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Genetic Evaluation and Trait Association Analysis for Yield Enhancement in Soybean (*Glycine max* L. Merrill)

Yamini Gautam [a], M.K. Tripathi [a*], Riya Mishra [a], Goutam Mohbe [a], Anurag Sharma [a], Sanjeev Sharma [a], Jagendra Singh [a] and Lalita Bishnoi [b]

[a] Department of Genetics & Plant Breeding, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, M.P., India.
[b] Sardarkrushinagar Dantiwada Agricultural University, Dantiwada, Gujarat, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Glycine max [L.] Merrill is an internationally significant leguminous crop, appreciated for its high protein (~40%) and oil (~20%) content. Enhancing seed yield, a polygenic trait influenced by multiple agronomic characters, remains a major breeding objective. Present investigation was conducted during *Kharif*, 2024 at the Research Farm, Zonal Agricultural Research Station, Morena, RVSKVV, Gwalior, M. P., India, using 60 genetically diverse genotypes laid out in a Randomized

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*Corresponding author: Email: drmanojtripathi64@gmail.com;

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Block Design with two replications. Substantial genetic variability was observed for main yield attributing traits. Phenotypic coefficients of variation (PCV) exceeded genotypic coefficients (GCV), indicating environmental influence; however, small PCV-GCV differences for many traits suggested existence of a strong genetic basis. High heritability (>99%) and genetic advance as percentage of mean (GAM) were investigated for numbers of seeds per plant, biological and seed yield per plant signified that traits governed largely by additive gene action. Correlation analysis revealed significant positive associations of seed yield with numbers of seeds and pods per plant, biological yield, harvest index and hundred-seed weight. Path coefficient analysis identified biological yield as having the highest direct positive effect on seed yield, tracked by harvest index and numbers of seeds per plant. Whereas, negative direct effects of some traits were offset by strong indirect contributions *via* key yield contributing components. These findings highlighted that traits of high breeding value, offering essential guidance for selection indices in soybean improvement. Integrating these findings with molecular tools could accelerate the development of high-yielding, climate-resilient cultivars suitable to diverse agro-ecological zones.

Keywords: Correlation analysis; genetic advance; genetic variability; heritability; path coefficient analysis.

1. INTRODUCTION

Glycine max [L.] Merrill stands as one of the most purposefully important leguminous crops cultivated worldwide, owing to its exceptional nutritional composition, broad industrial utility, and agronomic versatility (Upadhyay *et al.,* 2020; Mishra et al., 2021). Its seeds contain around 40% high-quality protein and 20% oil, making soybean a vital component in human diets, animal feed formulations, and numerous industrial applications (Sharma *et al.,* 2021a; Mishra *et al.,* 2024a). Soy-derived protein, rich in essential amino acids, serves as a main alternative to animal protein in vegetarian and vegan diets. Instantaneously, soybean oil is extensively used in cooking, food processing, and non-food industries, including biodiesel, pharmaceuticals, cosmetics, lubricants and printing inks (Tripathi *et al.,* 2022; Sharma *et al.,* 2023; Mishra *et al.,* 2024b, Mishra *et al.,* 2024c). In livestock production, soybean meal produced after oil extraction aids as a high-protein feed ingredient that boosts productivity in poultry, cattle and aquaculture. Moreover, soybean products such as tofu, soy milk and textured vegetable protein are associated with health benefits like cholesterol reduction and improved heart health (Mishra *et al.,* 2025a; Department of Agriculture & Farmers Welfare, 2023). Agronomically, soybean subsidizes to environmental sustainability by fixing atmospheric nitrogen through symbiosis with *Rhizobium* bacteria, thereby reducing dependency on synthetic nitrogen fertilizers, improving soil fertility, and lowering production costs (Mishra *et al.,* 2021b; Nakei *et al.,* 2022; Hu *et al.,* 2023).

As per the USDA report (2023–24), global soybean production increased by 5.3%, reaching 394.71 million metric tons, with Brazil, the United States, Argentina, China and India collectively contributing over 88% of total output. India ranks fifth globally, producing 12.58 million metric tons from 12.56 million hectares, though its productivity (0.9 t/ha) remains significantly below the global average (USDA report, 2024-25; Mishra et al., 2024a; Mishra et al., 2025b; U.S. Department of Agriculture, 2024). Madhya Pradesh, recognized as the "Soybean State" of India, leads the country in both area (5.51 million hectares) and production (5.39 million metric tons), contributing approximately 45% to the national output with an average yield of 978 kg/ha (Soybean outlook, 2025; Agricultural Statistics at a Glance 2022, E&S division, DA & FW). Its adaptability to diverse agro-climatic zones, short growing season, and compatibility with multiple cropping systems make soybean a crop of global relevance. The rising global demand-fueled by population growth, dietary transitions, livestock sector expansion and renewable energy needs has intensified the need for soybean yield enhancement under variable environmental conditions (Mishra *et al.,* 2021c; Malik *et al.,* 2024; Jia *et al.,* 2025). However, seed yield in soybean is a complex quantitative trait governed by multiple morphological, physiological and phenological factors, often influenced by genotype × environment interactions. Therefore, systematic genetic improvement through plant breeding remains critical (Agricultural Market Intelligence Centre, 2025). Understanding the extent of genetic variability, heritability and genetic advance is fundamental for devising efficient selection strategies that ensure sustainable genetic gains

(Gnanasekaran *et al.,* 2024; Begna & Teressa, 2024). Simultaneously, assessing trait interrelationships through statistical tools such as correlation (Miller *et al.,* 1958) and path coefficient analyses (Wright, 1921), delivers insights into the direct and indirect effects of various yield attributing traits (Senthilnathan, 2019). This knowledge supports informed selection and management practices, ultimately enhancing yield potential and resource efficiency by farmers involved in soybean production (Barpanda et al., 2022; Zheng et al., 2022; Karunathilake et al., 2023). Correlation analysis reveals the degree and direction of association among traits, while path analysis partitions these associations into direct and indirect effects, helping to identify key traits for selection (Skelly *et al.,* 2019; Reddy *et al.,* 2022). Together, these tactics offer a vigorous framework for trait prioritization and the development of high-yielding, climate-resilient cultivars tailored to specific agro-ecological conditions. Thus, present investigation was conducted to investigate a combined study on genetic variability, heritability, and genetic advance estimates and inter-trait relationships to achieve enhanced productivity, ecological resilience, and long-term food and nutritional security.

2. MATERIALS AND METHODS

2.1 Experimental Site

The field experiment was conducted during the *Kharif*, 2024 at the Research Farm, Department of Genetics and Plant Breeding, Zonal Agricultural Research Station, Morena, affiliated with Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, Madhya Pradesh, India. Geographically, Morena is located at 26.5°N latitude and 78.0°E longitude, with an average elevation of 177 meters above mean sea level. The experimental site was characterized by uniform topography, medium-black soil and the absence of standing water, providing a suitable agro-ecological setting for soybean cultivation.

Table 1. List of soybean genotypes along with their source

S. No.	Genotypes	Source	S. No.	Genotypes	Source
1.	JS-26	JNKVV, Jabalpur	31.	Rajsoya-24	RAK, Sehore
2.	JS-20-79	JNKVV, Jabalpur	32.	DLSB-40	RAK, Sehore
3.	JS-20-116	JNKVV, Jabalpur	33.	DS 1510	Delhi
4.	JS-22-01	JNKVV, Jabalpur	34.	Himaso 1695	RAK, Sehore
5.	JS-22-12	JNKVV, Jabalpur	35.	CAUMS-3	RAK, Sehore
6.	JS-23-05	JNKVV, Jabalpur	36.	Cat492A	RAK, Sehore
7.	JS-24-26	JNKVV, Jabalpur	37.	Cat 87	RAK, Sehore
8.	JS-25-03	JNKVV, Jabalpur	38.	NRC-142	NSRI, Indore
9.	JS-21-07	JNKVV, Jabalpur	39.	NRC-201	NSRI, Indore
10.	Js-21-17	JNKVV, Jabalpur	40.	NRC-255	NSRI, Indore
11.	JS-20-94	JNKVV, Jabalpur	41.	NRC-166	NSRI, Indore
12.	RVS-23-26	RVSKVV, Gwalior	42.	NRC-152	NSRI, Indore
13.	RVS-23-10	RVSKVV, Gwalior	43.	NRC-138	NSRI, Indore
14.	RVS-23-15	RVSKVV, Gwalior	44.	NRC-192	NSRI, Indore
15.	RVS-23-23	RVSKVV, Gwalior	45.	NRCSL-7	RAK, Sehore
16	RVS-2001-4	RVSKVV, Gwalior	46.	NRCSL-4	RAK, Sehore
17.	RVS-23-5	RVSKVV, Gwalior	47.	KDS-1203	RAK, Sehore
18.	RVS-23-12	RVSKVV, Gwalior	48.	KDS-1201	RAK, Sehore
19.	RVS-23-20	RVSKVV, Gwalior	49.	KDSIS-1394	RAK, Sehore
20.	RVSM-2012-4	RAK, Sehore	50.	KSS-213	RAK, Sehore
21.	RSC-10-46	Raipur	51.	KBSL-23-36	RAK, Sehore
22.	RSC-10-52	Raipur	52.	BAUS(M)-6	Ranchi
23.	AS-26	RAK, Sehore	53.	Pusa Sipani BS 8	RAK, Sehore
24.	ASB-85	RAK, Sehore	54.	PS 1569	RAK, Sehore
25.	ASB-93	RAK, Sehore	55.	MAUS-787	RAK, Sehore
26.	AMS-264	PDKV, Akola	56.	MAUS-791	RAK, Sehore
27.	AMS-2021-3	PDKV, Akola	57.	MACS-824	RAK, Sehore
28.	AMS-100-39	PDKV, Akola	58.	SL-311	PAU, Ludhiana
29.	AUKS-21-5	RAK, Sehore	59.	SL-1315	PAU, Ludhiana
30.	TS-208	RAK, Sehore	60.	VLS-104	RAK, Sehore

2.2 Experimental Details

The experiment was laid out in a Randomized Block Design (RBD) with two replications to ensure statistical accuracy and minimize environmental variability. A total of sixty soybean genotypes were evaluated for their performance under field conditions. To ensure a broad genetic base, seeds were acquired from multiple reputed institutions, including the College of Agriculture, JNKVV, Jabalpur, M.P., India, RAK College of Agriculture, Sehore and RVSKVV, Gwalior (Table 1). Each genotype was sown in rows with a row-to-row spacing of 30 cm and plant-to-plant spacing of 10 cm, facilitating proper growth and aeration. The length of each row was 5 meters, providing adequate plot size for reliable phenotypic assessment. Standard agronomic practices were followed uniformly across the experimental field to ensure optimal crop establishment and to allow for the accurate evaluation of genetic potential.

2.3 Statistical Analysis

The experimental data were subjected to statistical analysis to assess genetic variability, heritability, genetic advance, correlation and path coefficient analysis using standard procedures. All statistical computations were carried out using the Agri Analyzer software for trait-wise descriptive statistics and OPSTAT, a web-based statistical tool developed by CCS HAU, Hisar, for analysis of variance (ANOVA) and multivariate analysis to ensure precision and reliability in interpretation.

3. RESULTS AND DISCUSSION

3.1 Genetic Variability, Heritability and Genetic Advance

The analysis of genetic variability, heritability and genetic advance among 60 soybean genotypes revealed substantial differences across investigated traits (Table 2). In all cases, phenotypic coefficients of variation (PCV) exceeded genotypic coefficients of variation (GCV), indicated environmental influence; nevertheless, the narrow gap between PCV and GCV for several traits suggested strong genetic control, supported the efficacy of phenotypic selection (Saicharan *et al.,* 2022; Chacko *et al.,* 2023).

High variability (>20%) was observed for numbers of seeds per plant (GCV: 31.25%; PCV: 31.26%), numbers of primary branches, harvest index, biological and seed yield, suggested for high selection potential. Moderate variability (10–20%) was addressed for 100-seed weight and plant height, while phenological traits *e.g*., days to flowering, podding and maturity demonstrated low variability (<10%) (Yimram *et al.,* 2009; Terfa & Gurmu, 2020).

Broad-sense heritability was found high for the most of the traits (75.74%–99.98%), with maximum values for numbers of pods, numbers of seeds per plant and days to maturity, indicated strong genetic determination as earlier mentioned by Toker (2004) and Akram *et al.* (2016). Genetic advance as percentage of the mean (GAM) was recorded highest for numbers of seeds per plant (64.38%), tracked by numbers of branches, harvest index, biological and seed yield. This emphasized that these traits predominantly governed by additive gene action (Getnet *et al.,* 2018; Jayaprada *et al.,* 2021). Thus, traits like numbers of seeds per plant, biological yield and harvest index with high heritability and GAM emerged as prime candidates for selection in soybean improvement programmes targeting high-yielding and climate-resilient cultivars (Baraskar *et al.,* 2014; Nayak *et al.,* 2024).

3.2 Correlation Coefficient Analysis

In the present investigation, genotypic and phenotypic correlation analysis were conducted to understand the interrelationships between seed yield per plant and various yield attributing traits in 60 soybean genotypes. At the genotypic level (Table 3; Fig. 1), seed yield per plant exhibited a highly significant and positive association with numbers of seeds per plant (0.729), numbers of pods per plant (0.505), biological yield (0.448), harvest index (0.386), and hundred-seed weight (0.265). These traits also displayed strong interrelationships, such as the high correlation between numbers of pods per plant and numbers of seeds per plant (0.637), and between harvest index and numbers of seeds per plant (0.376). This indicates that improvement in these traits may contribute significantly to enhance seed yield as earlier investigated by Bambodkar *et al.* (2020) and Barpanda *et al.* (2024). Traits such as days to flowering, days to podding, and days to maturity, generally demonstrated weak or non-significant correlations with seed yield. Some even exhibited negative associations with major yield traits, suggesting their limited direct role in yield enhancement under the investigated circumstances. For instance, days to podding had significant negative correlations with numbers of pods per plant and 100-seed weight at the genotypic level. Similar results also reported by Painkra *et al.* (2018), Sharma *et al.* (2021b) and Ragade *et al.* (2025).

At the phenotypic level (Table 4; Fig. 2), the trends were consistent with the genotypic correlations. Seed yield per plant displayed significant positive correlations with numbers of seeds per plant (0.721), numbers of pods per plant (0.500), biological yield (0.444), harvest index (0.396), and hundred-seed weight (0.237). Numbers of primary branches also demonstrated a positive association with seed yield including several component traits in experiments of Guleria *et al.* (2019) and Patil *et al.* (2024), suggesting its importance as a secondary selection criterion. The negative correlation between biological yield and harvest index indicates a trade-off between total biomass production and resource allocation to seed formation (Chavan *et al.,* 2016; Amogne *et al.,* 2020). However, the strong positive association of biological yield with seed yield implies that genotypes with higher biomass, if coupled with a favourable harvest index, can be highly productive (Silva *et al.,* 2015; Sulistyo *et al.,* 2018; Miranda *et al.,* 2020). Similarly, the positive relationship between 100-seed weight and both harvest index and seed yield highlights the role of seed size in yield enhancement. The weak correlations of phenological traits such as days to flowering, podding, and maturity with seed yield suggested that delayed flowering or prolonged maturity may not contribute effectively to yield under rainfed *Kharif* conditions (Jain *et al.,* 2014; Karyawati & Puspitaningrum, 2021). These findings are likely influenced by environmental stresses such as irregular rainfall, drought, or waterlogging, which are common in the soybean-growing regions of India during this season (Nair *et al.,* 2024; Murali *et al.,* 2025). Overall, the results highlight the importance of selecting genotypes with higher numbers of pods and seeds per plant, better harvest index, and greater biological yield for improving soybean productivity. These traits can serve as reliable selection indices in soybean breeding programmes aim to yield enhancement under rainfed conditions (Borowska & Prusiński, 2021; Mishra *et al.,* 2025b).

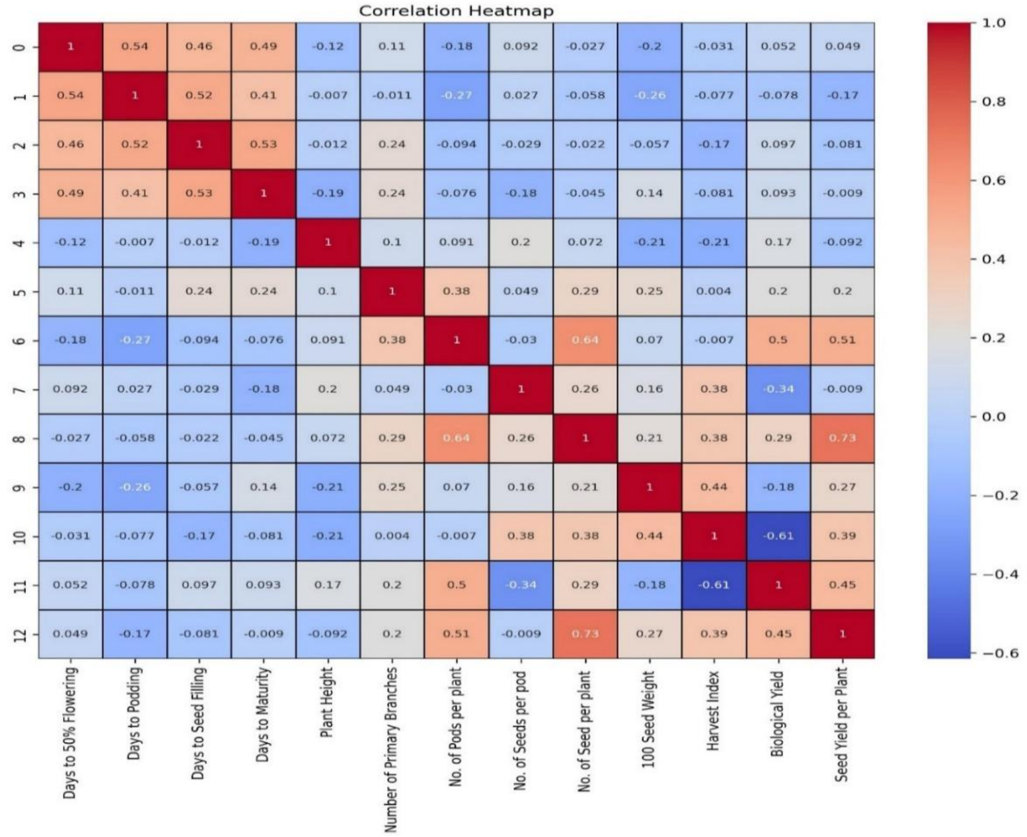

Fig. 1. Genotypic correlation heatmap for different traits in soybean

Table 2. Grand Mean, range, coefficient of variation and heritability for different characters in soybean genotypes

Trait	Grand Mean	Range		GCV (%)	PCV (%)	ECV (%)	Heritability (%)	Genetic Advance (%)	GA as % of Mean
		Maximum	Minimum						
Days to 50% flowering	40.292	47.000	33.000	7.339	7.349	0.386	99.72	6.083	15.098
Days to podding	53.175	62.000	47.000	7.527	7.533	0.292	99.85	8.239	15.494
Days to seed filling	64.558	75.000	54.000	6.726	6.730	0.241	99.87	8.939	13.846
Days to maturity	95.725	110.000	63.000	8.501	8.503	0.212	99.94	16.757	17.506
Plant height (cm)	37.500	56.333	28.000	14.484	14.517	0.976	99.55	11.164	29.770
Numbers of primary branches	4.294	7.333	2.000	27.924	28.218	4.063	97.93	2.445	56.924
Numbers of pods per plant	66.330	103.667	29.667	25.706	25.709	0.401	99.98	35.121	52.948
Numbers of seeds per pod	2.719	3.667	2.000	12.104	13.908	6.850	75.74	0.590	21.701
Numbers of seeds per plant	115.233	223.333	41.333	31.254	31.257	0.404	99.98	74.185	64.379
100-seed weight	9.173	13.465	5.176	16.770	19.067	9.072	77.36	2.787	30.386
Harvest index	41.406	64.251	22.360	27.727	28.120	4.681	97.23	23.320	56.321
Biological yield	25.884	41.407	11.231	27.090	27.177	2.174	99.36	14.398	55.627
Seed yield per plant	10.227	19.637	5.249	26.690	27.007	4.125	97.67	5.557	54.337

Classes of Heritability (%): High >70%, Moderate 50-70%, Low <50%
Classes of GA as percentage of mean at 5%: High >20%, Moderate 10-20%, Low <10%

Table 3. Estimates of correlation coefficient at genotypic level among different characters in soybean

Days to 50% flowering	Days to podding	Days to seed filling	Days to maturity	Plant height (cm)	Numbers of primary branches	Numbers of pods per plant	Numbers of seeds per pod	Numbers of seed per plant	100-seed weight	Harvest index	Biological yield	Seed yield per plant
1.000	0.543 **	0.458 **	0.489 **	-0.120	0.114	-0.181	0.092	-0.027	-0.199	-0.031	0.052	0.049
	1.000	0.521 **	0.414 **	-0.007	-0.011	-0.268 *	0.027	-0.058	-0.255 *	-0.077	-0.078	-0.168
		1.000	0.534 **	-0.012	0.239	-0.094	-0.029	-0.022	-0.057	-0.173	0.097	-0.081
			1.000	-0.193	0.242	-0.076	-0.180	-0.045	0.145	-0.081	0.093	-0.009
				1.000	0.105	0.091	0.203	0.073	-0.206	-0.213	0.168	-0.092
					1.000	0.380 **	0.049	0.287 *	0.249	0.004	0.198	0.197
						1.000	-0.030	0.637 **	0.070	-0.007	0.503 **	0.505 **
							1.000	0.258 *	0.164	0.377 **	-0.343 **	-0.009
								1.000	0.213	0.376 **	0.290 *	0.729 **
									1.000	0.442 **	-0.176	0.265 *
										1.000	-0.615 **	0.386 **
											1.000	0.448 **
												1.000

Table 4. Estimates of correlation coefficient for phenotypic level among different characters in soybean

Days to 50% flowering	Days to podding	Days to seed filling	Days to maturity	Plant height (cm)	Numbers of primary branches	Numbers of pods per plant	Numbers of seeds per pod	Numbers of seeds per plant	100-seed weight	Harvest index	Biological yield	Seed yield per plant
1.000	0.542 **	0.457 **	0.489 **	-0.120	0.113	-0.181 *	0.081	-0.027	-0.167	-0.031	0.051	0.048
	1.000	0.521 **	0.413 **	-0.007	-0.012	-0.267 **	0.027	-0.058	-0.224 *	-0.076	-0.078	-0.165
		1.000	0.533 **	-0.012	0.236 **	-0.094	-0.025	-0.022	-0.051	-0.171	0.096	-0.081
			1.000	-0.192 *	0.239 **	-0.076	-0.160	-0.045	0.127	-0.080	0.093	-0.010
				1.000	0.104	0.091	0.174	0.072	-0.181 *	-0.210 *	0.168	-0.090
					1.000	0.376 **	0.042	0.283 **	0.220 *	0.007	0.194 *	0.195 *
						1.000	-0.025	0.637 **	0.061	-0.005	0.501 **	0.500 **
							1.000	0.226 *	0.138	0.329 **	-0.297 **	0.000
								1.000	0.186 *	0.370 **	0.289 **	0.721 **
									1.000	0.389 **	-0.156	0.237 **
										1.000	-0.609 **	0.396 **
											1.000	0.444 **
												1.000

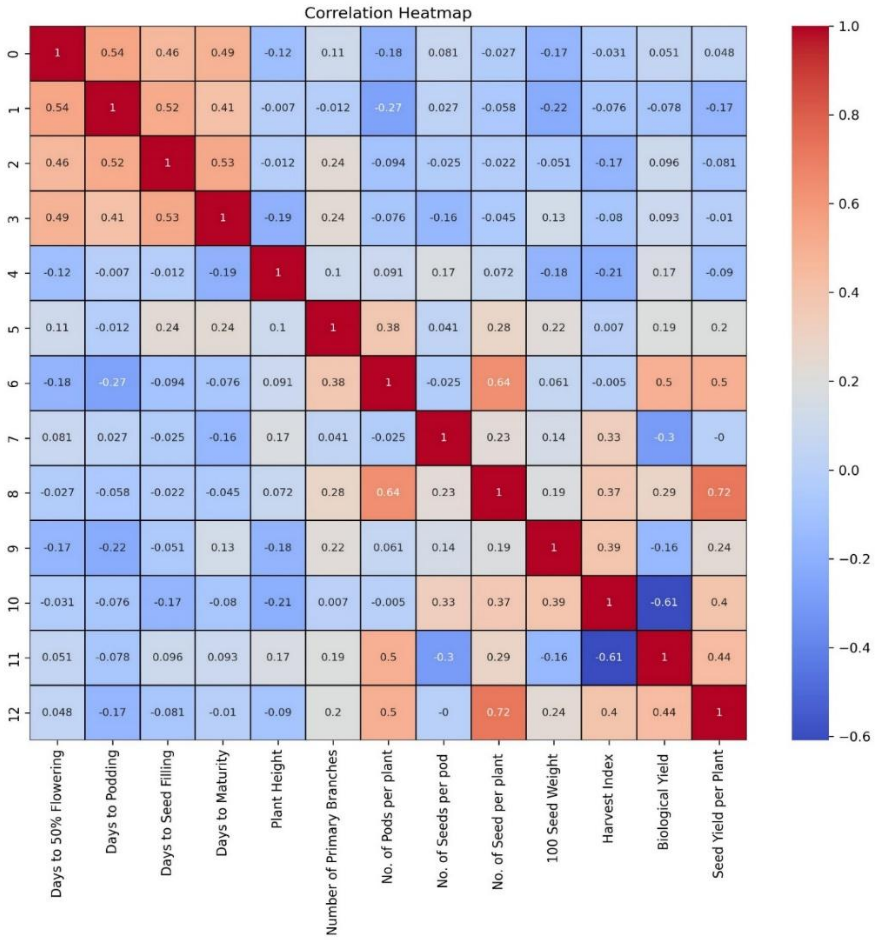

Fig. 2. Phenotypic correlation heatmap for different traits in soybean

3.3 Path Coefficient Analysis

The path coefficient analysis conducted at both genotypic and phenotypic levels revealed detailed insights into the direct and indirect effects of various yield contributing traits on seed yield per plant in soybean (Table 5; Table 6). The results advised that biological yield per plant exhibited the highest positive direct effect on seed yield at both genotypic (0.999) and phenotypic (1.065) levels, tracked by harvest index and numbers of seeds per plant. This highlights the importance of these traits as primary contributors to seed yield enhancement as previously documented by Amogne *et al.* (2020) and Patil *et al.* (2024).

At the genotypic level, harvest index (0.992) and numbers of seeds per plant (0.127) also showed remarkable positive direct effects, whereas traits for instance days to maturity (-0.073), plant height (-0.051), numbers of pods per plant (-0.107), numbers of seeds per pod (-0.064), and days to podding (-0.031) had negative direct effects on seed yield. Similarly, at the phenotypic level, besides biological yield and harvest index, numbers of seeds per plant (0.120) contributed positively, while days to maturity (-0.068), plant height (-0.057), numbers of pods per plant (-0.105), and numbers of seeds per pod (-0.047) negatively influenced seed yield directly.

The indirect effects further elucidated complex interrelationships among traits. Markedly, biological yield exerted strong positive indirect effects *via* numbers of seeds per plant, numbers of seeds per pod, and phenological traits like days to flowering and podding, but was negatively influenced through harvest index, plant height, and numbers of pods per plant. Harvest index, while showed a strong direct effect, was influenced indirectly by traits such as numbers of seeds per plant, plant height, and days to maturity, while negatively impacted by biological yield and seed filling duration.

Table 5. Path coefficient analysis showing the direct and indirect effect of 13 characters on the seed yield at phenotypic level

Traits	Days to 50% flowering	Days to podding	Days to seed filling	Days to maturity	Plant height (cm)	Numbers of primary branches	Numbers of pods per plant	Numbers of seeds per pod	Numbers of seeds per plant	100-seed weight	Harvest index	Biological yield	Seed yield per plant
Days to 50% flowering	0.053	-0.016	0.003	-0.033	0.007	0.000	0.019	-0.004	-0.003	-0.001	-0.030	0.054	0.048
Days to podding	0.029	-0.029	0.003	-0.028	0.000	0.000	0.028	-0.001	-0.007	-0.002	-0.075	-0.083	-0.165
Days to seed filling	0.024	-0.015	0.005	-0.036	0.001	0.000	0.010	0.001	-0.003	0.000	-0.171	0.103	-0.081
Days to maturity	0.026	-0.012	0.003	-0.068	0.011	0.000	0.008	0.008	-0.006	0.001	-0.080	0.099	-0.010
Plant height (cm)	-0.006	0.000	0.000	0.013	-0.057	0.000	-0.010	-0.008	0.009	-0.002	-0.209	0.179	-0.090
Numbers of primary branches	0.006	0.000	0.001	-0.016	-0.006	0.001	-0.039	-0.002	0.034	0.002	0.007	0.207	0.1945 *
Numbers of pods per plant	-0.010	0.008	-0.001	0.005	-0.005	0.000	-0.105	0.001	0.077	0.001	-0.005	0.534	0.5004 **
Numbers of seeds per pod	0.004	-0.001	0.000	0.011	-0.010	0.000	0.003	-0.047	0.027	0.001	0.328	-0.316	0.000
Numbers of seed per plant	-0.001	0.002	0.000	0.003	-0.004	0.000	-0.067	-0.011	0.120	0.002	0.368	0.308	0.7205 **
100- seed weight	-0.009	0.006	0.000	-0.009	0.010	0.000	-0.006	-0.006	0.022	0.008	0.387	-0.166	0.2374 **
Harvest index	-0.002	0.002	-0.001	0.006	0.012	0.000	0.001	-0.015	0.044	0.003	0.996	-0.649	0.3963 **
Biological yield	0.003	0.002	0.001	-0.006	-0.010	0.000	-0.052	0.014	0.035	-0.001	-0.607	1.066	0.444 **

Table 6. Path coefficient analysis showing the direct and indirect effect of 13 characters on the seed yield at genotypic level

Traits	Days to 50% flowering	Days to podding	Days to seed filling	Days to maturity	Plant height (cm)	Numbers of primary branches	Numbers of pods per plant	Numbers of seeds per pod	Numbers of seeds per plant	100-- seed weight	Harvest index	Biological yield	Seed yield per plant
Days to 50% flowering	0.058	-0.017	0.004	-0.036	0.006	0.000	0.019	-0.006	-0.003	-0.001	-0.031	0.056	0.049
Days to podding	0.032	-0.031	0.004	-0.030	0.000	0.000	0.029	-0.002	-0.007	-0.001	-0.078	-0.084	-0.168
Days to seed filling	0.027	-0.016	0.008	-0.039	0.001	0.000	0.010	0.002	-0.003	0.000	-0.174	0.103	-0.081
Days to maturity	0.029	-0.013	0.004	-0.073	0.010	0.000	0.008	0.012	-0.006	0.001	-0.081	0.100	-0.009
Plant height (cm)	-0.007	0.000	0.000	0.014	-0.051	0.000	-0.010	-0.013	0.009	-0.001	-0.213	0.179	-0.092
Numbers of primary branches	0.007	0.000	0.002	-0.018	-0.005	0.001	-0.041	-0.003	0.036	0.001	0.004	0.212	0.197
Numbers of pods per plant	-0.011	0.008	-0.001	0.006	-0.005	0.000	-0.107	0.002	0.081	0.000	-0.007	0.537	0.505 **
Numbers of seeds per pod	0.005	-0.001	0.000	0.013	-0.010	0.000	0.003	-0.064	0.033	0.001	0.378	-0.367	-0.009
Numbers of seed per plant	-0.002	0.002	0.000	0.003	-0.004	0.000	-0.068	-0.017	0.127	0.001	0.376	0.310	0.7292 **
100- Seed Weight	-0.012	0.008	0.000	-0.011	0.011	0.000	-0.008	-0.011	0.027	0.005	0.443	-0.188	0.265 *
Harvest index	-0.002	0.002	-0.001	0.006	0.011	0.000	0.001	-0.024	0.048	0.002	0.992	-0.657	0.386 **
Biological yield	0.003	0.002	0.001	-0.007	-0.009	0.000	-0.054	0.022	0.037	-0.001	-0.616	0.999	0.448 **

Traits such as numbers of pods per plant and numbers of seeds per pod, despite having negative direct effects, contributed positively to seed yield through their strong indirect effects *via* biological yield, numbers of seeds per plant, and harvest index. Days to maturity, plant height, and phenological traits generally had minimal or negative direct effects, yet their indirect contributions through key yield components were non-negligible.

These findings suggested that selection for high biological yield, efficient partitioning (harvest index), and greater seed numbers per plant can effectively increase seed yield in soybean. The predominance of biological yield as a central contributor to yield highlights the importance of biomass accumulation under field conditions (Sulistyo *et al.,* 2018; Ragade *et al.,* 2025). However, its negative association with harvest index designates a trade-off between vegetative growth and reproductive efficiency, necessitating a balanced selection approach. The positive direct and indirect effects of numbers of seeds per plant reaffirm its utility as a reliable yield predictor (Karyawati & Puspitaningrum, 2021; Nasir *et al.,* 2023). In contrast, traits like numbers of pods per plant and numbers of seeds per pod, though showing negative direct effects, may still be valuable through their interactions with other traits (Bisinotto *et al.,* 2017; Veeramani *et al.,* 2023). Moreover, the greater magnitude of both direct and indirect effects at the genotypic level compared to the phenotypic level suggests that genetic factors play a stronger role than environmental influences in determining these relationships, highlighting the potential of genetic improvement for yield enhancement (Obua *et al.,* 2024; Mishra *et al.,* 2025b).

4. CONCLUSION

The present investigation revealed significant genetic variability and robust interrelationships among yield and yield contributing traits in sixty soybean genotypes, offering valuable insights for crop improvement. Correlation and path coefficient analyses recognized key traits such as numbers of seeds per plant, biological yield, harvest index and seed yield per plant as critical determinants of yield. Remarkably, biological yield exhibited the highest positive direct effect on seed yield, followed by harvest index and numbers of seeds per plant, suggesting their prioritization in selection strategies. Although some traits like numbers of pods per plant and plant height displayed negative direct effects, their positive indirect effects accentuate the complexity of trait interactions and the need for balanced, multi-trait selection. The consistently higher phenotypic over genotypic coefficients of variation across traits indicated environmental influence; however, the narrow differences between them and the high heritability estimates for most traits advised predominant genetic control and the reliability of phenotypic selection. Moreover, high genetic advance for main characters implies additive gene action, making these characters ideal targets for genetic gain. Together, these findings establish a solid foundation for soybean breeding programmes. By integrating these insights with modern tools such as marker-assisted and genomic selection, breeders can accelerate the development of high-yielding, climate-resilient cultivars adapted to diverse agro-climatic conditions. This research strengthens the genetic base of soybean and contributes meaningfully to global food and nutritional security.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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