Original Research Article

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

ABSTRACT

Background and methods: A study with 21 soybean genotypes including three checks was conducted in *kharif* 2021 at Experimental Farm of Genetics and Plant Breeding, CSK HPKV Palampur to determine the genetic variability, heritability and genetic advance for 13 agro-morphological and seed yield component traits for selection criteria in a breeding program. The experiment was laid out in RBD design with plot size of 3 × 1.35=4.05 m^2 and replicated three times.

Results: The results of analysis of variance revealed significant variation among the genotypes for these traits, indicating that the planting materials were genetically divergent from each other. The estimates of genetic variability showed that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits explaining the important role played by environmental factors in the expression of the traits. High PCV coupled with moderate GCV values were detected for harvest index (27.93%, 11.84%) portraying the presence of sufficient genetic variation for selection in these traits. High heritability estimates coupled with high genetic advance (as % of mean) were observed for plant height and 100-seed weight which could be ascribed to the predominance of additive gene effects and high selective index and therefore, selection pressure could profitably be applied on these characters for genetic improvement in soybean.

Keywords: Variability, Soybean, Heritability, Genetic Advance, PCV, GCV

INTRODUCTION

The subgenus *Glycine* consists of 26 wild perennial species while *Glycine soja* is the wild annual progenitor of cultivated 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 (Singh 2017).

Soybean is a world leading oilseed crop having major contribution in total world oilseed production. Three main oilseeds groundnut, soybean and rapeseed-mustard accounts for over 88% of total oilseeds output in India (Anonymous 2019a). The edible oil industry is one of the most important 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 (Narayan 2017). 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 (Anonymous 2019b).

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 supplies 35-40% of high-quality protein and approximately 18-22% of vegetable oil for animal feed and human consumption (Wilson 2004). It is an exceptionally nutritive protein food with all the essential amino acids such as glycine, tryptophan and lysine, similar to cow’s milk and animal proteins. 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. Due to the high protein content, soybean flour is often used to competent cereal flours mainly sorghum and maize lacking essential amino acids to boost their nutritional value (Tukamuhabwa and Oloka 2016). Soybean as a leguminous crop also has the capacity for soil fertility as it can fix approximately 300 kg ha^{-1} of nitrogen from the atmosphere into the soil (Keyser and Li 1992).

Variability can be defined as the availability of differences among the individuals of plant population which usually arises as a result of differences either in genetic makeup of the individuals of a plant population or in the environment in which the plants are grown. The large amount of variability present in any genetic material indicates the scope for further improvement of the crop (Baig et al. 2018). The existence of genetic variability is essential for performance of selection in any breeding programme. Selection as a breeding method will be meaningful if there is an appreciable quantity of genetic differences within the various genotypes used in the breeding programme. However, selection responds only to variation 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, pod blight (*Colletotrichum truncatum*), frogeye leaf spot (*Cercospora sojina*), brown spot (*Septoria glycines*) and bacterial pustules *(Xanthomonas axonopodis* pv*. glycines*).

Heritability estimates reveal the extent of transmission of quantitative traits such as plant height, number of branches, pods per plant, seeds per pod and seed yield from one generation to the other, as performance of selection is based on the transmittable aspect of the differences. Heritability estimation help the plant breeder to effectively assign the necessary strategies to be adopted for a successful selection of the desired traits and to achieve the highest genetic gain within the shortest possible time and resources. Broad sense heritability is estimated using the total genetic variance while narrow sense heritability represents only additive component of the variation and is fixable. Higher heritability can be more easily manipulated by selection as compared to the traits with lower heritability. Similarly, genetic advance is also a useful tool in estimating the gain under specified selection intensity. However, when genetic advance is considered along with heritability, it becomes a more important measure in predicting responses to selection than the heritability estimates alone.

Seed yield, a complex character controlled by polygenes, is the most important trait in breeding soybean, depending on both the phenotypic potential and environmental conditions. Being a quantitative trait, the expression of seed yield is measured by the interaction of the genetic and environmental factors. This indicate that variability of quantitative trait is caused by genetic variability, environmental variability and variability of their interactions. Therefore, this study was undertaken to estimate the extent of variability (genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance in soybean for effective selection in a breeding programme.

MATERIALS AND METHODS

Site description: The field experiment was conducted at Research Farm of 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 the precipitation of about 2500 mm annually. The pH of the soil is acidic with 5.0-5.6. The region comes under mid hill zone of Himachal Pradesh.

Experimental materials and design: A total of 21 genotypes (including three checks *viz*., Hara Soya, Him Soya and Shivalik) of soybean were evaluated (Table 1, Plate 1). The experiment was laid out in 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^2. The standard agronomic management practices were followed to raise the crop.

Table 1. List of genotypes for the experiment

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% flowering, days to 75% maturity, plant height (cm), number of branches per plant, number of nodes per plant, internodal length, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%) was recorded. All the data except days to 50% flowering and days to 75% maturity (plot basis) was collected by randomly selecting 5 competitive plants and their means.

Statistical data analyses: The data obtained was subjected to statistical software 'R' and further re-evaluated using TNAUSTAT (Manivannan 2014).

Estimation of Genotypic and Phenotypic Variances

The genotypic and phenotypic variances were estimated according to the formula suggested by Johnson et al. (1955). The error MS was considered as environmental variances (σ^2_e).

Genotypic variances (σ^2_g) and phenotypic variances (σ^2_p) were calculated using the following formula:

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

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

where, GMS and EMS are the genotypic mean squares and error mean squares respectively and r is the number of replications.

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

Phenotypic and genotypic coefficients of variation were estimated as per the formula prescribed by Burton and Devane (1952).

$$\text{PCV (\%)} = \frac{\sqrt{\text{Vp}}}{\text{X}} \times 100$$

where,

Vp = phenotypic variance, Vg = genotypic variance

X = general mean of the character under investigation

- **Estimation of Heritability**

Heritability (h^2_{bs}) was calculated in broad sense by using the following formula given by Singh and Chaudhary (1985).

$$h^2 \quad (\%) = \frac{\text{Vg} \times 100}{\text{Vp}}$$

Vp = phenotypic variance, Vg = genotypic variance

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

The expected genetic advance (GA) for different traits under selection was estimated using the formula suggested by Johnson et al. (1955).

Genetic advance (GA) = $h^2_{bs} \times i \times \sigma_p$ **or** $i \times Vg / \sqrt{Vp}$

where,

h^2_{bs} = Heritability broad sense (decimal)

i = selection differential at 5 per cent selection intensity i.e., 2.06

σ_p = Phenotypic standard variation

Vg = genotypic variance, Vp = 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 by using formula Johnson et al. (1955).

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

where,

X = General mean of the population

GA= Genetic advance

Plate1: Field view of the experiment

(a) (b) (c)

(d)

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

RESULTS AND DISCUSSION

- **Analysis of variance**

Genetic variability is the pre-requisite for success of any crop improvement programme. Analysis of variance is an analysis tool used to split an observed variability found inside a data set and indicate source of variation due to replication, treatments and uncontrolled environmental conditions. For this experiment the results of ANOVA revealed that the mean sum of squares due to treatments were significant for all the traits under study, which indicated the enormous phenotypic variability among the genetic materials studied (Table 2, Plate 2).

Table 2. Analysis of variance for yield and related component 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 ≤ 0.05, df= Degree of freedom

- **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 hence, could be utilized for improvement in the seed yield in soybean. All the 21 genotypes showed wide range of variation for most of the traits under study (Table 3), indicated the scope for selection of these traits for further breeding work.

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

Characters	Mean± SE	Range		PCV	GCV	h^2 (bs)	GA	GA (as % mean)
		Mini.	Max.					
Days to 50% flowering	63.98± 1.17	58.33	73.66	6.56	5.75	76.88	6.65	10.39
Days to 75% maturity	120.38± 0.91	114.66	129.33	3.30	3.03	84.15	6.90	5.73
Plant height (cm)	58.67± 2.57	48.13	79.33	14.54	12.42	72.83	12.80	21.83
Branches per plant	4.07± 0.23	3.50	5.43	13.13	8.76	44.47	0.49	12.03
Nodes per plant	9.47± 0.53	8.30	11.20	10.73	4.58	18.21	0.38	4.02
Internodal length (cm)	4.42± 0.28	3.93	5.36	11.35	3.24	8.13	0.08	1.90
Pods per plant	53.90± 6.57	38.56	69.26	23.23	9.66	17.30	4.46	8.28
Pod length (cm)	3.78± 0.14	3.50	4.16	7.52	3.64	23.45	0.14	3.63
Seeds per pod	2.34± 0.09	2.15	2.56	7.36	3.66	24.80	0.08	3.76
100-seed weight (g)	15.46± 0.18	12.84	19.81	10.48	10.28	96.30	3.22	20.80
Seed yield per plant (g)	25.79± 1.71	15.33	30.00	16.17	11.41	49.78	4.28	16.59
Biological yield per plant (g)	49.19± 6.40	35.06	60.16	23.63	7.16	9.19	2.20	4.47
Harvest Index (%)	55.07±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. (2020)
2	**GCV**	<10%	10-20 %	>20%	Pallavi et al. (2018)
3	**h^2_{bs}**	<30%	30-60 %	>60%	Johnson et al. (1955)
4	**GAM**	<10%	10-20 %	>20%	Johnson et al. (1955)

The level of varietal differences present among soybean genotypes were 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 long range of differences was observed for all the traits. The estimates of genotypic (GCV) and phenotypic (PCV) coefficients of variability revealed that the values of PCV were higher than GCV for all the traits probably due to 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% flowering, days to 75% maturity, plant height and 100-seed weight indicated that these characters were less influenced by the environment. Similar results were obtained by Sawale et al. (2014), Malik et al. (2011) and Mahbub et al. (2015). High PCV coupled with moderate GCV values were detected for harvest index (27.93%, 11.84%) as also observed by Kumar et al. (2018), Sureshrao et al. (2014) indicating the wider 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%). These results were in conformity with the findings of Datt et al. (2011), Kumar et al. (2018) and suggests that there is scope to enrich the variation for these characters. Low PCV and GCV values were observed for days to 50% flowering (6.56%, 5.75%), days to 75 % maturity (3.30%, 3.03%), number of seeds per pod (7.36%, 3.66%) and pod length (7.52%, 3.64%). This may be due to the involvement of environment and genotype × environment effects in character expression.

As genotypic coefficient of variation represents only the extent of genetic variability present for a character, therefore, it should be considered in combination with heritability and genetic advance to assess the effect of phenotypic selection. In this experiment, the highest broad sense heritability values were recorded for 100-seed weight (96.30%), days to 75% maturity (84.15%), days to 50% flowering (76.88%) and plant height (72.83%) (Table 4). The high heritable variation of these characters would be useful in the improvement of these traits. Heritability in broad sense estimates coupled with genetic advance will be more effective and reliable in predicting the response to selection (Johnson et al. 1955). Heritability in broad sense involves both the additive and non-additive gene effects. High heritability (broad sense) together with high genetic advance were observed for characters plant height and 100-seed weight indicating the predominance of additive gene action in the inheritance of these characters and selection can be effective for these traits based on phenotypic expression. Jain et al. (2017) reported the same findings and confirmed that the characters with high heritability allow more success in selection, so that the chance of obtaining superior progenies with selected individuals is larger. High/ moderate heritability with moderate genetic advance as per cent of mean was recorded for days to 50% flowering, branches per plant, seed yield per plant indicating that these characters were less influenced by environment but governed by additive and non-additive gene action. These results were in accordance with Abady et al. (2013), Khan et al. (2015) and Chandel et al. (2013). High magnitude of broad sense heritability and low magnitude of genetic advance was detected for days to 75% maturity which may be due to lack of genetic variability for that trait. In such a situation, advancement in these traits through usual selection may not be effective. However, recombination breeding and recurrent selection is advocated for improvement of such traits. Low estimate of heritability with low genetic advance expressed as percentage of mean was observed for nodes per plant, internodal length, pods per plant, pod length, seeds per pod and biological yield per plant suggested the presence of non-additive gene action and influence of environment in the expression of this character. Thus, the selection would be less effective for these characters.

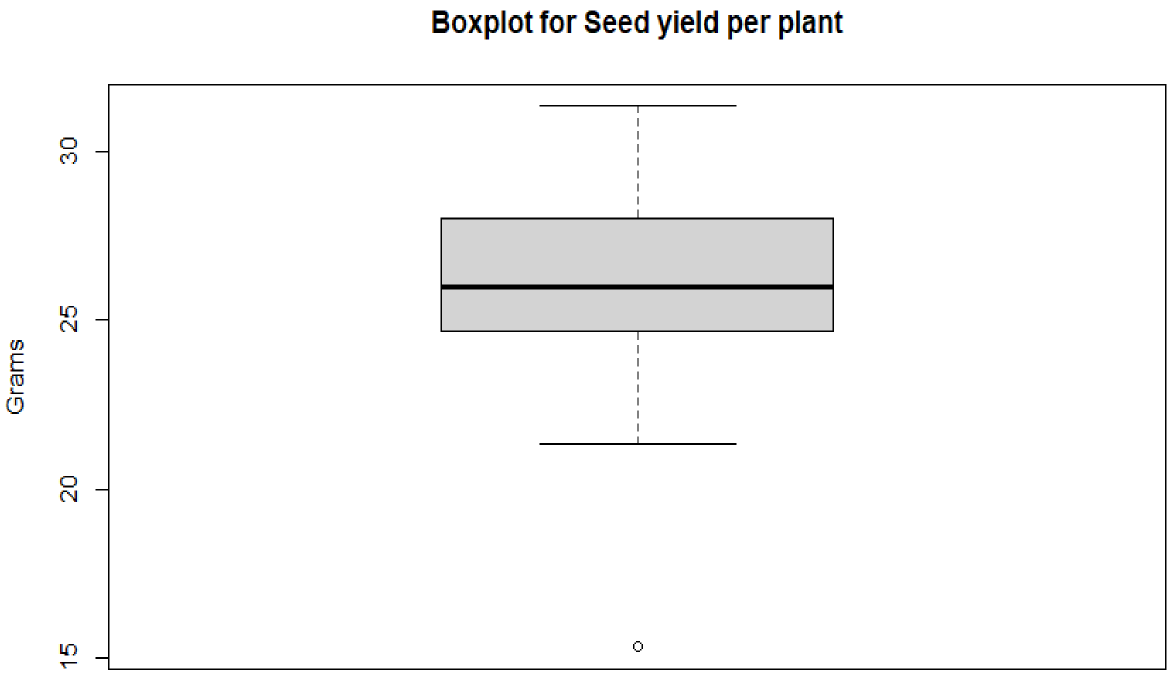

Figure 1 : Box plot for seed yield per plant

The box plot of seed yield is used to plot the distribution of a data set of the experiment. The boxplot graphs is encoding five characteristics of distribution of data by showing the reader their position and length. The box ranged from Q1 (the first quartile) to Q3 (the third quartile) of the distribution and the range represents the 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 the middle of the data set. It means that 50% of the data is greater than the median.

CONCLUSION

The analysis of variance revealed the enormity of phenotypic variability that exists among the soybean genotypes. On the basis of mean performance, 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 found to be superior for seed yield per plant while the genotypes P101-18-1-3-2, 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, Shivalik showed early flowering. The values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters indicating the influence of environmental factors in expression of these traits. Estimates of heritability were shown to be high for days to 50% flowering, days to 75% maturity, plant height and 100-seed weight. However, 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) were observed for plant height and 100-seed weight which could be ascribed to the predominance of additive gene effects and high selective index and therefore, selection pressure could profitably be applied on these characters for genetic improvement in soybean.

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