PS1029	BAU, Ranchi
23	**BAUS -194**	(NRC37 x JS335) x NRC121	BAU, Ranchi
24	**BAUS -103**	JS-335 x MACS-58	BAU, Ranchi
25	**BAUS -141**	JS97-52 x AG525	BAU, Ranchi
26	**BAUS -140**	(NRC37 x JS97-52) x NRC-21	BAU, Ranchi
27	**BAUS -138**	JS 97-52 x EC 572086	BAU, Ranchi
28	**BAUS - 135**	JS20-98 x JS 20-34	BAU, Ranchi
29	**BAUS - 136**	JS 97-52 x NRC121	BAU, Ranchi
30	**BAUS -102**	JS-97-52 x Bragg	BAU, Ranchi

Source of variation	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**No. of branches /plant**	**100 seed weight (g)**	**No. of seeds/ pod**	**No. of pods/ plant**	**Grain yield/ plant (g)**	**Grain yield /plot (Kg/plot)**	**Protein (%)**	**Oil (%)**
Replication d.f(2)	3.033	4.033	134.373	0.026	0.584	0.144	109.767	0.059	0.002	0.055	0.143
Treatment d.f(29)	33.962**	81.922**	232.774**	1.634**	4.514**	0.454**	308.839**	25.888**	0.067**	3.381**	2.810**
Error d.f (58)	2.413	5.183	23.792	0.227	0.312	0.087	62.016	3.814	0.005	0.538	0.291

Table 2: Analysis of variance (mean sum squares) for yield attributing characters and quality traits.

Source of variation	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**No. of branches /plant**	**100 seed weight (g)**	**No. of seeds/ pod**	**No. of pods/ plant**	**Grain yield/ plant (g)**	**Grain yield /plot (Kg/plot)**	**Protein (%)**	**Oil (%)**
Replication d.f(2)	3.033	4.033	134.373	0.026	0.584	0.144	109.767	0.059	0.002	0.055	0.143
Treatment d.f(29)	33.962**	81.922**	232.774**	1.634**	4.514**	0.454**	308.839**	25.888**	0.067**	3.381**	2.810**
Error d.f (58)	2.413	5.183	23.792	0.227	0.312	0.087	62.016	3.814	0.005	0.538	0.291

** = Significant at 1 % and * = Significant at 5 % level of significance

Table 3: Genetic estimates of PCV, GCV, heritability and GAM.

S. No.	**Characters**	**GCV**	**PCV**	**h^2 (%)**	**GA**	**GA Mean (%)**
1	**Days to 50% flowering**	7.21	8.00	**81.34**	6.03	13.40
2	**Days to maturity**	4.44	4.87	**83.15**	9.50	8.35
3	**Plant height (cm)**	12.71	14.72	**74.54**	14.84	**22.60**
4	**No. of branches /plant**	17.76	**21.64**	**67.36**	1.16	**30.02**
5	**100 seed weight (g)**	10.63	11.76	**81.81**	2.21	19.81
6	**No. of seeds/ pod**	12.90	16.87	58.43	0.55	**20.31**
7	**No. of pods/ plant**	16.03	**21.22**	57.02	14.11	**24.93**

8	**Grain yield /plant (kg)**	**24.28**	**29.92**	**65.86**	4.54	**40.59**
9	**Protein (%)**	2.41	3.02	**63.81**	1.60	3.97
10	**Oil (%)**	5.24	6.08	**74.25**	1.63	9.30
11	**Grain yield /plot (kg/plot)**	**21.65**	**23.91**	**82.00**	0.27	**40.39**

Table 4: Correlation Matrix (Above diagonal Genotypic and below diagonal Phenotypic

Germplasm	**Grain yield /plot (kg/plot)**	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**No. of branches /plant**	**100 seed weight (g)**	**No. of seeds/ pod**	**No. of pods/ plant**	**Grain yield /plant (g)**	**Protein (%)**	**Oil (%)**
Grain yield /plot (kg/plot)	1	-0.139	0.006	0.466**	0.920**	0.856**	0.116	0.593**	0.809**	0.042	0.169
Days to 50% flowering	-0.137	1	0.707**	0.260*	-0.157	-0.106	0.028	-0.336**	-0.036	0.163	-0.210*
Days to maturity	0.003	0.733**	1	0.169	-0.003	0.117	-0.01	-0.004	0.198	0.328**	-0.313**
Plant height (cm)	0.429**	0.221*	0.161	1	0.393**	0.169	0.156	0.484**	0.142	0.305**	-0.307**
No. of branches /plant	0.854**	-0.13	0.015	0.310**	1	0.781**	0.16	0.523**	0.738**	0.04	0.242*
100 seed weight (g)	0.793**	-0.092	0.108	0.171	0.660**	1	0.119	0.536**	0.899**	0.156	0.141
No. of seeds/ pod	0.026	0.097	0.034	0.084	0.074	0.053	1	-0.052	0.278**	0.343**	-0.055
No. of pods/ plant	0.459**	-0.192	0.022	0.356**	0.399**	0.361**	0.058	1	0.526**	-0.06	0.349**
Grain yield /plant (kg)	0.706**	-0.093	0.098	0.172	0.640**	0.733**	0.063	0.401**	1	-0.036	0.271**
Protein (%)	0.04	0.058	0.18	0.195	0.001	0.102	0.088	0.013	0.016	1	-0.560**
Oil (%)	0.126	-0.146	-0.259*	-0.201	0.157	0.13	-0.007	0.224*	0.209*	-0.488**	1

** = Significant at 1 % and * = Significant at 5 % level of significance

Table 5 : Path coefficient analysis showing direct effect (diagonal) and indirect effects (off diagonal) at genotypic and phenotypic level

		Days to 50% flowering	**Days to maturity**	**Plant height (cm)**	**No. of branches /plant**	**100 seed weight (g)**	**No. of seeds/ pod**	**No. of pods/ plant**	**Grain yield /plant (kg)**	**Grain yield per plot (r)**
Days to 50% flowering	G	-0.174	-0.036	0.104	-0.059	-0.025	-0.004	0.071	-0.015	-0.139
	P	-0.013	-0.056	0.047	-0.062	-0.035	-0.005	-0.005	-0.008	-0.137
Days to maturity	G	-0.123	-0.051	0.068	-0.001	0.027	0.002	0.001	0.083	0.006
	P	-0.009	-0.077	0.034	0.007	0.041	-0.002	0.001	0.008	0.003
Plant height (cm)	G	-0.045	-0.009	0.399	0.149	0.040	-0.025	-0.103	0.060	0.466**
	P	-0.003	-0.012	0.212	0.147	0.065	-0.004	0.008	0.015	0.429**
No. of branches /plant	G	0.027	0.000	0.157	0.378	0.183	-0.025	-0.111	0.311	0.920**
	P	0.002	-0.001	0.066	0.476	0.252	-0.004	0.009	0.054	0.854**
100 seed weight (g)	G	0.018	-0.006	0.068	0.295	0.235	-0.019	-0.114	0.379	0.856**
	P	0.001	-0.008	0.036	0.314	0.382	-0.003	0.009	0.062	0.793**
No. of seeds/ pod	G	-0.005	0.001	0.062	0.061	0.028	-0.158	0.011	0.117	0.116
	P	-0.001	-0.003	0.018	0.035	0.02	-0.051	0.001	0.005	0.026
No. of pods/ plant	G	0.058	0.000	0.193	0.198	0.126	0.008	-0.212	0.222	0.593**
	P	0.002	-0.002	0.076	0.19	0.138	-0.003	0.024	0.034	0.459**
Grain yield /plant (kg)	G	0.006	-0.010	0.057	0.279	0.211	-0.044	-0.112	0.421	0.809**
	P	0.001	-0.007	0.037	0.305	0.28	-0.003	0.009	0.084	0.706**

** = Significant at 1 % and * = Significant at 5 % level of significance

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