



## Genetic Variability Analysis for Agro-morphological and Seed Yield Component traits of Soybean (*Glycine max* (L.) Merrill) Genotypes under Mid Hill Zone of Himachal Pradesh

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### 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

**Aim, Design and Methodology:** A research with 21 soybean genotypes including three checks was carried out in *kharif* 2021 at Research Farm of Genetics and Plant Breeding, CSK HPKV Palampur to estimate the genetic variation, heritability and genetic advance for 13 agro-morphological & seed yield component traits that can be used as selection criteria in breeding programmes. RBD design was used to set up the experiment with a plot size of  $3 \times 1.35=4.05 \text{ m}^2$  and replicated three times.

**Results and Conclusion:** The results of the analysis of variance revealed that the genotypes varied considerably for days to 50 percent flowering, days to 75 percent maturity, plant height (cm), number of nodes per plant, inter-nodal length (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed yield per plant (g), 100-seed weight (g), biological yield per plant (g) and harvest index (%) showing the genetic divergence of the planting materials from one another. According to the estimates of genetic variability, the phenotypic coefficient of variation for all the traits were greater than the genotypic coefficient of variation explaining the important role played by environmental factors in the manifestation of the traits.

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Higher values of PCV coupled with moderate GCV values were detected for harvest index (27.93%, 11.84%) indicating the presence of sufficient genetic variation for selection in such traits. High heritability estimates along with high genetic advance (as percent of mean) were recorded for plant height and 100-seed weight which could be ascribed to predominance of additive gene action and high selective index and therefore, selection pressure could be applied profitably to such traits for genetic modification in soybean.

**Keywords:** Variability; soybean; heritability; genetic advance; PCV; GCV.

## 1. INTRODUCTION

There are 26 wild perennial species in the genus *Glycine* while *Glycine soja* is the wild annual progenitor of domesticated soybean [*Glycine max* (L.) Merrill]. The annual dicot legume is strictly self-pollinated (cleistogamous) and characterized by white to purple-pink flowers with tubular calyx of five sepals, a corolla of five parts (a standard petal, two wing petals, and two keel petals), ten diadelphous stamens (nine joined, one free), and a simple carpel [1,2].

Soybean is a world-leading oilseed crop having a major contribution to total world oilseed production. Groundnut, soybean and rapeseed-mustard account for more than 88% of India's total oilseed production [3]. The edible oil industry is one of the most significant sector of agriculture in India where soybean occupies an important position. Out of total 89% of imported crude edible oil, 21% is contributed by soybean oil [4]. Covering around 600 hectares area, soybean is traditionally grown as a food crop in some parts of Himachal Pradesh. With the production of 1006.2 tones, soybean is grown both as monoculture as well as in mixture with other crops like maize, ragi and other millets [5].

The versatile crop is considered as 'Golden bean', 'Wonder crop', 'Poor man's meat', 'Yellow jewel', 'Meat of the field' and 'Miracle crop' because it provides 18-22% of vegetable oil and 35-40% of high-quality protein for animal feed and human consumption [6]. Similar to cow's milk and animal proteins, it is an exceptionally nutritive protein food with all the necessary amino acids including glycine, tryptophan and lysine. However, it is also a good source of unsaturated fatty acids and minerals like calcium and phosphorus including vitamins A, B, C and D which makes it ideal for reducing cardiovascular disease. As it contains a lot of protein, soybean flour is frequently used to improve the nutritional value of cereal flours, particularly sorghum and maize, which lack several crucial amino acids [7]. Leguminous crops like soybean have the ability

to improve soil fertility as it can fix approximately 300 kg ha<sup>-1</sup> of atmospheric nitrogen into the soil [8].

The presence of variations within a population of plant individuals is known as variability and these differences typically originate from variations in the genetic makeup of the population's members or in the environment in which the plants are cultivated. The large amount of variation present in any genetic material indicates the scope for further improvement of the crop [9]. The existence of genetic variation is must for effectiveness of selection in any breeding programme. Selection as a breeding method will be useful if there is a significant quantity of genetic variations among the genotypes used in the breeding programme. However, selection responds only to variations controlled genetically as they are heritable while this is not in the case of environmental variations.

With the aforementioned importance of soybean, still the production and productivity of soybean in India as well as in the state is low. The major production constraints that have been responsible for low productivity of the crop includes, narrow genetic base/low yield, poor crop management, poor soil fertility, lack of high yielding potential varieties and foliar diseases, which includes, frog-eye leaf spot (*Cercospora sojina*), pod blight (*Colletotrichum truncatum*), brown spot (*Septoria glycines*) and bacterial pustules (*Xanthomonas axonopodis* pv. *glycines*).

Studies of heritability show transfer of quantitative attributes like plant height, pods per plant, seeds per pod, number of branches and seed yield from one generation to the next, as performance of selection depends on the transmittable aspect of the differences. Estimation of heritability assists the plant breeder to efficiently allocating the techniques that must be taken for a proper selection of the desired characteristics and to obtain the largest genetic gain in the least amount of time and resources.

Broad sense heritability is assessed using the total genetic variance while narrow sense heritability represents only additive component of the variation and is fixable. Traits with higher heritability are more amenable to selection manipulation as compared to the traits with lower heritability. Similarly, genetic advance is also a helpful method in determining the gain under particular selection intensity. However, genetic advance becomes a more significant factor in predicting responses to selection when heritability estimates are also taken into account.

Seed yield, a complex character controlled by polygenes, is the most crucial feature in breeding soybean, relies on both the phenotypic potential as well as environmental conditions. Being a quantitative trait, the expression of seed yield is assessed by the relationship of the genetic and environmental variables. This suggests that genetic variation, environmental variation and variation of their interactions contribute to the variability of quantitative traits. Therefore, it was decided to conduct this study in order to determine the degree of variability (GCV, PCV, heritability and genetic advance) in soybean to

facilitate efficient selection in breeding programme.

## 2. MATERIALS AND METHODS

**Site Description:** The field experiment was carried at Experimental Farm of the Department of Genetics and Plant Breeding, CSK HPKV, Palampur, Himachal Pradesh during *kharif* 2021. The Site is located at 32°09' N latitude and 76°55' E at the altitude of 1290 m above sea level with a precipitation of about 2500 mm annually. The pH of the soil is acidic from 5.0-5.6. The area is part of Himachal Pradesh's mid-hill zone.

**Experimental Materials and Design:** A total of 21 genotypes (including 3 checks *viz.*, Hara Soya, Shivalik and Him Soya) of soybean were evaluated (Table 1, Plate 1). The experiment was accomplished in a randomized block design with three replications. Each genotype in the plot was grown in three rows of 3m lengths with the plot size of 3 × 1.35=4.05 m<sup>2</sup>. The regular agronomic management procedures were followed to grow the crop.

**Table 1. Enlisted genotypes used in study**

Sr. no.	Genotype	Flower color	Pod Pubescence color	Pod color	Seed color
1	P101-18-1-3-2	Purple	Tawny	Brown	Yellow
2	P104-5-12-1-1	White	Grey	Yellow	Yellow
3	P 164-4-3-6-2	White	Tawny	Brown	Yellow
4	P 104-9-1	White	Grey	Yellow	Yellow
5	P 99-1-3-1	Purple	Tawny	Brown	Yellow
6	P 104-9-3	White	Grey	Yellow	Yellow
7	P 112-16-1-1-1	Purple	Tawny	Brown	Yellow
8	P 104-4-1-3-1	Purple	Grey	Black	Yellow
9	P 19-4-1-3-1	Purple	Tawny	Brown	Yellow
10	P 99-3-1-1	Purple	Tawny	Brown	Yellow
11	P 104-5-12-2	White	Grey	Yellow	Yellow
12	P 120-9-1-4	Purple	Tawny	Brown	Yellow
13	P 112-11-3-1	Purple	Tawny	Brown	Yellow
14	P 101-20-2-3	Purple	Tawny	Brown	Yellow
15	P 108-14-2-4-1	White	Tawny	Brown	Yellow
16	P 104-7-1	White	Grey	Yellow	Yellow
17	P 99-4-1-2	White	Tawny	Brown	Yellow
18	P 108-14-2-3-2	White	Tawny	Brown	Yellow
19	Hara Soya (Check)	White	Tawny	Brown	Green
20	Him Soya (Check)	Purple	Tawny	Brown	Yellow
21	Shivalik (Check)	White	Grey	Yellow	Yellow

**Data collection:** The data on various characters viz., days to 50 percent flowering, days to 75 percent maturity, plant height (cm), number of nodes per plant, inter-nodal length, number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed yield per plant (g), 100-seed weight (g), biological yield per plant (g) and harvest index (%) was collected. All the data except days to 50 percent flowering and days to 75 percent maturity (plot basis) was collected by randomly selecting five competitive plants and their means.

**Estimation of Genotypic and Phenotypic Variances:** The genotypic and phenotypic variances were calculated as per the formula proposed by Johnson et al. [11]. The error MS was estimated and considered as environmental variances ( $\sigma^2_e$ ), genotypic variances ( $\sigma^2_g$ ) and phenotypic variances ( $\sigma^2_p$ ) using the following formula:

$$\sigma^2_g = (GMS - EMS)/r \text{ with } (n - 1) \text{ df}$$

$$\sigma^2_p = \sigma^2_g + \sigma^2_e \text{ or } V_p = V_g + V_e$$

**Statistical data analyses:** The data obtained was subjected to statistical software 'R' and further re-evaluated using TNAUSTAT [10].

where, GMS = genotypic mean squares, EMS= error mean squares, r= number of replications.

- **Estimation of Genotypic and Phenotypic Coefficient of Variation**

PCV and GCV were estimated as per the formula prescribed by Burton and Devane [12].

$$PCV (\%) = \frac{\sqrt{V_p}}{\bar{X}} \times 100 \quad GCV (\%) = \frac{\sqrt{V_g}}{\bar{X}} \times 100$$

where,

$V_p$  = phenotypic variance,  $V_g$  = genotypic variance  
 $\bar{X}$  = general mean of the character under investigation

- **Estimation of Heritability**

Heritability ( $h^2_{bs}$ ) was calculated in broad sense by using the formula given by Singh and Chaudhary [13].

$$h^2_{bs} (\%) = \frac{V_g \times 100}{V_p}$$

$V_p$  = phenotypic variance,  $V_g$  = genotypic variance

- **Estimation of Genetic Advance (GA)**

The expected genetic advance (GA) for all the traits under selection was estimated using the formula suggested by Johnson et al. [11].

$$\text{Genetic advance (GA)} = h^2_{bs} \times i \times \sigma_p \text{ or } i \times V_g / \sqrt{V_p}$$

where,

$h^2_{bs}$  = Heritability broad sense (decimal)  
*i* = selection differential at 5% selection intensity i.e., 2.06  
 $\sigma_p$  = Phenotypic standard variation  
 $V_g$  = genotypic variance,  $V_p$  = phenotypic variance

- **Estimation of Genetic Advance expressed as Percent of Mean**

Genetic gain (GG) is the genetic advance expressed as per cent of mean. The genetic advance in percent of mean was calculated using formula by Johnson et al. [11].

Genetic advance as percent of mean / (Genetic Gain (%)) =  $(GA/\bar{X}) \times 100$

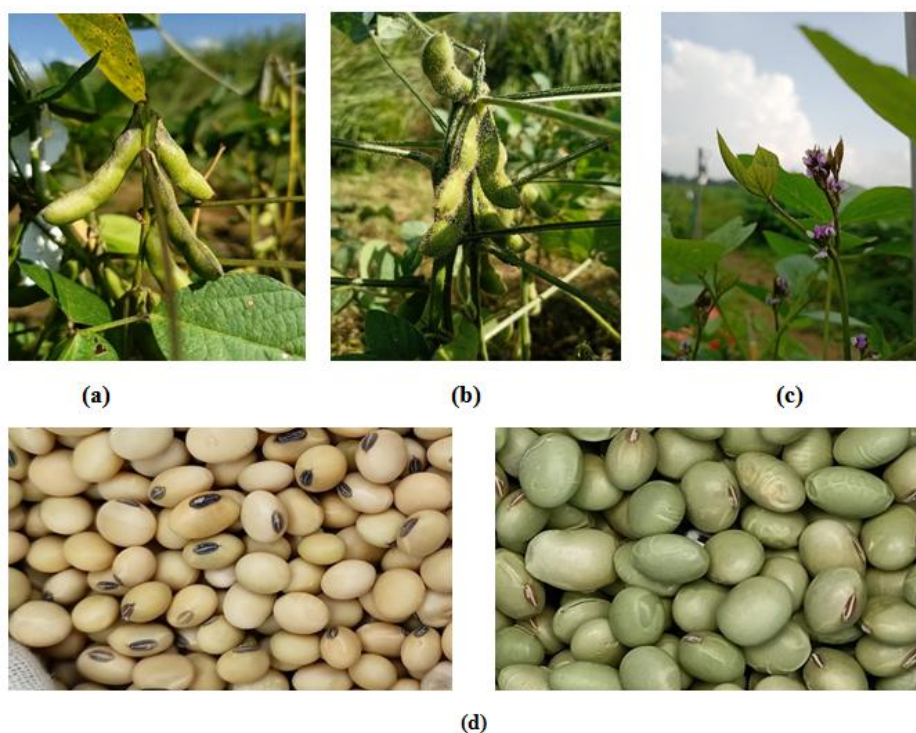
where,

$\bar{X}$  = General mean of the population

GA= Genetic advance



**Plate 1. Field view of the experiment**



**Plate 2. (a) Pods without pubescence (b) Pods with grey pubescence (c) Purple colored flower (d) Seed color variation**

### 3. RESULTS AND DISCUSSION

**Analysis of Variance:** Genetic variability is the necessity for the success of any crop

improvement programme. ANOVA is an analysis tool used to split an observed variability found inside a data set into replication, treatments and uncontrolled environmental conditions. For this



experiment, the results of ANOVA revealed that the treatment mean sum of squares were significant for all the traits under study representing the enormous phenotypic variability present among the genetic material studied (Table 2, Plate 2).

**Genetic parameters of variability:** In the present investigation, the genotypes P 104-9-3,

P 19-4-1-3-1, P 99-3-1-1, P 99-4-1-2, P 108-14-2-3-2 and Shivalik gave significantly higher seed yield per plant thus, could be utilized for seed yield improvement in soybean. Presence of a wide range of variation among all the genotypes for most of the traits (Table 3), indicated the scope for selection of these traits for further breeding work.

**Table 2. Analysis of variance for seed yield and related traits in soybean**

Sr. No.	Characters	Mean Sum of Squares		
		Replication	Treatments	Error
	Df	2	20	40
1	Days to 50% flowering	14.82	3,821.85*	26.39
2	Days to 75% maturity	27.03	4,181.29*	16.32
3	Plant height (cm)	40.84	2,794.91*	17.73
4	Branches per plant	9.29	3,833.12*	78.78
5	Nodes per plant	24.54	3,978.87*	27.19
6	Internodal length (cm)	100.92	3,206.64*	21.81
7	Pods per plant	23.48	3,917.99*	55.97
8	Pod length (cm)	17.36	2,973.94*	29.91
9	Seeds per pod	44.86	3,881.03*	76.85
10	100-seed weight (g)	59.99	4,105.00*	70.44
11	Seed yield per plant (g)	63.39	3,028.86*	42.66
12	Biological yield per plant (g)	3.02	3,869.16*	21.68
13	Harvest Index (%)	16.59	2,632.28*	36.66

\*Significance at  $P \leq 0.05$ ,  $df = \text{Degree of freedom}$

**Table 3. Genetic parameters of variability for yield and related traits in soybean**

Characters	Mean $\pm$ SE	Range		PCV	GCV	$h^2$ (bs)	GA	GA (as % mean)
		Mini.	Max.					
Days to 50% flowering	63.98 $\pm$ 1.17	58.33	73.66	6.56	5.75	76.88	6.65	10.39
Days to 75% maturity	120.38 $\pm$ 0.91	114.66	129.33	3.30	3.03	84.15	6.90	5.73
Plant height (cm)	58.67 $\pm$ 2.57	48.13	79.33	14.54	12.42	72.83	12.80	21.83
Branches per plant	4.07 $\pm$ 0.23	3.50	5.43	13.13	8.76	44.47	0.49	12.03
Nodes per plant	9.47 $\pm$ 0.53	8.30	11.20	10.73	4.58	18.21	0.38	4.02
Internodal length (cm)	4.42 $\pm$ 0.28	3.93	5.36	11.35	3.24	8.13	0.08	1.90
Pods per plant	53.90 $\pm$ 6.57	38.56	69.26	23.23	9.66	17.30	4.46	8.28
Pod length (cm)	3.78 $\pm$ 0.14	3.50	4.16	7.52	3.64	23.45	0.14	3.63
Seeds per pod	2.34 $\pm$ 0.09	2.15	2.56	7.36	3.66	24.80	0.08	3.76
100-seed weight (g)	15.46 $\pm$ 0.18	12.84	19.81	10.48	10.28	96.30	3.22	20.80
Seed yield per plant (g)	25.79 $\pm$ 1.71	15.33	30.00	16.17	11.41	49.78	4.28	16.59
Biological yield per plant (g)	49.19 $\pm$ 6.40	35.06	60.16	23.63	7.16	9.19	2.20	4.47
Harvest Index (%)	55.07 $\pm$ 8.04	40.36	86.91	27.93	11.84	17.97	5.69	10.34

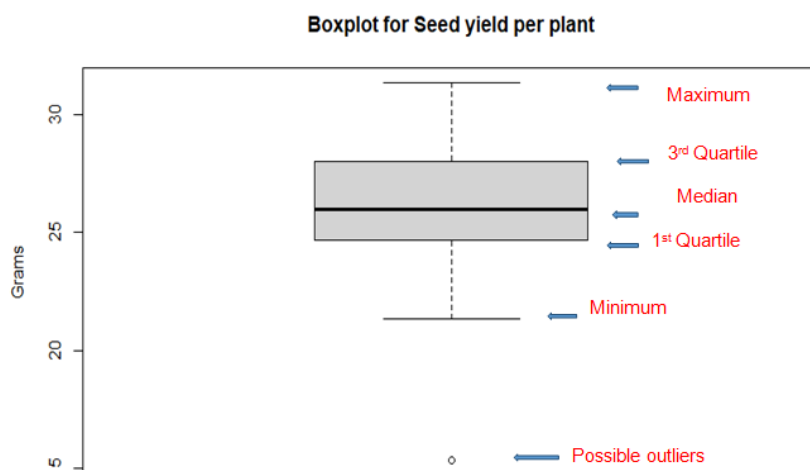
**Table 4. Range wise categorization of genetic parameters of variability**

Sr. no.	Parameters	Low	Moderate	High	Reference
1	PCV	<10%	10-20 %	>20%	Jandong et al. [14]
2	GCV	<10%	10-20 %	>20%	Pallavi et al. [15]
3	$h^2_{bs}$	<30%	30-60 %	>60%	Johnson et al. [11]
4	GAM	<10%	10-20 %	>20%	Johnson et al. [11]

The level of varietal differences present among soybean genotypes was estimated on the basis of genetic parameters viz., genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance coupled with various traits (Table 3). A wide range of differences was observed for all the traits. The results revealed that the values of PCV were higher than GCV for all the traits probably due to the interaction of the soybean genotypes with the environment or other environmental factors influencing the expression of these characters (Table 3). Narrow differences observed between the PCV and GCV for characters such as days to 50 percent flowering, days to 75 percent maturity, plant height and 100-seed weight indicated that these characters were less influenced by the environment. These findings were in accordance with Sawale et al. [16], Malik et al. [17] and Mahbub et al. [18]. High PCV coupled with moderate GCV values were detected for harvest index (27.93%, 11.84%) as also observed by Kumar et al. [19], Suresh Rao et al. [20] indicating the wide adaptability of these traits in the genotypes studied. Moderate PCV and GCV were recorded for seed yield per plant (16.17%, 11.41%) and 100-seed weight (10.48%, 10.28%). Similar results were in conformity with the findings of Datt et al. [21], Kumar et al. [19] and suggests that there is scope to enrich the variation for these characters. Low PCV and GCV values for days to 50 percent flowering (6.56%, 5.75%), days to 75 percent maturity (3.30%, 3.03%), number of seeds per pod (7.36%, 3.66%) and pod length (7.52%, 3.64%) were may be due to the involvement of environment and genotype  $\times$  environment effects in character expression.

To evaluate the impact of phenotypic selection, the genotypic coefficient of variation should be taken into account together with heritability and genetic progress since it only captures the level of genetic variability present for a character. The experiment's 100-seed weight (96.30%), days to 75% maturity (84.15%), days to 50% flowering

(76.88%), and plant height (72.83%) all recorded the greatest broad sense heritability values (Table 4). High heritability for these traits would be useful in the improvement of these characters. Estimates of heritability in broad sense combined with genetic advance will increase the accuracy and reliability of predicting the response to selection [11]. Broad sense heritability includes both additive and non-additive gene effects. For characters plant height and 100-seed weight, high heritability (broad sense) and high genetic advance were observed, indicating the predominance of additive gene action in the inheritance of these characters and the potential for effective selection for these traits based on phenotypic expression. Jain et al. [22] reported the same results and indicated that the traits with high heritability allow for greater selection success, increasing the likelihood of having superior progenies from selected individual. Days to 50 percent flowering, branches per plant, and seed yield per plant showed high or moderate heritability with moderate genetic advance as a percentage of the mean, indicating that these traits were more controlled by additive and non-additive gene activity than by environmental factors. These results were in accordance with Abady et al. [23], Khan et al. [24] and Chandel et al. [25]. Days to 75 percent maturity showed high broad sense heritability and low magnitude of genetic advance, which may be indicative of limited genetic variability for that attribute. In such a situation, advancement of these traits through phenotypic selection may not be effective. Recombination breeding and recurrent selection are encouraged for the enhancement of these features, nonetheless. Nodes per plant, internodal length, pods per plant, pod length, seeds per pod, and biological yield per plant all showed low estimates of heritability with low genetic advance expressed as a percentage of the mean, showing the presence of non-additive gene action and the influence of environment in the expression of this characteristic. Therefore, selection would be less effective for these traits.



**Fig. 1. Box plot for seed yield per plant**

The distribution of an experiment's data set is plotted using a box plot. The boxplot graphs is encoding five characteristics of distribution of data by showing the reader their position and length. The box contained values from the first to the third quartiles of the distribution, and the range corresponds to the interquartile range (IQR) (interquartile range). However, the maximum 30 (Shivalik) and minimum 15.33 (P101-18-1-3-2) values can be depicted by horizontal bars. The median (26), represented by a line across the box, is in the middle of the data set. It means that 50% of the data is greater than the median.

#### 4. CONCLUSION

The enormous phenotypic variation among the soybean genotypes was shown by the analysis of variance. The genotypes P 104-9-3, P 19-4-1-3-1, P 99-3-1-1, P 99-4-1-2, P 108-14-2-3-2, and Shivalik were discovered to have superior seed yield per plant based on mean performance, whereas the genotypes P 101-18-1-3-2, P 164-4-3-6-2, P 99-1-3-1, P 112-16-1-1-1, P 101-20-2-3, P 108-14-2-3-2, Hara Soya, and Shivalik showed early flowering. The phenotypic coefficient of variation (PCV) values was larger than genotypic coefficient of variation (GCV) values, showing environmental influence in the manifestation of these traits. Estimates of heritability were shown to be high for days to 50 percent flowering, days to 75 percent maturity, plant height and 100-seed weight. However, a high magnitude of genetic advance was observed for plant height and 100-seed weight. High heritability estimates coupled with high genetic advance (as % of mean) was observed for plant height and 100-seed weight

which could be ascribed to the predominance of additive gene effects and high selective index. As a result, applying selection pressure to these traits could be profitable for soybean genetic improvement.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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