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ESTIMATION OF GENETIC PARAMETERS AND TRAIT INTERRELATIONSHIPS FOR YIELD IMPROVEMENT IN A MINI CORE ACCESSION OF SOYBEAN (*Glycine max* L. Merrill)

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ABSTRACT

A detailed experiment was conducted at ICAR- National Institute of Seed Science and Technology, Kushmaur, Mau, Uttar Pradesh to assess the analysis of variance, association analysis and the direct and indirect effect of various traits on seed yield with 170 mini core accessions. We included 10 ago-morphological traits which showed clear significant effect. The analysis of variance clearly showed that the genotypes had significant effect on almost traits. High genotypic coefficient observed for yield related traits and for flowering, while high heritability recorded for days to 50% flowering and days to maturity. Positive correlation with seed yield was observed for harvest index, biological yield, number of pods per plant. Harvest index and biological yield showed highest positive direct effect on seed yield per plant. Positive indirect effect on seed yield per plant were also found by total branches followed by number of pods per plant, seeds per pod and test weight also found positive indirect effect via biological yield per plant. Harvest index and biological yield reduced each other's contribution to seed yield per plant via significant negative indirect effect. Biological yield, harvest index and number of pods per plant are the most reliable contributors to seed yield. A balanced multi trait selection strategy using these traits will accelerate the development of high yielding and better adopted genotypes.

Key word : Correlation, Seed yield per plant, Path coefficient, Heritability, Genetic advance.

Introduction

Soybean (*Glycine max*) is the leading oilseed crop with production of 428.11 million metric tons in 2025-26 with an average growth rate of 2 % over the past 10 years (Soybeans | USDA Foreign Agricultural Service, n.d.). India held the 6th position in production with 11.03 million metric tons after Brazil, USA, Argentina, China, and Paraguay and contribute 3% of total world production (Soybeans | USDA Foreign Agricultural Service, n.d.). It was introduced in India by Roxburgh in 1832 from its native place China and its cultivation was initiated in

Kolkata botanic garden (Rani & Kumar, 2022). Soybean is self-pollinated crop from Leguminosae family that exhibit determinate (vegetative growth ceases after flowering), Indeterminates (vegetative growth and flowering occur simultaneously) and semi determinate (vegetative growth occur for a limited time after flowering) type growth habit (Bernard, 1972) with yellow, black, brown and red seed coat colour. Soybean possess a high protein content with poor digestibility due to trypsin inhibitor substance in seed (Kumar *et al.*, 2019). Soybean is short day crop with reversion of flowering stage into

vegetative phase in long day condition (Rani & Kumar, 2022; Yadava *et al.*, 2022). It has the high market value due to its high protein (40%) content and oil content (18-20%) with low glycemic index which make it good for diabetic (Rani & Kumar, 2022; Yadava *et al.*, 2022). Soybean products have grassy and beany flavor due to unsaturated fatty acid of lipoxygenase (Wilson, 1996). Soybean is rich source of fiber, vitamins, minerals and bioactive compounds. It supports bones and hearts health with regulate the blood sugar and reduce the menopausal symptoms and inflammation. Soybean also promotes digestion, satiety, muscle maintenance, immune function, healthy skin and brain function. Regular consumption support hormonal balance, healthy aging and protection against chronic diseases. Existing genetic variability is required for improvement and selection. This allows the breeders to estimate phenotypic basis of selection through genetic difference. Grain yield is a complex quantitative trait because its expression is determined through various traits, therefore, identifying and understanding the traits contributing to grain yield is essential for developing effective selection strategy (El-Mohsen *et al.*, 2013). Heritability denotes the proportion of phenotypic variation that is valuable for genetic differences and provides information about the response of a traits for selection. Traits with high heritability are typically improved more effectively through selection because a larger proportion of the observed variation is associated with genetic factors. Broad-sense heritability considers the total genetic variance and is useful for assessing the genetic contribution in creating variation among genotypes. Genetic advance is also an important parameter for estimating the expected improvement in a trait under a given selection intensity. The combined consideration of heritability and genetic advance provides more useful information about the expected response to selection than heritability alone (Johnson *et al.*, 1955). Grain yield is a major objective of soybean breeding; its expression is influenced by both genetic and environmental factors. Since grain yield is a complex quantitative trait, its variation is affected by genetic effects, environmental conditions, and their interaction (Bos & Caligari, 1995; Soldati, 1995). Estimating genetic variability, heritability, and genetic advance for yield and its related traits is important for identifying suitable traits for effective selection and genetic improvement in soybean.

Analysis of trait association analysis provides valuable information on the relationships among yield and its component traits, which can help in identifying appropriate characters for indirect selection (Silva *et al.*, 2022). Because correlation by itself does not clarify the nature

of these associations, path coefficient analysis can be applied to distinguish direct effects from indirect effects mediated by other traits and identify the traits with greater contributions to grain yield (Jain *et al.*, 2015). The combined use of correlation and path coefficient analysis provides a better understanding of the relationships among different traits and assist in identifying those traits that exert direct and indirect effects on yield. Hence, the present study was carried out to evaluate the genetic variability among 170 soybean segregants using genetic parameters including variability, heritability, and genetic advance as a percentage of the mean. The study also sought to establish the associations between yield and its contributing traits using correlation analysis and to identify the traits having direct and indirect effects on yield through path coefficient analysis. These analyses were used to identify useful traits for selection and to aid the genetic improvement of soybean under the target production conditions.

Material and Method

Experimental site and Plant material

This study utilized a minicore collection consisting of 170 germplasm accessions including certain cultivated soybean varieties, that was collected from ICAR-National institute of seed science and technology, Kushmaur, Mau (Table 1). The minicore collection was evaluated in an alpha lattice design with two replications over two successive *Kharif* season 2024 and 2025 at ICAR- NISST, Kushmaur, Mau. Uttar Pradesh, India, which is situated at 25.94° N latitude and 83.56° E longitude. Each replication consisted of 17 incomplete blocks with 10 plots in each block with following the required agronomic practices.

Phenotypic Data Collection of quantitative characters

Systematic observation, collection and analysis of the agronomic characters were included to evaluate the performance of the crop. The count of days until 50% flowering referred to how many days were required for 50% of the plant to attain flowering and days to maturity spanned the time from sowing until physiological maturity. Plant height (cm) was measured from the soil surface to apical tip of main stem at maturity. The Number of pods per plant was determined by counting the total developed pods from each plant. Total branches per plant were counted at maturity to assess the branching capacity of individual plants. Seed size and uniformity of weight were evaluated by weighing a hundred seed and recording the 100 seed weight in grams. Harvest index (%) was calculated as the proportion of seed yield relative to biological yield and expressed as percentage. Biological

Table 1: List of 170 soybean mini core accessions used in study.

S.No.	Genotype	S.No.	Genotype	S.No.	Genotype	S.No.	Genotype	S.No.	Genotype
1	GW6_W	35	GW95_W	69	GW159_W	103	GW223_W	137	GW303_W
2	NRC130	36	GW96_W	70	GW160_W	104	GW226_W	138	GW306_W
3	GW11_W	37	GW97_W	71	GW161_W	105	GW227_W	139	GW307_W
4	GW12_W	38	GW102_W	72	GW163_W	106	GW231_B	140	GW308_B
5	GW14_W	39	GW104_W	73	GW167_W	107	GW237_W	141	GW309_BR
6	GW15_W	40	GW105_W	74	GW171_W	108	GW238_G	142	GW310_W
7	GW18_G	41	GW107_W	75	GW172_W	109	GW240_W	143	GW311_W
8	GW22_W	42	GW113_W	76	GW174_W	110	GW242_G	144	GW312_W
9	GW27_BR	43	GW114_W	77	GW175_W	111	GW243_W	145	GW313_W
10	GW33_W	44	GW133_W	78	GW176_W	112	GW247_W	146	GW314_W
11	GW34_W	45	GW120_W	79	GW179_W	113	GW248_W	147	GW318_W
12	GW35_B	46	GW121_B	80	GW181_W	114	GW250_W	148	GW319_B
13	GW37_W	47	GW134_W	81	GW183_W	115	GW252_W	149	GW320_W
14	GW38_W	48	GW126_W	82	GW187_W	116	GW253_W	150	1_NRC-86_W
15	GW40_W	49	GW127_W	83	GW188_W	117	GW254_B	151	2_GP-551_G
16	GW41_W	50	GW128_W	84	GW190_W	118	GW256_W	152	3_PK-262_W
17	GW32_W	51	GW129_W	85	GW192_W	119	GW257_W	153	5_NRC-37_W
18	GW43_W	52	GW131_W	86	GW195_W	120	GW259_B	154	6_JS-20-48_W
19	GW46_W	53	GW135_W	87	GW200_W	121	GW260_BR	155	7_KDS-1096_W
20	GW49_W	54	GW136_W	88	GW201_W	122	GW262_W	156	11_KDS-992_W
21	GW51_W	55	GW137_W	89	GW203_W	123	GW264_B	157	15_KDS-1045_W
22	GW54_W	56	GW138_W	90	GW204_W	124	GW272_W	158	17_VLS-94_B
23	GW53_W	57	GW140_W	91	GW206_W	125	GW273_W	159	20_AGS-143_B
24	GW61_W	58	GW144_W	92	GW207_W	126	GW274_W	160	kali toor
25	GW65_W	59	GW142_W	93	GW208_W	127	GW280_W	161	JS335 (CHECK)
26	GW66_W	60	GW143_W	94	GW209_W	128	GW281_W	162	NRC150
27	GW68_W	61	GW145_W	95	GW210_B	129	GW283_W	163	JS20-98
28	GW74_W	62	GW148_W	96	GW211_G	130	GW284_W	164	JS20-94
29	GW81_W	63	GW140_W	97	GW212_G	131	GW288_W	165	NRC165
30	GW82_G	64	GW151_W	98	GW213_W	132	GW289_B	166	JS22-12
31	GW85_W	65	GW152_W	99	GW215_B	133	GW291_B	167	JS22-72
32	GW86_W	66	GW155_W	100	GW216_W	134	GW295_W	168	JS20-116
33	GW89_G	67	GW156_W	101	GW219_W	135	GW299_W	169	JS20-34
34	GW92_W	68	GW157_W	102	GW220_W	136	GW302_W	170	JS95-60

yield (g) was recorded through total dry biomass that was produced by each plant covering both vegetative and reproductive parts. These characters made it possible to grasp the plant structure, reproductive performance, and seed characteristics of the diverse genotypes.

Statistical analysis

All the statistical analysis were performed using R software (version 2026.06.0+242). Mean value was used for statistical analysis that is estimated from five randomly chosen plants from each plot. The comparison of genotypes, ANOVA and the experimental design was assessed through agricolae package which offers extensive functionality for experimental design, especially for agricultural and plant breeding experiment (PATTERSON & WILLIAMS, 1976). Correlation

Coefficient was calculated by correplot package (Aravind *et al.*, 2023).

Results

Variability and Genetic parameters

ANOVA, phenotypic variation and descriptive statistics in soybean genotypes:

The ANOVA showed that genotypes significantly influence nearly all the traits, as presented in Table 1. In this study, highly significant phenotypic variation was observed among the soybean genotypes for all the traits. The time needed to reach 50% flowering ranged from approximately 25 to 50 days. Likewise, maturity ranged from 70.59 to 114.60 days. High variation was observed for plant height with range from 40 to 177.47 cm with

Table 2: Analysis of variance for yield and contributing traits in soybean genotypes over the years *Kharif* season (2024 & 2025).

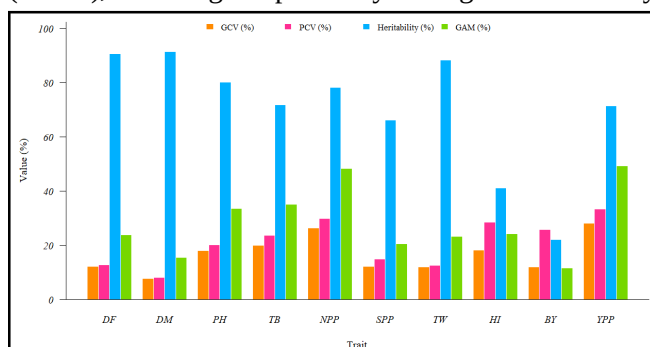
Source/traits	Environment	Replication within Environment	Genotypes (adj.)	Environment × Genotype	Blocks with in Replication × Environment	Error (intra-block)	Total
df	1	2	169	169	64	274	679
DF	2.14	0.015	85.386**	0.135**	0.034	0.028	14481.3
DM	12.856**	0.056	232.821**	0.025	0.033	0.035	39375.6
PH	1311.05**	8.293*	2902.29**	98.641**	2.052	1.704	509083
TB	3.125**	0.076	14.035**	3.469**	0.114	0.176	3017.05
NPP	7708.68**	37.312**	2356.14**	490.512**	3.75	4.592	490367
SPP	0.023	0.013	0.811**	0.018	0.023	0.027	149.012
TW	9.951**	0.045	6.222*	0.537**	0.037	0.062	1171.73
HI	15.303**	3.344*	760.653**	5.601**	0.892	1.085	129873
BY	2709.65**	46.976**	589.843**	135.145**	2.098	2.85	126242
SYPP	178.012**	3.169**	69.419**	16.622**	0.103	0.122	14765.4

**Significant at 1%, and * Significant at 5%, df; degree of freedom
DF-Days to 50 % flowering; **DM**-Days to maturity; **PH**- Plant height (cm); **TB**- total branches; **NPP**- no. of pods per plant; **SPP**- seed per pod; **TW**- Test weight (g.); **BY**-Biological yield (g.); **HI**-Harvest index (%); **SYPP**-Seed yield per plant (g).

mean of 115.68 cm. Adequate variation also observed for number of pods per plant ranged from 20.16 to 99.87 with an average of 64.27. Harvest index and seed yield per plant also exhibited variability, which is ranged from 13.39 to 69.46 % and 4.6 to 28.08 g per plant, respectively. These variabilities are summarized in Table 2.

Genotypic and Phenotypic variability:

All the characters exhibited higher phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV). This finding indicates that environment contributes on phenotypic traits. A Few traits showed high GCV value (>20), consisting of number of pods per plant (32.05%), harvest index (28.45%), biological yield (28.86%) and plant height (21.39%) suggesting sufficient genetic variability for these traits. Total branches per plant (20.11%) also exhibited high GCV although it was close to the threshold. Moderate GCV values (10-20%) were observed for seeds per pod (18.65%), days to 50% flowering (12.22%), and test weight (12.05%). Days to maturity showed a low GCV (7.88%), indicating comparatively lower genetic variability

**Fig. 1:** Genetic parameters for ten characters in 170 soybean genotypes.

for these traits. The highest PCV was recorded for number of pods per plant (36.77%) followed by biological yield (34.09%), seed yield per plant (33.41%) and harvest index (30.41%). The relatively small differences between GCV and PCV for days to flowering, days to maturity and test weight suggested lower environmental influence. However, the larger differences observed for biological yield and seed yield per plant indicated a higher environmental effect. Other estimates of genetic variability are presented in Table 2.

Heritability and Genetic advance:

Broad sense heritability showed a large variation among the soybean traits studied. High heritability was observed for most of the traits such as days to maturity (91.43%), days to 50% flowering (90.68%), test weight (88.54%), harvest index (87.52%), plant height (85.52%), seed per pod (84.27%), number of pods per plant (75.97%), total branch (71.79%) biological yield (71.67%) and seed yield per plant (71.31%). It suggests that these traits were highly influenced by genetic factors and could respond well to selection. The estimates of genetic advance also varied considerably among the traits. The highest genetic advance was recorded for plant height (48.24), followed by number of pods per plant (39.88), harvest index (21.92), biological yield (16.82) and days to maturity (14.92).

In terms of genetic advance as percentage of mean, number of pods per plant showed the highest value (57.63%) followed by harvest index (54.92%), biological yield (50.41%) seed yield per plant (49.16%). This finding suggests the possibility of improvement through selection. Days to maturity showed the lowest GAM (15.53%), indicating limited expected genetic gain through selection.

Table 3: genetic parameters for yield and yield components in soybean genotypes.

Trait	Mean	Range		GCV (%)	PCV (%)	Heritability (%)	GA	GA % of mean
		Minimum	Maximum					
DF	36.488	25	50	12.224	12.837	90.684	8.763	24.015
DM	96.072	70	115.92	7.875	8.235	91.431	14.923	15.534
PH	118.252	40	220	21.39	23.13	85.526	48.259	40.81
TB	7.954	2	16	20.109	23.732	71.797	2.796	35.152
NPP	68.212	15	160	32.053	36.773	75.974	39.314	57.636
SPP	2.4	1	4	18.657	20.323	84.278	0.848	35.334
TW	10.098	5.88	14.83	12.049	12.805	88.542	2.362	23.389
HI	39.91	12.428	69.885	28.457	30.418	87.522	21.92	54.922
BY	33.383	10	95	28.863	34.091	71.679	16.829	50.412
SYPP	12.446	4	28.08	28.221	33.419	71.314	6.119	49.166

DF-Days to 50 % flowering; **DM**-Days to maturity; **PH**- Plant height (cm); **TB**- total branches; **NPP**- no. of pods per plant; **SPP**- seed per pod; **TW**- Test weight (g.); **BY**-Biological yield (g.); **HI**-Harvest index (%); **SYPP**-Seed yield per plant (g).

Other estimates of heritability, genetic advance and genetic advance as percentage of mean are presented in Table 3.

Correlation patterns among traits:

The analysis of simple correlation coefficient (Table 4) revealed valuable association among all traits that will give opportunities for future breeding and crop improvement. We recorded strong positive correlation between seed yield per plant and several other traits like harvest index (0.631), number of pods per plant (0.488), biological yield (0.406), seed per pod (0.234). On the other hand, test weight (-0.015) showed negative correlation with seed yield per plant. Days to 50 % flowering showed non-significant positive correlation with days to maturity (0.450). Days to maturity were found to have positive association with days to 50% flowering, and significant positive correlation with harvest index (0.195*) and seed yield per plant (0.171). Plant height had a highly significant and positive correlation with total branch (0.375) and number of pods per plant (0.299), and significant positive correlation with test weight (0.156). Total branch exhibited a highly significant positive correlation with plant height

(0.375) and number of pods per plant (0.324), and significant positive correlation with seeds per pod (0.174) and test weight (0.181), while positive and non-significant association showed with days to maturity (0.071), harvest index (0.055), biological yield (0.086) and seed yield per plant (0.135). Number of pods per plant showed a highly significant and positive correlation with plant height (0.299), total branch (0.324), harvest index (0.320) and seed yield per plant (0.488) and significant positive correlation with seeds per pod (0.216) and biological yield (g) (0.188) with non-significant association observed for 50% flowering (0.001), days to maturity (0.036) and test weight (0.060). Seeds per pod had significant and positive correlation with total branch (0.174), number of pods per plant (0.216), and seed yield per plant (0.234). Test weight exhibited significant and positive correlation with plant height (0.156) and total branch (0.181). Positive and non-significant correlation was recorded with days to maturity (0.102), number of pods per plant (0.060), harvest index (0.011), and biological yield (0.008), while negative non-significant correlation was noted with days to 50%

Table 4: The correlation coefficients for yield and yield contributing traits in lentil genotypes over the years.

Trait	DF	DM	PH	TB	NPP	SPP	TW	HI	BY	YPP
DF	1.000	0.450***	-0.045	-0.115	0.001	0.141	-0.040	0.041	-0.052	0.051
DM		1.000	-0.033	0.071	0.036	0.142	0.102	0.195*	-0.062	0.171*
PH			1.000	0.375***	0.299***	0.054	0.156*	0.061	-0.003	0.060
TB				1.000	0.324***	0.174*	0.181*	0.055	0.086	0.135
NPP					1.000	0.216**	0.060	0.320***	0.188*	0.488***
SPP						1.000	-0.013	0.114	0.089	0.234**
TW							1.000	0.011	0.008	-0.015
HI								1.000	-0.421***	0.631***
BY									1.000	0.406***
SYPP										1.000

Significance: *P<=0.05 **P<=0.01 ***P<=0.001

DF-Days to 50 % flowering; **DM**-Days to maturity; **PH**- Plant height (cm); **TB**- Total branches; **NPP**- No. of pods per plant; **SPP**- Seed per pod; **TW**- Test weight (g.); **BY**-Biological yield (g.); **HI**-Harvest index (%); **SYPP**-Seed yield per plant (g)

Table 5: Estimates of direct (diagonal, shaded) and indirect effects of component traits on seed yield per plant.

Trait	DF	DM	PH	TB	NPP	SPP	TW	HI	BY	Total
DF	0.0435	0.0051	0.0001	-0.0012	0.0000	0.0055	0.0014	0.0389	-0.0419	0.0513
DM	0.0196	0.0114	0.0003	0.0007	0.0008	0.0055	-0.0035	0.1858	-0.0495	0.1709
PH	-0.0019	-0.0004	-0.0010	0.0039	0.0068	0.0021	-0.0053	0.0585	-0.0028	0.0599
TB	-0.0050	0.0008	-0.0004	0.0103	0.0074	0.0067	-0.0062	0.0521	0.0690	0.1349
NPP	0.0001	0.0004	-0.0003	0.0034	0.0229	0.0083	-0.0021	0.3047	0.1508	0.4881
SPP	0.0061	0.0016	-0.0001	0.0018	0.0049	0.0386	0.0005	0.1088	0.0714	0.2337
TW	-0.0018	0.0012	-0.0002	0.0019	0.0014	-0.0005	-0.0341	0.0104	0.0067	-0.0150
HI	0.0018	0.0022	-0.0001	0.0006	0.0073	0.0044	-0.0004	0.9531	-0.3376	0.6313
BY	-0.0023	-0.0007	0.0001	0.0009	0.0043	0.0034	-0.0003	-0.4014	0.8016	0.4056

Residual effect = 0.2166

DF-Days to 50 % flowering; DM-Days to maturity; PH- Plant height (cm); TB- Total branches; NPP- No. of pods per plant; SPP- Seed per pod; TW- Test weight (g); BY-Biological yield (g); HI-Harvest index (%); SYYP-Seed yield per plant (g)

flowering (-0.040). Highly positive significant association were found between harvest index and number of pods per plant (0.320), seed yield per plant (0.631), while harvest index showed highly significant negative with biological yield (-0.421). The main important finding is that the test weight showed negative association with seed yield per plant (-0.015), days to 50% flowering (-0.040) and seeds per pod (-0.013).

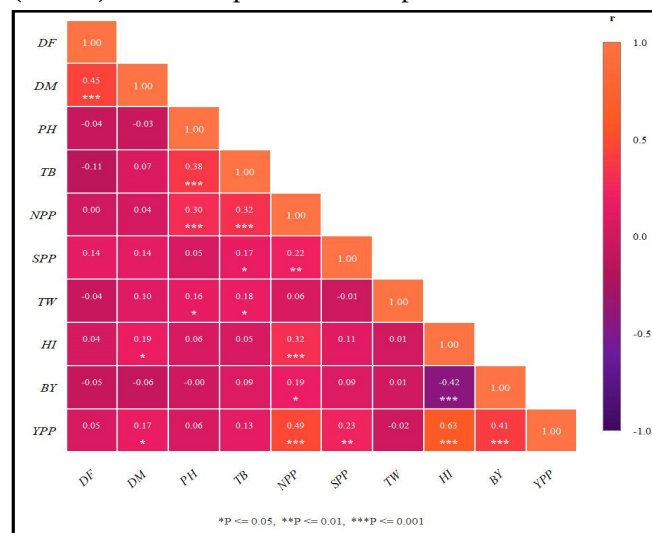
Path Coefficient analysis

The result of path coefficient analysis (Table 5) of the present study is presented in table 4 Maximum direct effect was contributed by harvest index (0.951) followed by biological yield (0.8016). The days to 50 % flowering (0.0435), seeds per pod (0.0386), number of pods per plant (0.0229), days to maturity (0.0114), and total branches (0.0103) also had positive but low direct effects on seed yield per plant. The indirect effect indicated that harvest index and biological yield are the principal pathways by which all other traits influenced the seed yield per plant. Days to 50 per cent flowering recorded its largest positive indirect effect via harvest index (0.0389), while its indirect effect via biological yield per plant was negative (-0.0419). Days to 50% flowering (0.0389), days to maturity (0.1858), plant height (0.0585), number of pods per plant (0.3047) and seed per pod (0.1088) exhibited largest positive indirect effect via harvest index. Positive indirect effects on seed yield per plant were also found by total branches (0.0690) followed by number of pods per plant (0.1508), seeds per pod (0.0714) and test weight (0.0067) also found positive indirect effect via biological yield per plant. Harvest index (-0.3376) and biological yield (-0.4014) reduced each other's contribution to seed yield per plant via significant negative indirect effect with counterbalancing each other.

Discussion

A well designed and appropriate breeding programme

executed for getting good quality, high yielding, resistant to biotic and abiotic stress with widely adoptable varieties in diverse environment. Such adoptability ensures stability under fluctuated environment which helps consistent productivity, which consequently highlights the importance of utilizing variable genetic resource to improve the yield potential (Verma *et al.*, 2024; Zong *et al.*, 2026). Existing genetic variability is prerequisite for success of any breeding programme, since it provides raw material for selection and crop improvement (Supraja *et al.*, 2026; Tekade *et al.*, 2025). The knowledge of variability helps the breeder in the selection of the various parent plants for creating of high yielding varieties. The Environmental factors also influence the expression of the agronomic traits in soybean. The genotypes showed a significant variation for almost all the traits under this study and the PCV was found to be higher than the GCV for all the traits that were studied. Among all the traits assessed, days to maturity was found to exhibit the lowest GCV (7.88%), which implies that this particular character is

**Fig. 2:** Simple correlation heat map for ten characters in 170 soybean genotypes.

strongly influenced by environment and it provides limited opportunity for genetic gain (Habib *et al.*, 2026), while days to 50 per cent flowering along with test weight exhibited merely a moderate level of genetic variability. On the other hand, number of pods per plant, biological yield and harvest index, recorded high GCV, which suggests the presence of ample genetic variability in these traits and identifies them as promising candidates for improvement through selection. The analysis of variance showed highly significant genotypic variation in genotypes for the investigated traits. The wide phenotypic range recorded for days to 50% flowering (25 to 50 days), plant height (40 to 177.47 cm), number of pods per plant (20.16 to 99.87) and seed yield per plant (4.6 to 28.08g) provided evidence for the variability within the experimental material. Comparable significant genotypic differences for phenological, morphological and yield related traits have been reported in soybean germplasm (S & Fakrudin, 2020). Similarly, highly significant differences were found among soybean genotypes for agronomic and yield related traits such as plant height and seed yield per plant (P.S. Shukla & Vikash Kumar Singh, 2017). Likewise, significant genotypic differences were recorded for all the traits particularly high GCV and PCV for seed yield per plant, biological yield and number of pods per plant (Kumari *et al.*, 2022; Rahaman *et al.*, 2022). Similar highly significant differences have been reported for yield and yield related traits by (Banerjee *et al.*, 2022; Baraskar *et al.*, 2026) in independent panels, while significant variation for all the traits was reported by (Belay *et al.*, 2023). These findings confirm the existence of exploitable variability in soybean genotypes and provide a basis for selecting superior genotypes. In the present study, broad sense heritability was high for all traits, ranging from 71.31% for seed yield per plant to 91.43% for days to maturity. High heritability accompanied by high genetic advance as a percentage of mean was found for number of pods per plant, harvest index, biological yield, seed yield per plant and plant height (Berhanu *et al.*, 2023; Manjunath *et al.*, 2020; Thio *et al.*, 2022), indicating that sufficient genetic variation exists and that additive gene effects are predominant in the inheritance of these traits, meaning that they can be used for direct phenotypic selection. A similar combination of high heritability and genetic advances have been observed for plant height, pods per plant, biological yield, harvest index, and seed yield per plant in soybean (Jawarkar *et al.*, 2025). Similar finding was observed in soybean, where high heritability coupled with adequate genetic advance was observed for several yield-contributing traits, that can use of heritability together with genetic advance become a reliable criterion for selection in crop improvement (J *et*

al., 2020). In the present study, days to maturity exhibited the highest heritability but showed the lowest genetic advance as a percentage of the mean suggesting a involvement of non-additive gene action or a narrow range of genetic variation for this trait. Considerable contribution of non-additive gene action was also found for this trait (Johnson *et al.*, 1955). An identical pattern was observed, in which high heritability led to effective additive gene action only when accompanied with high genetic advance, as observed for plant height in their study, whereas days to flowering, days to maturity and primary branches per plant combined low heritability with low genetic advance and were ascribed to non-additive gene action. An identical pattern was also observed with high heritability, transformed into effective additive gene action only when it was accompanied by high genetic advance as observed for plant height (Khan *et al.*, n.d.). Days to flowering, days to maturity, and primary branches per plant showed low heritability combined with low genetic advance and were attributed to non-additive gene action. Seed yield per plant exhibited a highly significant and positive correlation with harvest index, number of pods per plant and biological yield, along with a significant positive association with number of seeds per pod and days to maturity but test weight showed a negative non-significant association. Harvest index had a highly significant negative correlation with biological yield. Similarly, seed yield per plant showed significant positive relationship with biological yield and number of pods per plant, while (Mitiku *et al.*, 2025) recorded a similarly strong negative correlation between biological yield and harvest index that reflects the well-documented physiological trade-off between vegetative biomass accumulation and its efficient partitioning into seed. Seed yield per plant to be positively associated with harvest index and number of pods per plant that confirming these traits as dependable indicators for indirect selection of seed yield in soybean (Belay *et al.*, 2023). Path coefficient analysis showed that harvest index exerted the highest positive direct effect on seed yield per plant followed by biological yield, while the all-other traits contributed lower positive direct effects and test weight and plant height expressed negative direct effect. (Belay *et al.*, 2023) and (Mitiku *et al.*, 2025) similarly identified harvest index among the traits exerting the positive direct effect on seed yield per plant, while reported biological yield as the trait with the highest direct effect that are consistent with the present findings. The negative indirect effect between harvest index and biological yield exerted on one another indicates that these two traits act as counterbalancing pathways, each reducing other's contribution despite possessing a strong direct effect of its own. Number of

Pods per plant was the trait exerting the greatest direct effect (Pawar *et al.*, 2020), while hundred-seed weight was a different soybean (Khan *et al.*, n.d.). The dominant direct-effect trait was shown by (Silva *et al.*, 2022) to change across different environments confirms the path coefficients remain sensitive to genetic background and environment.

Conclusion

The soybean genotypes exhibited a wide range of genetic variance for all traits studied and the phenotypic coefficient of variation consistently exceeded the genotypic coefficient of variation, which indicates environmental influence on trait expression. However, several important yield-related traits such as number of pods per plant, biological yield and harvest index showed a high degree of genetic variation. This finding suggests good potential for selecting superior genotypes based on these traits. On the other hand, days to maturity showed comparatively low genetic variation despite recording the highest heritability, as environmental factors largely govern its expression rather than additive gene action. Traits such as number of pods per plant, harvest index, biological yield, seed yield per plant and plant height combined with high heritability with high genetic advance, making them reliable choices for direct selection. Correlation analysis demonstrated strong positive relationships between seed yield per plant and harvest index, number of pods per plant and biological yield this result indicates that improvement in these traits would contribute directly into higher seed yield, whereas harvest index and biological yield showed a strong negative relationship with each other. Path coefficient analysis confirmed harvest index and biological yield as the traits exerting the greatest direct influence on seed yield per plant, with the remaining traits acting mainly through these two pathways.

In conclusion, the results suggest that breeders should prioritize harvest index, biological yield and number of pods per plant, which combine high heritability, high genetic advance and a strong direct effect on seed yield, for effective selection. Future soybean breeding programmes can efficiently develop high-yielding genotypes by focusing on these traits while accounting for the counterbalancing relationship between harvest index and biological yield.

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