Original Research Article

Assessment of Genetic Variability, Trait Correlations, and Path Coefficients for Yield and Associated Traits in Soybean *(Glycine max* L. Merrill)

Abstract

This study evaluates genetic variability, heritability, and trait correlations among 52 advanced soybean breeding lines, with trial conducted during the Kharif season of 2023 at N.E. Borlaug Crop Research Centre, GBPUAT, Pantnagar, Uttarakhand. A randomized complete block design with three replications was employed, assessing traits such as plant height (PH), number of primary branches per plant (PBPP), number of nodes per plant (NPP), number of pods per plant (PPP),number of seeds per pod(SPP), days to 50% flowering(D50F), days to maturity(DM), and yield per plant(YPP). High genetic coefficients of variation for pods per plant and yield per plant, along with significant heritability and genetic advance, suggest that these traits are predominantly controlled by genetic factors and hold substantial potential for selection in breeding programs. Correlation analysis identified PPP as the most influential trait positively associated with YPP, indicating its suitability as a selection criterion. Path analysis further underscored PPP's direct impact on yield, while traits like seeds per pod and days to maturity also contributed positively. However, nodes per plant and days to flowering exhibited complex indirect effects on yield, emphasizing the need for a comprehensive selection approach that balances direct and indirect trait contributions. The results offer insights into optimizing selection strategies for soybean yield enhancement.

Key words: Soybean, correlation coefficient, path analysis, genetic variability, heritability, Genetic advance, Correlation.

Introduction

Soybean (*Glycine max* L. Merrill) belongs to the family Leguminosae, with a chromosome number of (2n=40). This leguminous crop thrives well in tropical, subtropical, and temperate climates. It is often referred to as the "Golden Bean," "Miracle Crop," or "Wonder Crop," soybean is valued for its diverse applications. Originally native to China, soybean was introduced to India in 1968 from the United States (Nagata 1970). Soybean ranks as the second most important oilseed crop in India, following mustard, due to its high nutritional value. It is rich in seed protein (approximately 40%) and contains a significant oil content (around 22%) with a high proportion of unsaturated fatty acids. This composition makes it highly desirable for human consumption and is utilized as a green vegetable, and its milk and oil are widely used in food preparation and various industrial products, while it also contributes to soil enrichment through nitrogen fixation in symbiosis with bacteria.

India has currently 12.07-million-hectare area with production of 13.98 million tons and productivity of 1158 kilogram per hectare (IISR 2023). Madhya Pradesh and Maharashtra alone contribute for more than 80 per cent of the country's total soybean production. In Uttarakhand, soybean occupies an area of 7960 ha with an annual production and average productivity of 8364 metric tons and 10.51 q/ ha, respectively (https://agriculture.uk.gov.in/pages/display/315-2023-24).

In selecting desirable genotypes for improved yield in a planned breeding program, it is essential to understand the nature and extent of variation in available breeding materials, the association of yield with contributing traits, and the precise contribution of these traits through direct and indirect effects.

Therefore, studying variability through estimates of the coefficient of variation, heritability, and genetic advance is essential to assess selection response. Variance component analysis (Jinks and Hayman, 1953), Hayman's graphical analysis (1954, 1956), and Griffing's (1956) combining ability analysis provide valuable insights into the inheritance of quantitative traits and aid in identifying superior parents and combinations likely to produce superior recombinants.

Correlation analysis offers insights into the degree of association between key plant traits and serves as a valuable indicator for predicting yield response based on changes in specific traits whereas Path coefficient analysis (Wright, 1921) is used to clarify the relationships among yield attributes and their contributions to overall yield. Studies on Correlation and path coefficient analyses are essential for establishing selection criteria in soybean improvement programs.

Genetic diversity analysis serves as a valuable approach for quantifying the extent of divergence between biological populations at the genotypic level and evaluating the relative contributions of various components to the overall divergence. The analysis of genetic diversity is a valuable tool for quantifying the degree of divergence between biological populations at the genotypic level and for assessing the relative contributions of different components to the total divergence. Path coefficient analysis, a standardized partial regression coefficient initially introduced by Wright (1921) and later expanded upon by Li (1956) and Dewey and Lu (1959), allows for the partitioning of the correlation coefficient into both direct and indirect effects.

The present experiment aims to determine the different variability parameters and their direct and indirect effects on seed yield of soybean.

Materials and Methods:

Present study was conducted during the *Kharif* 2023 at N.E. Borlaug Crop Research Centre, GBPUAT Pantnagar, Uttarakhand. Experimental material comprised of 52 advanced breeding lines as given in (Table 1). Each genotype was sown in three replications in a five rows plot, measuring 4-meters, spaced 45×5 (cm) apart using a randomized complete block design (RCBD).

S. No.	Genotypes	S. No.	Genotypes
1	DS13-18	27	RKS 54
2	NRC 127	28	JS 20-76
3	RVSM 2011-35	29	DS 97-12
4	PS 1569	30	MLT-19-15423
5	PS 1670	31	MLT-19-15523
6	Himso 1690	32	RVSM 2011-77
7	PS 1605	33	JS 21-71
8	JS 20-11	34	VLS 69
9	DS 13-12	35	SL 1074
10	UPSM 534×G. soja	36	NRC 128
11	UPSM 534	37	TGX 849-D-13-4
12	TGX 1681- 3f	38	MACS 1620
13	PS 26	39	AGS 25
14	RVSM 2011-10	40	EC 241780
15	PS 1661	41	DT 21
16	JS 20-69	42	Doko
17	MACS 303	43	CM 60
18	PS 1584	44	JS 20-34
19	PK 515	45	MAUS 768
20	PS 1225	46	Himso 1689
21	JS 20-116	47	Dsb 37
22	NRC-149	48	Dsb 21
23	PB 1	49	Hardee×G. soja
24	EC 241778	50	JS 335×G. soja
25	JS 20-98	51	Glycine soja
26	JS 20-01	52	NRCSL 4

Table 1: List of selected Soybean Advanced breeding Lines

Statistical Analysis:

Data was collected on five competitive randomly selected plants in each replication for yield and its related traits namely, plant height (PH), number of primary branches per plant (PBPP), number of nodes per plant (NPP), number of pods per plant (PPP), number of seeds per pod (SPP), days to 50% flowering (D50F), days to maturity (DM), Yield per plant (YPP). Genetic parameters, correlation coefficients were computed according to the method suggested by Singh and Chaudhry (1979). Path coefficients were worked out by the methods used by Dewey and Lu (1959).

Results and Discussion

Genetic parameters

The genetic coefficient of variation serves as a tool to quantify and compare the level of genetic diversity present across various quantitative and qualitative traits. The high PCV and GCV observed for pods per plant (PPP) **and** yield per plant (YPP) suggest that these traits have significant variability, which is largely genetic in nature as indicated by their high heritability values. This strong genetic influence, combined with high genetic advance as a percentage of mean, indicates that these traits are highly responsive to selection, making them ideal targets for yield improvement in soybean breeding programs. Similar finding was observed by Bhairav *et al.,* (2006) and Karad *et al.,* (2005) (Table 2). The high heritability coupled with high genetic advance observed for nodes per plant (NPP) also highlights its importance as a selectable trait with substantial genetic gain potential.

Traits such **as** plant height (PH)**,** with high heritability (97.869%) and moderate genetic advance, suggest that genetic improvement is possible but may yield moderate progress relative to other traits. In contrast, days to 50% flowering (D50F) and days to maturity (DM) show relatively low PCV and GCV values and moderate heritability, suggesting these traits are less variable and may be less responsive to selection. Similar results were reported earlier in soybean by Ramgiry and Raha (1997), Rajanna et al., (2000) and Singh and Yadav (2000). Mir and Tyagi (2010).

Overall, the high heritability and genetic advance in traits like pods per plant**,** nodes per plant, and yield per plant highlight them as critical traits for effective selection strategies aimed at improving soybean yield.

Correlation studies

The phenotypic and genotypic correlation coefficients between yield and yield components and inter-relationship among them were estimated and presented in the (Table 3).

The significant positive correlations observed in this analysis highlights pods per plant (PPP) as the most influential trait associated with yield per plant (YPP), both at the genotypic and phenotypic levels. This strong association suggests that increasing the number of pods per plant could directly contribute to higher yields, making PPP a prime target for selection in breeding programs. Nodes per plant (NPP) also contributes significantly to yield, reflecting its importance in enhancing yield potential when present in optimal numbers. The positive relationship between plant height (PH) and YPP indicates that taller plants may support more productive structures, possibly through increased photosynthetic capacity or a greater number of nodes. Additionally, the moderate positive correlation between days to 50% flowering (D50F) and YPP suggests that a slight delay in flowering time might allow for better plant development and a better yield, although this needs careful management to avoid adverse effects on maturity. Overall, selecting genotypes with higher values for PPP, NPP, and PH could be beneficial strategies for yield improvement in soybean. These results showed close resemblance with the report of Siahbidi *et al.* (2013).

Path coefficient analysis

The direct and indirect contributions of various yield components to grain yield, analyzed through path analysis at the phenotypic level, are detailed in (Table 4).

The path analysis reveals that pods per plant (PPP) plays a pivotal role in determining the dependent trait, with its high positive direct effect underscoring it as a critical target in selection for yield improvement in soybean. The significant positive contributions from seeds per pod (SPP) and days to maturity (DM) further emphasize the importance of reproductive traits in yield-related selection.

Traits like nodes per plant (NPP) and days to 50% flowering (D50F) showed significant negative direct effects, indicating potential trade-offs that breeders may need to manage. However, the positive indirect effects of plant height (PH) and nodes per plant (NPP) through pods per plant (PPP) suggest that their overall influence on yield can be favorable when PPP is optimized. This interaction indicates that while direct selection on these traits may not yield positive outcomes, they could contribute indirectly when pods per plant is emphasized. Similar results were also reported by Karnwal and Singh (2009), Yadav *et. al.* (2009) and Singh *et. al.* (1999). The complex interplay of indirect effects underscores the importance of a holistic approach in breeding programs, where direct and indirect influences are considered for trait improvement.

Conclusion

In conclusion, the findings of this study highlight pods per plant (PPP), nodes per plant (NPP), and yield per plant (YPP) as key traits with high genetic variation, heritability, and genetic advance, making them strong candidates for selection in soybean yield improvement programs. The significant positive correlations and direct effects of these traits on yield underline their potential as effective selection targets. Traits such as plant height (PH) and days to maturity (DM) also contribute positively, though often through indirect pathways, which suggests that an integrated approach considering both direct and indirect effects can optimize breeding outcomes. These insights provide a valuable foundation for developing high-yielding soybean varieties, emphasizing the need for targeted breeding strategies that leverage both genetic variability and trait interrelationships.

S. No.	Character	Mean	Range		PCV	GCV	h^2(bs)%	GA as % of mean
			Minimum	**Maximum**				
1	**PH (cm)**	39.674	23.36	66.5	25.405	25.132	97.869	51.218
2	**PBPP**	6.635	3.5	9	15.885	15.155	91.026	29.786
3	**NPP**	12.986	5.1	37.8	50.998	50.86	99.459	104.487
4	**PPP**	49.987	15.6	143.1	55.546	55.164	98.629	112.856
5	**SPP**	2.533	1.5	3.6	15.397	9.334	36.751	11.657
6	**D50F**	38	31	47	8.22	6.135	55.701	9.432
7	**DM**	98.013	83	120	7.432	6.973	88.018	13.476
8	**YPP(gm)**	13.029	3.07	51.15	68.286	65.362	91.619	128.88

Table 2: Estimation of genetic parameters for different traits in soybean:

S. No.	Character		PH (cm)	PBPP	NPP	PPP	SPP	D50F	DM	YPP
1	**PH (cm)**	P	1	0.491	0.537	0.687	0.132	0.237	0.483	0.614
		G	1	0.519	0.547	0.7	0.255	0.312	0.524	0.564
2	**PBPP**	P	0.491	1	0.042	0.216	0.166	0.001	0.081	0.276
		G	0.519	1	0.044	0.228	0.267	0.008	0.077	0.303
3	**NPP**	P	0.537	0.042	1	0.782	0.066	0.4	0.442	0.661
		G	0.547	0.044	1	0.789	0.107	0.527	0.469	0.692
4	**PPP**	P	0.687	0.216	0.782	1	0.112	0.405	0.384	0.906
		G	0.7	0.228	0.789	1	0.177	0.543	0.423	0.94
5	**SPP**	P	0.132	0.166	0.066	0.112	1	0.085	-0.057	0.315
		G	0.255	0.267	0.107	0.177	1	0.057	-0.126	0.238
6	**D50F**	P	0.237	0.001	0.4	0.405	0.085	1	0.252	0.305
		G	0.312	0.008	0.527	0.543	0.057	1	0.358	0.409
7	**DM**	P	0.483	0.081	0.442	0.384	-0.057	0.252	1	0.337
		G	0.524	0.077	0.469	0.423	-0.126	0.358	1	0.375
8	**YPP**	P	0.614	0.276	0.661	0.906	0.315	0.305	0.337	1

		G	0.564	0.303	0.692	0.94	0.238	0.409	0.375	1

Table 3: Genotypic & Phenotypic correlations between grain yield and its component traits

S. No.	Character	PH (cm)	PBPP	NPP	PPP	SPP	D50F	DM
1	**PH (cm)**	**-0.13**	0.03836	-0.05055	0.7093	0.0315	-0.01947	0.03453
2	**PBPP**	-0.0638	**0.078**	-0.00396	0.22295	0.03675	-0.00007	0.00579
3	**NPP**	-0.06978	0.00329	**-0.094**	0.80809	0.01462	-0.03292	0.03158
4	**PPP**	-0.08923	0.01686	-0.07363	**1.033**	0.0248	-0.0333	0.02744
5	**SPP**	-0.01844	0.01293	-0.0062	0.11537	**0.22197**	-0.00699	-0.00406
6	**D50F**	-0.03077	0.00007	-0.03768	0.41823	0.01887	**-0.08222**	0.01804
7	**DM**	-0.06278	0.00633	-0.04159	0.39652	-0.01261	-0.02075	**0.07147**

Table 4: Phenotypic path analysis table

RESIDUAL EFFECT=0.11613

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