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Assessment of genetic variability for yield and its component traits in soybean [*Glycine max* (L.) Merrill

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Abstract
The present study was undertaken to assess genetic variability parameters in a set of 50 soybean genotypes along with four standard checks, namely JS 20-94, JS 20-98, JS 22-12, and JS 335. The experiment was conducted during Kharif 2024 at the experimental farm of the *All India Coordinated Research Project on Soybean*, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani (M.S.), following a Randomized Block Design (RBD) with two replications. Data were collected on ten characters, and estimates were made for variability parameters such as range, mean, genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, genetic advance, and genetic advance expressed as a percentage of mean.
Results revealed that number of pods per plant recorded the highest genotypic and phenotypic variance, followed by plant height and days to 50% flowering. Seed yield per plant exhibited the greatest GCV and PCV, with number of pods per plant, number of branches per plant, and 100-seed weight showing the next highest values. Heritability estimates were maximum for days to 50% flowering, followed by days to maturity, seed yield per plant, number of pods per plant, plant height, 100-seed weight, number of nodes per plant, number of branches per plant, and number of pod clusters per plant. High genetic advance as a percentage of mean was recorded for seed yield per plant, followed by number of pods per plant, 100-seed weight, number of branches per plant, plant height, number of nodes per plant, number of pod clusters per plant, and days to 50% flowering.

Keywords: Genetic advance, genetic variability, heritability, soybean (*Glycine max* (L.) Merrill) and yield

Introduction
Soybean (*Glycine max* L. Merrill) is regarded as one of the most valuable crops because of its high protein and oil content. Belonging to the family Leguminosae, it is a self-pollinated species with a chromosome number of 2n = 40. Globally, soybean has become a crucial crop to meet the rising demand for food and livestock feed. Its versatility makes it important not only as a direct food source but also as a major ingredient in animal nutrition and as a raw material for various industrial uses, which has expanded its cultivation well beyond its center of origin. Owing to its exceptional nutritional profile, soybean is often termed a "wonder crop" and a cost-effective source of high-quality protein. The protein is complete, supplying all nine essential amino acids, which has earned soybean the name "miracle bean" in nutritional terms (Quayam *et al.*, 1985) [24]. Historical records suggest its domestication dates back to around the 11th century B.C. in the Yellow River Basin of China (Hymowitz and Newell, 1981) [12]. Soybean seeds contain about 40-42% high-quality protein and 18-22% oil, of which nearly 85% are unsaturated fatty acids, and they are naturally cholesterol-free while also rich in minerals. Due to these attributes, soybean has been aptly described as "the meat that grows on plants" (Arshad *et al.*, 2006) [3]. Today, it stands as the world's most widely produced oilseed crop, with its protein being particularly well balanced for essential amino acids and minerals.

Materials and Methods
The present investigation was conducted the experimental farm of "All India Coordinated Research Project on Soybean'' Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. (M.S.) during *Kharif*-2024 in Randomized Block Design with two replications. The field was

divided into two homogenous replication blocks. Fifty genotypes were planted randomly in two replications. Observation on ten characters were recoded on randomly selected five plants from each genotype and average value was used for statistical analysis. The data is subjected to different statistical analysis *viz.*, analysis of variance, magnitude of genetic variability was performed following standard procedures.

Results and Discussion

Analysis of Variance

Table 1 displays the analysis of variance for ten characters. Significant variations were found in the genotypes of every character under study, according to the investigation. This showed that all of the characters in the genotypes under investigation had enough variability, thus selection could be used to enhance the features. Ramteke *et al*. (2010) [25], Masreshaw *et al*. (2022) [17], and Patel *et al*. (2025) [22] have also reported similar findings.

Table 1: Analysis of variance (ANOVA) for yield and yield contributing characters.

Sr. No	Characters	Source of variation		
		Replications (df=1)	Treatments (df=49)	Error (49)
1	Days to 50% flowering	2.25	43.60**	0.43
2	Days to maturity	4.41	38.44**	0.43
3	Plant height (cm)	26.75	543.97**	7.96
4	Number of nodes per plant	0.21	16.67**	0.48
5	Number of branches per plant	5.06	1.57**	0.22
6	Number of pod clusters per plant	2.75	14.24**	2.58
7	Number of seeds per pod	0.01	0.04**	0.02
8	Number of pods per plant	2.83	736.90**	9.18
9	100 Seed weight (g)	0.01	7.60**	0.14
10	Seed yield plant (g)	0.58	22.45**	0.27

** Significant at 1%, * Significant at 5%

Genetic variability Parameters

The estimates of mean, range, genotypic coefficient of variability, phenotypic coefficient of variability, heritability, genetic advance and genetic advance as percent of mean for ten characters of soybean are shown in Table 2.

Coefficient of variation

Seed yield per plant recorded the highest genotypic coefficient of variation (GCV, 48.13) and phenotypic coefficient of variation (PCV, 48.72), followed by number of pods per plant (32.69 and 33.10), number of branches per plant (22.76 and 26.33), 100-seed weight (21.46 and 21.86), plant height (19.62 and 19.91), number of nodes per plant (15.26 and 15.70), and number of pod clusters per plant (14.07 and 16.90). Moderate variation was observed for days to 50% flowering (10.30 and 10.40), while the lowest values were noted for days to maturity (4.24 and 4.30) and number of seeds per pod (3.72 and 7.77).

The coefficients of variation were estimated following Burton (1952) [7] and categorized as low (<10%), moderate (10-20%) and high (>20%) as suggested by Sivasubramanian and Menon (1973) [28]. Based on this classification, high variability (both GCV and PCV) was observed for seed yield per plant, number of pods per plant, number of branches per plant, and 100-seed weight. Moderate variability was recorded for days to 50% flowering, plant height, number of nodes, and number of pod clusters, whereas days to maturity and number of seeds per pod exhibited low variability.

The present findings are in line with earlier reports. Patel *et al*. (2025) [22] and Saicharan *et al*. (2022) [26] also documented maximum GCV and PCV for seed yield per plant. Similar results for high variability in number of branches per plant were reported by Gobezie *et al*. (2024) [11], Chandrawat *et al*. (2017) [8], and Vasanth *et al*. (2023) [30]. Mitiku *et al*. (2025) [18] observed high GCV and PCV for 100-seed weight, while Bairagi *et al*. (2023) [4] and Parindiyal *et al*. (2023) [21] reported similar findings for number of pods per plant. Bhangare *et al*. (2024) [6] indicated moderate variability for plant height, number of nodes, pod clusters, and days to 50% flowering. Low estimates of GCV and PCV for days to maturity and number of seeds per pod were also reported by Khumukcham *et al*. (2022) [15] and Sidramappa *et al*. (2019) [27].

Across all traits, PCV values were marginally higher than GCV, suggesting some influence of environmental factors. However, the narrow difference between the two indicates that environmental effects were relatively minor, and the observed variability is largely genetic in nature.

Heritability

Heritability estimates among the studied traits varied from 22.91% to 98.03%. The values were computed following the method of Burton (1952) [7] and categorized as low (<30%), moderate (30-60%), and high (>60%). High heritability was recorded for most traits, with the maximum observed for days to 50% flowering (98.03%), followed by days to maturity (97.79%), seed yield per plant (97.59%), number of pods per plant (97.54%), plant height (97.11%), 100-seed weight (96.34%), number of nodes per plant (94.39%), number of branches per plant (74.72%), and number of pod clusters per plant (69.26%). The only trait showing low heritability was number of seeds per pod (22.91%).

Overall, high heritability values for most characters suggest that these traits are largely governed by additive gene effects and can be effectively improved through selection. The present findings are consistent with earlier reports: days to 50% flowering (Pushpa Reni and Koteshwara Rao, 2013; Dutta *et al*., 2021; Sidramappa *et al*., 2019) [23, 10, 27]; days to maturity (Khumukcham *et al*., 2022) [15]; plant height (Masreshaw *et al*., 2022; Patel *et al*., 2025) [17, 22]; number of nodes per plant (Joshi *et al*., 2018) [13]; number of branches per plant (Akram *et al*., 2016) [1]; number of pod clusters per plant (Bairagi *et al*., 2023; Vasanth *et al*., 2023) [4, 30]; number of pods per plant (Bhangare *et al*., 2024) [6]; 100-seed weight (Masreshaw *et al*., 2022) [17]; and seed yield per plant (Gobezie *et al*., 2024) [11].

Genetic Advance

Genetic advance was estimated following the method of Johnson *et al*. (1955) [14] and categorized as low (<10%), moderate (10-20%), and high (>20%). In the present study, genetic advance ranged from 0.08 to 38.80. The highest values were obtained for number of pods per plant (38.80) and plant height (33.23), indicating strong potential for improvement through selection. In contrast, low genetic advance was observed for days to 50% flowering (9.47), days to maturity (8.88), seed yield per plant (6.77), number of nodes per plant (5.69), number of pod clusters per plant (4.13), 100-seed weight (3.90), number of branches per plant (1.45), and number of seeds per plant (0.08).

These results align with earlier findings. Days to 50% flowering showed low genetic advance as reported by Khumukcham *et al*. (2022) [15] and Bhangare *et al*. (2024) [6]. Days to maturity also exhibited low estimates, consistent with Ramteke *et al*. (2010)

[25]. High genetic advance for plant height was similarly observed by Amogne (2022) [2]. For number of branches per plant, low estimates were reported by Neelima *et al*. (2018) [20] and Nayak *et al*. (2024) [19], while number of seeds per plant also showed low values, as supported by Thakur and Vedna Kumari (2024) [29] and Yechalew (2019) [31]. High genetic advance for number of pods per plant was reported by Khumukcham *et al*. (2022) [15] and Akram *et al*. (2016) [1]. In contrast, 100-seed weight and seed yield per plant showed low genetic advance, which is in agreement with Sidramappa *et al*. (2019) [27].

Genetic advance as percent of mean

Genetic advance expressed as a percentage of mean was computed according to Johnson *et al*. (1955) [14] and classified as low (<10%), moderate (10-20%), and high (>20%). In the present study, high genetic advance as percent of mean was recorded for seed yield per plant (97.96%), followed by number of pods per plant (66.51%), 100-seed weight (43.39%), number of branches per plant (40.53%), plant height (39.83%), number of nodes per plant (30.54%), number of pod clusters per plant (24.12%), and days to 50% flowering (21.01%). On the other hand, low genetic advance as percent of mean was observed for number of seeds per plant (3.66%) and days to maturity (8.68%). These findings are supported by earlier reports. High estimates of genetic advance as percent of mean for days to 50% flowering were reported by Sidramappa *et al*. (2019) [27], while days to maturity showed low values as noted by Ramteke *et al*. (2010) [25]. Plant height exhibited high values in the studies of Masreshaw *et al*. (2022) [17] and Patel *et al*. (2025) [22]. Similarly, high estimates were documented for number of nodes per plant (Parindyal *et al*., 2023 [21]), number of branches per plant (Nayak *et al*., 2024 [19]), and number of pod clusters per plant (Vasanth *et al*., 2023; Joshi *et al*., 2018) [30, 13]. Low genetic advance as percent of mean for number of seeds per pod was reported by Thakur and Vedna Kumari (2024) [29] and Yechalew (2019) [31]. For number of pods per plant, high values were also noted by Belay *et al*. (2022) [5] and Koraddi *et al*. (2019) [16]. Likewise, seed yield per plant showed high genetic advance as percent of mean, in agreement with Dubey *et al*. (2015) [9].

Table 2: Estimation of variability, heritability and genetic advance for seed yield and its component traits

Sr. No	Characters	Range	General Mean	Genotypic Variance ($\sigma^2 g$)	Phenotypic Variance ($\sigma^2 p$)	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (%)	Genetic adv. as (%) of mean
1	Days to 50% flowering	33.5 - 57.0	45.09	21.58	22.01	10.30	10.40	98.03	9.47	21.01
2	Days to maturity	91.5 - 113.5	102.31	19.00	19.43	4.24	4.30	97.79	8.88	8.68
3	Plant height (cm)	44.0 - 113.1	83.42	268.00	275.96	19.62	19.91	97.11	33.23	39.83
4	Number of nodes per plant	11.0 - 23.1	18.64	8.09	8.57	15.26	15.70	94.39	5.69	30.54
5	Number of branches per plant	1.9 - 5.4	3.60	0.67	0.90	22.76	26.33	74.72	1.45	40.53
6	Number of pod clusters per plant	8.30 - 22.25	17.16	5.83	8.42	14.07	16.90	69.26	4.13	24.12
7	Number of seeds per pod	2.0 - 2.7	2.41	0.01	0.03	3.72	7.77	22.91	0.08	3.66
8	Number of pods per plant	21.1 - 98.1	58.34	363.85	373.04	32.69	33.10	97.54	38.80	66.51
9	100 Seed wt. (g)	5.78 - 14.21	9.00	3.73	3.87	21.46	21.86	96.34	3.90	43.39
10	Seed yield plant (g)	2.93 - 23.66	6.91	11.09	11.36	48.13	48.72	97.59	6.70	97.96

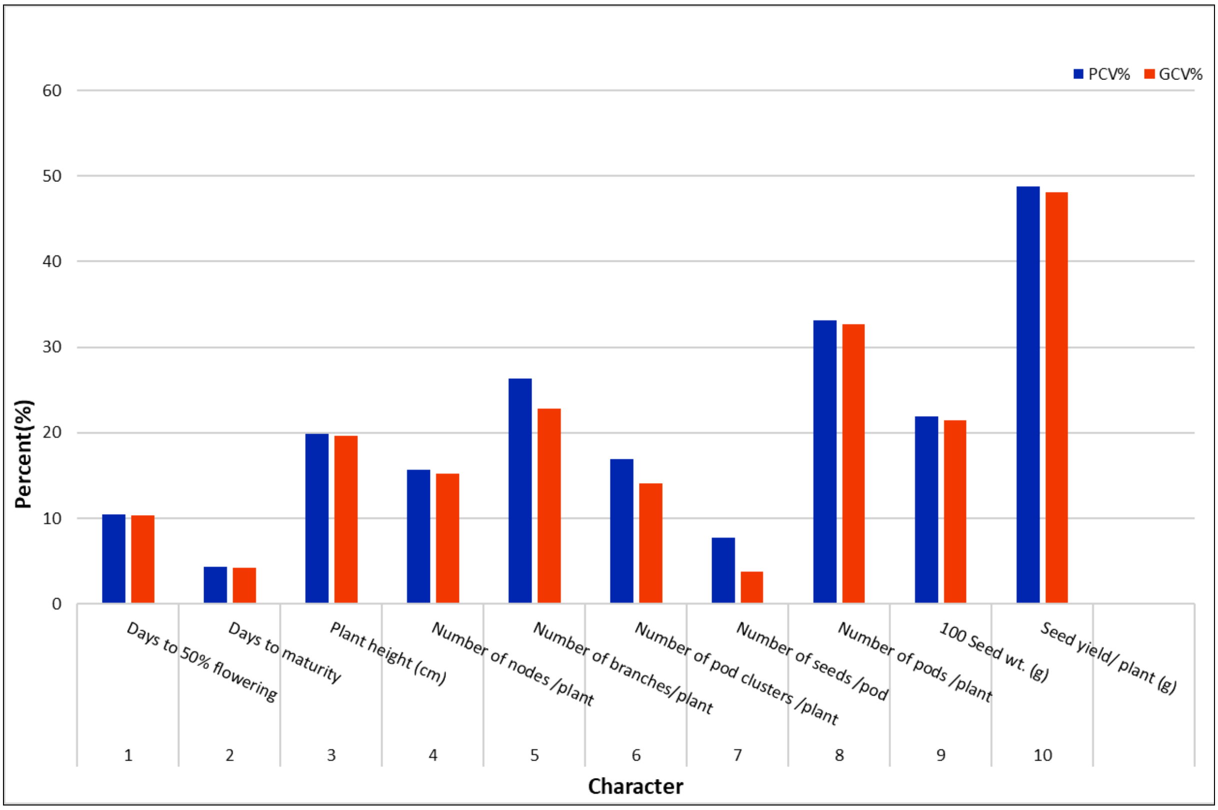

Fig 1: Graphical representation of genotypic and phenotypic coefficient of variation for various associated traits of seed yield.

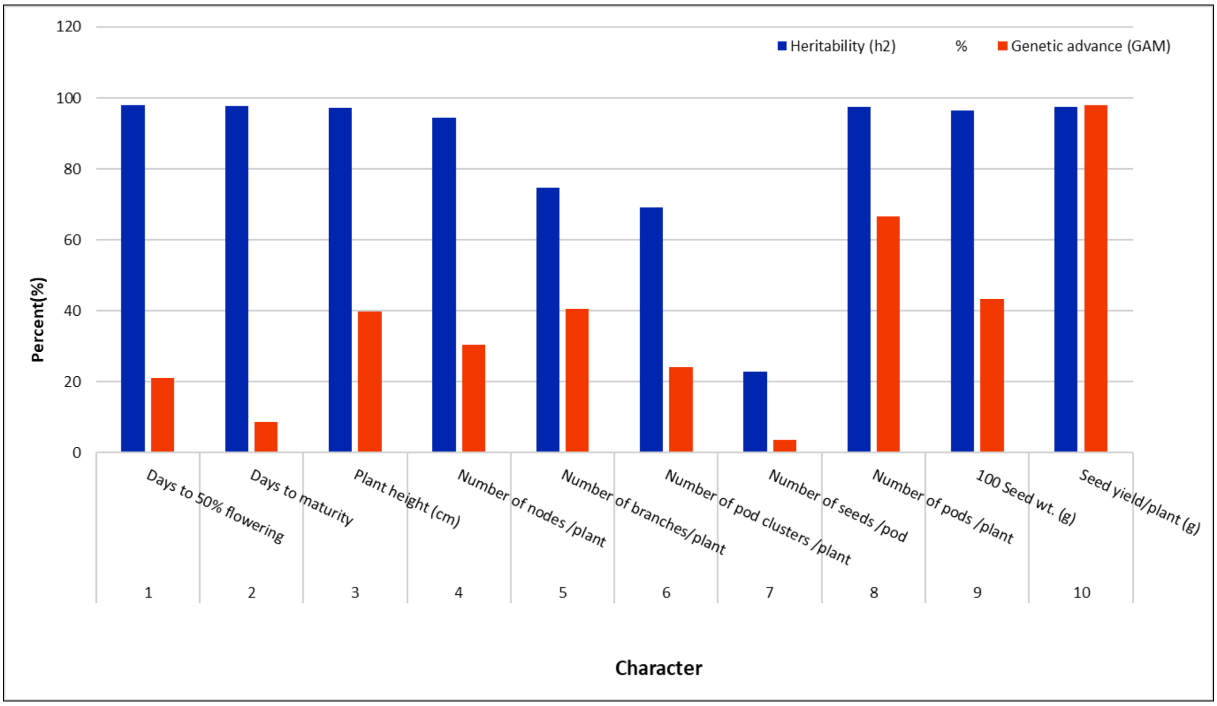

Fig 2: Estimation of heritability and genetic advance as percent of mean (GAM)

Conclusion

The analysis of variance demonstrated significant differences among all soybean genotypes for the traits under study, confirming the existence of considerable genetic variability and indicating ample scope for selection and genetic improvement. High estimates of both genotypic and phenotypic coefficients of variation were obtained for important yield-related traits such as seed yield per plant, number of pods per plant, number of branches per plant, and 100-seed weight, reflecting a wide range of variability and strong prospects for effective selection. The relatively small gap between GCV and PCV across traits suggested a limited influence of environmental factors, implying that most of these characters are predominantly governed by genetic control.

Specifically, high GCV and PCV values were recorded for seed yield per plant, number of pods per plant, number of branches per plant, and 100-seed weight. Moderate values were observed for plant height, number of nodes per plant, number of pod clusters per plant, and days to 50% flowering. In contrast, low GCV and PCV values were noted for days to maturity and number of seeds per pod. For all traits, genotypic variance was lower than phenotypic variance.

High heritability estimates in combination with high genetic advance as a percentage of mean were found for seed yield per plant, number of pods per plant, 100-seed weight, number of branches per plant, plant height, number of nodes per plant, number of pod clusters per plant, and days to 50% flowering. This pattern indicates that these traits are largely governed by additive gene action, and selection based on them would be effective.

In summary, the investigation highlighted that seed yield per plant, number of pods per plant, plant height, and 100-seed weight are highly heritable and responsive to selection, making them key targets in breeding programs for improving soybean productivity. These findings are consistent with earlier reports, thereby strengthening the evidence for significant genetic potential among the studied soybean genotypes.

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