

# Spectrum of Genetic Variability for Seed Yield and Yield-Contributing Traits in Soybean (*Glycine max* (L.) Merrill)

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**Abstract—** The present investigation entitled “Spectrum of Genetic Variability for Seed Yield and Yield-Contributing traits in Soybean (*Glycine max* (L.) Merrill)” was undertaken to assess the extent of variability, heritability, and genetic advance in eight soybean genotypes. The experiment was laid out in a Randomized Block Design with three replications during the Kharif season of 2024 at the School of Agricultural Sciences, G.H. Raison University, Saikheda. Observations were recorded for nine characters: days to 50% flowering, days to maturity, plant height, number of primary branches per plant, pod length, number of pods per plant, number of seeds per pod, 100-seed weight, and seed yield per plant. Analysis of variance revealed significant differences among genotypes for all traits, indicating considerable genetic variability. A wide range of variation was recorded for seed yield per plant, number of pods per plant, and plant height, suggesting ample scope for selection. Phenotypic coefficient of variation (PCV) values were slightly higher than genotypic coefficient of variation (GCV) for all traits, suggesting minimal environmental influence. High heritability coupled with high genetic advance as percent of mean was observed for number of primary branches per plant, number of pods per plant, 100-seed weight, and seed yield per plant, indicating the predominance of additive gene action and effectiveness of direct selection for yield improvement. These findings provide valuable insights for breeders to develop high-yielding and stable soybean varieties adapted to diverse agro-climatic conditions, hereby enhancing productivity and profitability.

**Index Terms —** *Glycine max*, genetic variability, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance, yield components, soybean breeding.

## I. INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is one of the most important grain legume crops grown worldwide, recognized for its dual value as a rich

source of high-quality protein (approximately 40%) and oil (around 20%), making it an essential commodity for food, feed, and various industrial applications. In addition to its nutritional significance, soybean plays a pivotal role in sustainable agriculture by contributing to soil fertility through biological nitrogen fixation. Globally, soybean has emerged as a major oilseed crop, with India being among the leading producers. Over the past few decades, soybean cultivation in India has expanded considerably, particularly in states such as Madhya Pradesh, Maharashtra, and Rajasthan. Despite this expansion, the productivity of soybean in the country remains below the global average, largely due to a narrow genetic base in cultivated varieties, environmental stresses, and inadequate exploitation of existing genetic variability.

Genetic variability is the fundamental prerequisite for crop improvement, as it determines the potential for selection and genetic enhancement of desirable traits. Effective plant breeding relies on the presence of sufficient heritable variation within a population, enabling breeders to identify superior genotypes for yield and adaptability. Quantitative traits such as seed yield and its contributing characters are governed by polygenes and are often influenced by the environment, making it essential to distinguish between genetic and environmental components of variation. Statistical parameters such as the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) help measure the extent of variability, while heritability (in the broad sense) and genetic advance provide insight into the proportion of heritable variation and the expected improvement through selection. A high heritability estimate coupled with a high genetic advance as a percentage of mean is indicative of the predominance of additive gene action, thereby

suggesting that direct selection can be effective for genetic improvement.

Considering the significance of genetic variability in crop enhancement, the present study was undertaken to assess the magnitude of variability, heritability, and genetic advance for key yield and yield-contributing traits in soybean. The findings aim to identify traits with the greatest potential for genetic improvement and provide a basis for formulating effective breeding strategies to enhance productivity in this important oilseed crop.

## II. MATERIAL AND METHODS

The present investigation was carried out during the Kharif season of 2024 at the Research Farm, School of Agricultural Sciences, G.H. Rasoni University, Saikheda. The experimental material comprised eight soybean genotypes namely KDS 726, KDS 992, DS 228, MAUS 71, MAUS 81, MAUS 162, MAUS 612, and JS 335. The field trial was laid out in a Randomized Block Design (RBD) with three replications. Each experimental plot measured 3 m × 3 m, maintaining a spacing of 45 cm between rows and 5 cm between plants to ensure uniform crop growth. Observations were recorded on nine quantitative traits, viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, pod length (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g), and seed yield per plant (g). The collected data were subjected to statistical analysis using the method of analysis of variance (ANOVA) as suggested by Panse and Sukhatme (1985). Estimates of genotypic variance ( $\sigma^2_g$ ), phenotypic variance ( $\sigma^2_p$ ), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense ( $h^2_b$ ), and genetic advance (GA) were computed following the procedures outlined by Burton and De Vane (1953) and Johnson et al. (1955). Data were analyzed using R studio for Analysis of Data.

## III. RESULT AND DISCUSSION

### 1. Analysis of variance

Variance assessment (ANOVA) indicated marked and substantial differences among eight soybean entries across all nine measured quantitative attributes (Table 4.1). The average sum of squares attributed to genotype effects was extremely significant ( $p < 0.01$ ) for parameters such as duration to 50% blooming, maturity period, stem height,

count of primary branches per plant, pod length, pods per plant, seeds per pod, 100-seed mass, and grain yield per plant. Herein, strong statistical significance suggests that the observed phenotypic variation is largely attributed to genetic differences rather than environmental influence.

### 2. Mean performance and range variation for quantitative traits

The eight soybean genotypes exhibited significant variability across all traits studied (Table 4.2):

- Days to 50% flowering: Ranged from 36.67 days (JS 335) to 45.00 days (MAUS 162), with a mean of 40.92 days, distinguishing early and late flowering types.
- Days to maturity: Varied slightly from 96.00 days (MAUS 612) to 102.33 days (KDS 726), with a mean of 99.62 days, reflecting low variability for crop duration.
- Plant height (cm): Showed wide variation, ranging from 38.33 cm (MAUS 612) to 52.67 cm (KDS 726), with a mean of 41.30 cm, indicating substantial diversity in vegetative growth.
- Number of primary branches per plant: Displayed high variability, with values from 3.60 (MAUS 81, MAUS 162) to 6.00 (KDS 726), with a mean of 4.47.
- Pod length (cm): Exhibited moderate variation, ranging from 3.53 cm (JS 335) to 3.96 cm (KDS 726), with a mean of 3.72 cm.
- Number of pods per plant: Varied considerably from 32.33 (MAUS 612) to 42.33 (KDS 726), with a mean of 38.13, highlighting ample scope for selection.
- Number of seeds per pod: Ranged from 2.33 (MAUS 71, MAUS 81) to 2.93 (KDS 726, KDS 992), with a mean of 2.67, suggesting exploitable genetic variation.
- 100-seed weight (g): Showed notable variability, from 11.71 g (MAUS 81) to 15.68 g (KDS 726), with a mean of 13.34 g, classifying genotypes into small- and large-seeded types.
- Seed yield per plant (g): Displayed the widest variation, from 9.58 g (MAUS 71) to 19.45 g (KDS 726), with a mean of 13.65 g, confirming its potential as a key selection criterion.

Overall, the traits number of branches per plant, pods per plant, 100-seed weight, and seed yield per plant exhibited the highest variability, making them promising targets for selection in soybean improvement.

### 3. Parameters of genetic variability

This study evaluated genetic parameters to determine the extent of variability and scope for selection in soybean genotypes (Table 4.3).

- Genotypic variance ( $\sigma^2_g$ ): Highest values were observed for plant height (18.69), pods per plant (14.36), and seed yield per plant (9.61), while pod length (0.02) and seeds per pod (0.05) showed very low variability.
- Phenotypic variance ( $\sigma^2_p$ ): Maximum variance was recorded for plant height (24.28), pods per plant (15.04), and seed yield (9.76), while pod length (0.04) showed the least variation.
- Genotypic coefficient of variation (GCV%): Ranged from 2.24% (days to maturity) to 22.72% (seed yield per plant). High values were observed for seed yield, primary branches, 100-seed weight, and plant height, suggesting greater genetic diversity.
- Phenotypic coefficient of variation (PCV%): Varied from 2.29% (days to maturity) to 22.90% (seed yield). Traits like seed yield, primary branches, plant height, and 100-seed weight exhibited higher variability, indicating

influence of both genetic and environmental factors.

- Heritability ( $h^2$ ): All traits recorded high heritability (>70%). Seed yield per plant (98.38%), number of primary branches (98.28%), and days to 50% flowering (97.26%) showed the highest values, suggesting reliable transmission to the next generation.
- Genetic advance (GA): Highest GA was observed for plant height (7.81), pods per plant (7.63), and seed yield (6.33), indicating good potential for selection. Pod length (0.28) and seeds per pod (0.39) showed the lowest GA.
- Genetic advance as percent of mean (GAM): Ranged from 4.54% (days to maturity) to 46.42% (seed yield). High GAM was observed for seed yield, primary branches, and 100-seed weight, highlighting their effectiveness for selection-based improvement.

Traits such as seed yield, number of pods per plant, 100-seed weight, and primary branches exhibited high GCV, PCV, heritability, and GAM, confirming their predominance of additive gene action and reliability for selection in soybean improvement programs.

Table 4.1 Analysis of variance for traits studied in genotypes of soyabean

Source of variation	Degree of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	Pod length (cm)	No. of pods per plant	No. of seeds per pod	100 Seed weight (g)	Seed yield per plant (g)
MEAN SUM OF SQAURE (MSS)										
Replication	2	0.04	0.67	4.33	0.22	0.01	104.62	0.01	0.34	2.29
Genotype	7	24.93**	15.12**	61.67**	2.41**	0.07**	43.75**	0.16**	7.03**	28.98**
Error	14	0.23	0.19	5.59	0.01	0.02	0.68	0.02	0.10	0.16

\*\*\* Significant at 5% and 1% levels, respectively

Table 4.2 Mean performance of genotypes for yield and yield contributing nine characters in soybean

Sr. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 seed weight (g)	Seed yield per plant (g)
1.	KDS 726	43.33	102.33	52.67	6.00	3.96	42.33	2.93	15.68	19.45
2.	KDS 992	42.33	100.00	40.67	5.00	3.85	41.80	2.93	13.60	16.67
3.	DS 228	39.00	101.67	41.17	5.33	3.87	35.80	2.67	12.98	12.36
4.	MAUS 71	39.33	100.33	39.57	4.33	3.63	34.40	2.33	11.93	9.58
5.	MAUS 81	43.00	96.33	44.33	3.60	3.58	41.53	2.33	11.71	11.36
6.	MAUS 162	45.00	101.00	41.30	3.60	3.69	40.20	2.80	12.02	13.58
7.	MAUS 612	38.67	96.00	38.33	3.67	3.65	32.33	2.67	15.42	13.25
8.	JS 335	36.67	99.33	40.27	4.20	3.53	36.67	2.67	13.34	12.98
	Mean	40.92	99.62	42.29	4.47	3.72	38.13	2.67	13.34	13.65
	C.V.	1.17	0.44	5.59	2.24	3.80	2.16	5.30	2.37	2.93
	F ratio	107.38	79.37	11.02	171.39	15.54	64.45	9.05	67.87	183.64

	S.E. $\pm$	0.28	0.25	1.36	0.07	0.04	0.47	0.08	0.18	0.23
	C.D. 5%	0.84	0.76	4.14	0.21	0.12	1.44	0.23	0.56	0.69

Table 4.2 Parameters for genetic variability for yield and yield contributing characters in soybean

Sr. No.	Traits	Range		Mean	Range Coefficient (%)	Variance		GCV (%)	PCV (%)	$H^2_{bs}$ (%)	Genetic advance	Genetic advance as % of mean
		Min	Max			Genotypic	Phenotypic					
1	Days to 50% flowering	36.67	45.00	40.92	20.36	8.23	8.46	7.01	7.11	97.26	5.82	14.24
2	Days to maturity	96.00	102.33	99.62	6.35	4.98	5.17	2.24	2.29	96.31	4.71	4.54
3	Plant height (cm)	38.33	52.67	41.30	33.91	18.69	24.28	10.22	11.66	76.97	7.81	18.48
4	No. of primary branches per plant	3.60	6.00	4.47	53.69	0.80	0.81	20	20.17	98.28	1.82	40.84
5	Pod length (cm)	3.53	3.96	3.72	11.56	0.02	0.04	3.98	4.37	82.95	0.28	7.46
6	No. of pods per plant	32.33	42.33	38.13	26.23	14.36	15.04	9.94	10.17	95.49	7.63	20
7	No. of seeds per pod	2.33	2.93	2.67	22.47	0.05	0.07	8.28	9.68	72.86	0.39	14.54
8	100 seed weight (g)	11.71	15.68	13.34	29.76	2.31	2.41	11.40	11.65	95.71	3.06	22.96
9	Seed yield per plant (g)	9.58	19.45	13.65	72.31	9.61	9.76	22.72	22.90	98.38	6.33	46.42

#### IV. CONCLUSION

The present investigation revealed considerable genetic divergence among the evaluated soybean genotypes with respect to seed yield and its component traits. The combination of high heritability and substantial genetic advance for traits such as seed yield per plant, number of pods per plant, and 100-seed weight suggests the predominance of additive gene action, indicating that direct selection for these traits would be highly effective. Genotypes including KDS 726, KDS 992, and MAUS 162 consistently exhibited superior performance and thus represent promising genetic resources for utilization in soybean improvement programmes. Overall, the findings underscore the significance of exploiting inherent genetic variability, coupled with favorable trait associations, to develop high-yielding and stable soybean cultivars.

#### REFERENCE

- [1] BAIRAGI, S., JADHAV, P. S., KHARE, M. AND SHINDE, S. V., 2023, Assessment of genetic variability and heritability in soybean [*Glycine max* (L.) Merrill]. Electron. J. Plant Breed., 14(1): 326-332.
- [2] BARPANDA, A., RAGHU, K. A., MANDAL, S., DAS, S. AND SINGH, A., 2024, Study of genetic variability and character association in soybean [*Glycine max* (L.) Merrill]. Legume Res., 47(1): 102-107.
- [3] DARAI, R., KHADKA, K., SHARMA, D., SAPKOTA, M., POKHREL, D. R. AND SAPKOTA, S., 2020, Genetic variability and diversity analysis in soybean [*Glycine max* (L.) Merrill] genotypes of Nepal. J. Agric. Nat. Resour., 3(1): 74-87.
- [4] DIXIT, D., CHOUDHARY, A. K., SAINI, D. K. AND KUMAR, R., 2023, Genetic variability, correlation and path coefficient analysis in soybean [*Glycine max* (L.) Merrill]. J. Food Legumes, 36(3): 237-242.
- [5] GAIKWAD, A. P., PAWAR, V. Y., SABALE, S. N. AND KADAM, S. S., 2020, Genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. J. Pharmacogn. Phytochem., 9(4): 1938-1941.
- [6] KHUMUKCHAM, S., KHUMAN, A., KSHETRIMAYUM, K. AND SINGH, K. C.,

- 2022, Genetic variability studies in soybean [*Glycine max* (L.) Merrill]. J. Pharmacogn. Phytochem., 11(2): 1177-1181.
- [7] KUMARI, A., SAHU, A., RANI, P. AND RAO, A., 2020, Path coefficient analysis for yield and its contributing characters in soybean [*Glycine max* (L.) Merrill]. Int. J. Curr. Microbiol. App. Sci., 9(9): 2375-2380.
- [8] KUMARI, P., SHARMA, S., GUPTA, S. AND SINGH, A., 2021, Genetic variability studies in soybean [*Glycine max* (L.) Merrill]. Legume Res., 44(3): 345-350.
- [9] KUMAWAT, R. R., VERMA, M. M., JAT, G. AND KUMAR, A., 2023, Genetic parameters and variability studies in soybean [*Glycine max* (L.) Merrill]. J. Food Legumes, 36(2): 172-176.
- [10] MEENA, R. K., YADAV, R. K. AND BHATI, P. K., 2023, Genetic variability and path coefficient analysis in soybean [*Glycine max* (L.) Merrill]. J. Pharmacogn. Phytochem., 12(3): 455-459.
- [11] MISHRA, A., KUMAR, D. AND RAJ, R., 2023, Genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. J. Food Legumes, 36(3): 229-233.
- [12] MONDAL, T. AND DAS, S., 2020, Genetic variability and path analysis in soybean [*Glycine max* (L.) Merrill]. J. Pharmacogn. Phytochem., 9(1): 1800-1803.
- [13] MOFOKENG, M. A., KALINDA, C. AND MPANZA, N., 2021, Genetic variability studies for yield and yield components in soybean [*Glycine max* (L.) Merrill]. Afr. J. Agric. Res., 16(5): 675-683.
- [14] RANI, P., KUMARI, A. AND SHARMA, R., 2022, Genetic variability and heritability in soybean [*Glycine max* (L.) Merrill]. Int. J. Agric. Sci., 14(2): 75-78.
- [15] SHARMA, V., SHARMA, R., YADAV, A. AND KUMARI, P., 2023, Genetic variability studies for yield and yield-related traits in soybean [*Glycine max* (L.) Merrill]. J. Food Legumes, 36(2): 177-182.