

Original Research Article

Genetic Parameters Studies for Yield, Yield contributing and Morphological Traits in Soybean (*Glycine max* (L.) Merrill)

Abstract

Soybean (*Glycine max* (L.) Merrill) is the only oilseed crop having richest source of quality protein (~ 40%) apart from 20% edible and having share of 22 % edible oil requirement of the country. The present study was carried out to estimate the important genetic parameters such as genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h^2) and expected genetic advance (EGA). Thirty-five soybean genotypes collected from different centers of the country were studied for nine yield, yield contributing and morphological characters at All India Coordinated Research Project on Soybean during *kharif*, 2013. The analysis of variance revealed that the sufficient variability was present in the material for all the characters. The value of phenotypic coefficient of variation (PCV) is greater than genotypic coefficient of variation (GCV). The high GCV and PCV were observed for number of pods per plant, number of branches per plant, seed yield per plant and plant height. High heritability estimates coupled with high expected genetic advance were observed for the characters seed yield per plant, number of pods per plant, number of branches per plant and plant height indicating the presence of additive gene action. Therefore, more emphasis should be focused on these traits during selection for genetic improvement of soybean.

Key words : Soybean, GCV, PCV, Heritability, Genetic advance, Variability

1. Introduction

In India, soybean (*Glycine max* (L.) Merrill) cultivation was started during 1960s with few thousand hectares area and within six decades, it occupies number one position in terms of area (119.9 lakh hectares) with total production of 118.8 Million Metric Tonnes (Anonymous, 2021). It contributes nearly 42% share in total oilseed crops and fulfills 22 % edible oil requirement of the country. Soybean is often termed as ‘miracle golden bean of 21st century’, because it contains around 20% oil and 40% protein, well balanced in essential amino acids, 20 % rich in poly unsaturated fatty acids specially omega 6 and omega 3 fatty acids. The iso-flavones of soybean have been found to possess numerous health benefits as they exhibited properties like preventing cancer, combating menopausal problem and helping to recover from diabetes (Chauhan and

Joshi, 2005). However, apart from numerous health benefits, it also contains many kinds of anti-nutritional factors, such as trypsin inhibitor, lectin, α -amylase inhibiting factor, goitrin, soybean antigen etc. (Liener, 1994 and Grant, 1989). The development of superior variety can be based on the magnitude of genetic variability in the base material and the extent of heritability of desirable characters. Presence of sufficient genetic variability is pre-requisite in breeding program of any crop for development of variety or hybrid with desired traits. Although increased seed yield is the ultimate aim of the plant breeders, seed yield itself is a product of interaction of many component traits which influence it directly or indirectly. Therefore, variability existing within each component trait must be exploited by selection to realize maximum gain in seed yield (Gohil *et al.* 2006).

Seed yield is very complex character being dependent on number of genetic factors interacting with environment. For the improvement of crop yield, the breeder has to select superior individuals based on their phenotypic expression. Selection based on phenotypic expression is sometimes misleading as the development of the character is the result of interaction of the heritable and non-heritable factors. It highlights the imperative need for partitioning the overall variability into its heritable and non-heritable components and genetic parameters like the genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and expected genetic advance (EGA). The development of superior variety with desired traits can be based on the magnitude of the genetic variability in the base material and the extent of heritability of desirable characters (Dhillon *et al.*, 2005). The existence of variability is essential for resistance to biotic and abiotic factors and for varietal adaptability. Selection is also effective when there is sufficient genetic variability present among the individuals in the population. Hence, the magnitude of genetic variability present in a population is of prime importance to any plant breeder for starting and judicious breeding programme. In the present study, efforts have been made to analyze the components of variability regarding future breeding programmes.

2. Materials and Methods

The experimental material consists of thirty-five newly developed promising genotypes of soybean (*Glycine max* (L.) Merrill) developed at different centers from various states of the country and three national checks viz., Bragg, JS93-05, JS 97-52 and two local checks viz., MAUS 71 and MAUS 81 (Table 1). The experiment was carried out in randomized block

design with three replications at All India Co-ordinated Research Project on Soybean, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani in medium black soil during *kharif* season of 2013-2014. Each entry was planted in three rows of 3 m length with row to row distance of 45 cm and plant to plant distance of 5 cm. Recommended fertilizer dose of 30:60:30:30 NPKS (kg/ha.) were advocated at the time of sowing. Two hand weeding were undertaken at the interval of 20 and 45 days after sowing. Two sprayings of insecticides were undertaken to control the leaf miner and leaf rolling caterpillar.

Observations were recorded on nine yield and yield contributing and morphological characters viz., days to first flowering, days to 50 % flowering, days to maturity, plant height(cm.), number of branches per plant, number of pods per plant, 100 grain weight (gm.), oil content(%) and grain yield per plant(gm.). All recommended agronomical package of practices were followed for satisfactory crop growth. The analysis of variance for randomized block design was done using the method given by Panse and Sukhatme (1967). The data was collected and analyzed for genotypic and phenotypic coefficients of variation, heritability (broad sense) and expected genetic advance as % of mean. The genotypic and phenotypic coefficient of variation (GCV and PCV) was calculated according to method suggested by Burton (1952). Heritability (broad sense) was estimated according to the method indicated by Allard (1960). The genetic advance (at 5 % selection intensity) was calculated for each character using the formula suggested by Johnson *et al.*, (1955).

Table 1 : List of soybean genotypes studied for genetic variability studies along with developing Institute

Sr.No	Genotype	Origin	Sr.No	Genotype	Origin
1.	VLS 75	VPKAS, Almora	21.	PS 1466	GBPUOAT, Pantnagar
2.	JS(SH)2003-2	RVSKVV, Sehore	22.	TS 9	Trombay, Mumbai
3.	DSb 16	UAS, Dharwad	23.	KS 1	Krishidhan seeds, Jalna
4.	VLS 74	VPKAS, Almora	24.	MACS 1259	ARI, Pune
5.	PS 1472	GBPUOAT, Pantnagar	25.	NRC 84	DOSR, Indore
6.	DS 12-13	IARI, New Delhi	26.	AMS 323	Dr. PDKV, Akola
7.	Himso 1679	CSKHPAU, Palampur	27.	PS 1469	GBPUOAT, Pantnagar
8.	NRC 82	DOSR, Indore	28.	JS 90-21	JNKVV, Jabalpur
9.	JS 20-19	JNKVV, Jabalpur	29.	SL 794	PAU, Ludhiana
10.	NSO 84	Nirmal Seeds, Pachora	30.	SH1	CCSHAU, Hissar
11.	PS 1475	GBPUOAT, Pantnagar	31.	KHSb 6	UAS, Bangalore
12.	SL 799	PAU, Ludhiana	32.	TS7	Trombay, Mumbai
13.	NRC 83	DOSR, Indore	33.	KDS 343	MPKV, Rahuri
14.	MACS 1281	ARI, Pune	34.	KS 3	Krishidhan seeds, Jalna
15.	SH 2	CCSHAU, Hissar	35.	MACS 1238	ARI, Pune
16.	KDS 319	MPKV, Rahuri	36.	MAUS 71(LC)	VNMKV, Parbhani
17.	MAUS 394	VNMKV, Parbhani	37.	MAUS 81(LC)	VNMKV, Parbhani

18.	MACS 1254	ARI,Pune	38.	Bragg (NC)	USA (GBPUOAT,Pantnagar)
19.	SL 795	PAU,Ludhiana	39.	JS 93-05(NC)	JNKVV,Jabalpur
20.	Dsb 15	UAS,Dharwad	40.	JS 97-52(NC)	JNKVV,Jabalpur

3. Results and Discussion

In the genetic improvement of soybean, the knowledge of genetic variability, heritability and genetic advance is a pre-requisite to develop varieties having desirable characters. The heritable variation is masked by non-heritable variation which creates difficulty in exercising selection. Hence, it becomes necessary to split overall variability into heritable and non-heritable components with the help of specific genetic parameters. It may enable the breeder to adopt a proper breeding strategy since environmental conditions that affect many characters of economic importance.

3.1 Mean performance

Mean performance of thirty-five genotypes of soybean along with three national and two local checks for morphological, yield and yield contributing traits is presented in Table 2.

3.1.1 Morphological characters

Among the soybean genotypes tested, NRC 82 and NRC 83 (27.00 days) recorded lowest day's for first flowering followed by SL 794 (28.00 days) as compared to standard check, JS 97-52 (32.00 days). Similar trend of result was observed for days to 50 % flowering. Similarly, these two genotypes viz., NRC 82 (29.00 days) and NRC 83 (30.66 days) also recorded lowest days to 50 % flowering followed by SL 794 (31.66 days) as compared to standard check, JS 97-52 (35.00 days). For days to maturity, only two genotypes viz., SL 794 (71.00 days) and NRC 82 (85.33 days) recorded earliness as compared to earliest maturing standard check, JS 93-05 (86.33 days). The genotype, DS 12 (58.00 cm) recorded highest plant height followed by KDS 319 (53.66 cm), MACS 1259 (52.00 cm) and MACS 1281 (50.00 cm).

3.1.2 Yield and yield contributing characters

Out of thirty-five genotypes tested, three genotypes recorded significantly superior seed yield per plant over the highest yielding standard check, MAUS 81. The genotype DSb 16 (6.60 g) recorded highest seed yield per plant followed by TS 9 (6.00 g) and MACS 1259 (5.96 g). For number of pods per plant, twelve genotypes recorded significantly superior number of pods per plant over the standard check, Bragg. The genotype TS 9 (60.00) recorded highest number of pods per plant followed by JS (SH) 2003-2 (51.00) and DSb 16 (48.33) as compared to standard

checks, Bragg (32.00) and MAUS 71 (31.00). The genotype, PS 1472 (6.33) recorded highest number of branches per plant followed by the genotypes, viz., Himso 1679 (6.00), PS 1475 (6.00), NRC 84 (6.00) and KSHb 6 (6.00) in comparison with the standard checks viz., MAUS 71 (5.66) and JS 93-05 (5.33). For the trait 100 seed weight, the genotype DSb 15 (15.86 g) recorded highest test weight followed by PS 1472 (14.93 g), VSL 75 (13.66 g) and KSHb 6 (13.66 g) which was found far more than the check varieties viz., Bragg (10.20 g) and MAUS 71 (10.10 g). Twenty genotypes recorded significantly superior 100 seed weight over the standard check, Bragg. As regards the oil content, the genotypes viz., JS 90-21 and NRC 83 (21.80 %) recorded highest oil content and was found superior over standard checks, viz., MAUS 81 (21.40 %) and MAUS 71 (21.00 %).

Table 2: Mean Performance of Soybean Genotypes for morphological, yield and yield contributing traits

	Genotype	Morphological characters					Yield and yield contributing characters			
		Days to first flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number branches per plant	Number of pods per plants	100 seed weight (g)	Oil content (%)	Seed yield per plant (g)
1	2	3	4	5	6	7	8	9	10	11
1	VLS-75	34.00	37.00	102.33	39.00	4.33	37.33	13.66	20.20	4.80
2	JS (SH) 2003-2	31.00	34.33	87.33	37.33	4.00	51.00	9.20	17.53	3.36
3	DSb16	32.00	34.00	98.66	44.66	5.00	48.33	12.60	16.26	6.60
4	VLS 74	33.00	36.33	95.33	34.00	4.66	25.66	10.73	18.13	3.53
5	PS 1472	31.00	34.00	105.00	34.66	6.33	27.00	14.93	15.53	4.16
6	DS 12-13	40.00	42.66	107.33	58.00	5.33	27.00	12.53	19.96	5.43
7	Himso 1679	31.00	33.33	102.33	45.66	6.00	31.33	12.10	15.86	3.43
8	NRC 82	27.00	29.00	85.33	30.33	3.00	37.66	7.86	15.63	2.23
9	JS 20-19	32.00	34.33	87.00	32.00	4.00	40.00	11.7	17.90	3.23
10	NSO 84	31.00	34.00	92.00	40.00	4.00	23.66	10.0	16.86	4.30
11	PS 1475	32.00	34.66	106.33	35.00	6.00	25.66	12.70	16.06	4.16
12	SL 799	32.00	35.00	103.33	47.33	4.33	21.66	11.76	16.00	4.50
13	NRC 83	27.00	30.66	89.33	31.00	3.66	20.00	13.00	21.80	3.46
14	MACS 1281	35.00	37.66	94.66	50.00	4.33	39.66	11.30	17.26	4.90
15	SH – 2	32.00	33.00	100.67	28.66	2.66	31.00	11.60	16.86	1.71
16	KDS 319	35.00	37.33	86.66	53.66	4.66	34.00	11.20	20.03	3.66
17	MAUS 394	34.00	36.66	95.33	39.66	2.66	30.00	9.23	19.03	3.70
18	MACS 1254	36.00	39.33	100.66	38.00	2.31	39.33	11.10	19.40	4.40
19	SL 795	32.00	34.00	105.33	34.33	3.66	38.33	10.66	18.30	4.00
20	DSb 15	31.00	33.66	107.66	37.00	4.00	24.00	15.86	18.50	5.40
21	PS 1466	33.00	35.33	106.33	40.00	4.33	30.66	11.53	19.30	4.46
22	TS 9	37.00	39.33	99.66	48.00	3.66	60.66	11.20	21.13	6.00
23	KS 1	32.00	34.66	91.33	44.33	4.00	41.00	10.30	20.70	4.35
24	MACS 1259	32.00	35.33	98.66	52.00	2.33	26.66	10.50	20.36	5.96
25	NRC 84	32.00	35.33	87.33	36.66	6.00	20.00	9.40	16.83	3.63
26	AMS 323	33.00	35.33	97.33	39.66	3.33	27.00	9.26	21.00	3.73
27	PS 1469	33.00	36.00	102.66	36.00	4.00	18.00	12.66	16.83	4.26
28	JS 90-21	38.00	33.33	94.33	30.00	3.00	19.33	8.03	21.80	3.26
29	SL 794	28.00	31.66	71.00	36.36	3.00	21.00	10.53	16.63	4.43

30	ASH 1	32.00	35.66	96.66	26.33	2.66	18.66	9.20	18.23	2.26
31	KSHb 6	37.00	40.33	106.66	47.33	6.00	43.66	13.66	18.73	4.80
32	TS 7	37.00	40.00	92.66	39.00	3.66	30.66	13.00	19.30	3.70
33	KDS 343	37.00	40.33	101.33	46.00	3.33	42.33	9.73	20.23	4.63
34	KS 3	37.00	40.00	108.33	36.66	4.33	26.00	11.80	13.23	4.56
35	MACS 1238	34.00	37.36	88.33	34.66	2.66	28.00	9.16	18.36	3.36
Checks										
36	MAUS 71	34.00	37.33	94.33	46.66	5.66	31.00	10.10	21.00	3.93
37	MAUS 81	33.00	37.66	94.66	40.00	4.33	27.00	9.10	21.40	4.80
38	Bragg	33.00	36.33	98.33	40.00	4.00	32.00	10.20	18.00	4.53
39	JS-93-05	36.00	39.66	86.33	34.33	5.33	20.00	9.10	20.00	4.20
40	JS 97-52	32.00	35.00	98.66	44.33	3.33	10.00	9.33	31.30	4.23
	Range	27-40	29-42	85-107.33	26.3-58	2.3-6.33	18-60.66	7.86-15.86	15.53-21.80	1.71-6.60
	G.Mean	32.96	35.92	96.66	39.64	4.10	30.48	11.04	18.68	4.40
	SE±	0.37	0.29	5.24	1.22	0.38	1.29	0.31	0.31	0.39
	C.D. at 5%	1.21	0.80	14.50	3.38	1.07	3.57	0.86	0.87	1.09

3.2 Range of variability

The analysis of variance revealed highly significant differences among the mean square due to genotypes for all the characters studied, suggesting the presence of sufficient amount of variability in the material used (Table 3). The characters under investigation were analyzed for genotypic variance (σ^2_g), phenotypic variance (σ^2_p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and expected genetic advance as % of mean (EGA) and are presented in Table 4.

Table 3 : Analysis of variance for yield, yield contributing and morphological characters in soybean

Source of Variation	D.F	Mean Sum of squares								
		Morphological characters					Yield contributing characters			
		Days to first flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number branches per plant	Number of pods per plant	100 seed weight (g)	Oil content (%)	Seed yield per plant (g)
1	2	3	4	5	6	7	8	9	10	11
Replication	2	28.981	0.476	66.860	3.634	1.675	53.434	0.224	0.759	2.929
Treatment	39	23.055 **	24.29 **	192.92 **	156.297 **	3.644 **	290.289 **	9.814 **	10.676 **	2.866 **
Error	78	0.761	0.252	82.41	4.342	0.452	4.997	0.291	0.300	0.473

* and ** : Significant at 5 and 1 % respectively.

Table 4 : Parameters of Genetic Variability for yield, yield contributing and morphological characters in Soybean

Sr. No.	Character	Range	General mean	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	GCV(%)	PCV(%)	Heritability (%)	Expected genetic advance (%)
1	Days to first flowering	27.00-40.00	32.96	7.43	8.19	8.26	8.68	90.71	16.22
2	Days to 50% flowering	29.00-42.66	35.92	8.01	8.26	7.88	8.06	96.94	15.98
3	Days to maturity	71.0-108.33	96.66	48.12	48.46	7.11	7.13	99.30	14.60
4	Plant height (cm)	26.33-58.00	39.64	53.45	53.76	18.46	18.52	99.42	37.93
5	Number branches per plant	2.33-6.33	4.10	1.06	1.51	25.15	30.03	70.00	43.40
6	Number of pods per plant	18.0-60.66	30.48	95.09	100.95	31.99	32.82	95.00	64.23
7	100 seed weight (g)	7.86-15.86	11.04	3.17	3.46	16.13	16.86	91.59	31.81
8	Oil content (%)	15.53-21.80	18.68	8.43	8.80	14.37	16.10	30.00	5.13
9	Seed yield per plant (g)	1.71-6.60	4.15	0.95	0.96	23.59	23.61	99.00	48.59

A wide range of variability was observed for majority of yield contributing characters. Range of variation based on mean was more for traits viz., number of pods per plant, plant height, days to maturity, seed yield per plant, days to 50% flowering, days to first flowering, 100 seed weight, oil content and number of branches per plant. Similar results were obtained by Santosh *et al.* (2020), Chettri *et al.* (2005), Dhillon *et al.* (2005), Gupta and Punetha (2007), Aditya *et al.* (2011) and Akram *et al.* (2016).

Estimates for phenotypic variance are higher than the genotypic variance for all the characters. High genotypic variances were observed for character number of pods per plant followed by plant height, days to maturity, days to flowering, days to 50 % flowering and seed yield per plant. High phenotypic variances were observed for number of pods per plant, plant height and oil content. The present findings are in agreement with those reported by Dhillon *et al.* (2005), Gohil *et al.* (2006), Sirohi *et al.* (2007), Ghodrati (2013) and Baraskar *et al.* (2014).

3.3 Genotypic and phenotypic coefficient of variation

In the present investigation, the phenotypic coefficient of variation was more significant than the genotypic coefficient of variation. Still, the differences between them were found to be

of lower magnitude indicating that there is a small effect of environment on characters under study and selection may be effective for necessary of these traits. The highest values of genotypic coefficient of variation and phenotypic coefficient of variation were recorded for characters viz., number of pods per plant, number of branches per plant, seed yield per plant and plant height indicating the possibilities of enhancement of these traits through selection. Similar observations were made by Bhairav *et al.*(2006), Gohil *et al.* (2006),Sirohi *et al.* (2007), Malik *et al* (2011), Aditya *et al.*(2011) and Islam *et al.*(2015).The low estimates of the phenotypic coefficient of variation and genotypic coefficient of variation observed for days to first flowering, days to 50% flowering, days to maturity and oil content. These results are in conformity with reports of earlier workers viz., Dhillon *et al.* (2005), Karnwal and Singh (2009), Karad *et al.* (2005), Sahay *et al.* (2005), Gupta and Punetha (2007),Ghodrati (2013), Malek *et al* (2014) and Baraskar *et al.*(2014).

3.4 Heritability and genetic advance

The knowledge about the heritability of a trait is helpful to enable the plant breeder to decide the appropriate selection procedure to be followed for improvement of the trait under a given situation. The high heritability estimates is more useful in predicting yield under phenotypic selection than heritability estimates alone (Johnson *et al.* 1955). In the present investigation, range of heritability was from 30 % for oil content to 99.42 for plant height. The desirable broad sense heritability (more than 60%) was observed for days to flowering (90.71%), days to 50% flowering (96.94) and days to maturity (99.30 %). These results are in agreement with those results obtained by Gohil *et al.* (2006) and Gupta and Punetha (2007). Bhairav *et al.* (2006), Baraskar *et al.*(2014), Islam *et al.* (2015) , Kushwantoro (2017) and Jain and Ramgiry (2000) reported high genetic advance for number of branches per plant, pods per plant, seed yield per plant and plant height, suggesting that additive gene effects controlled all these characters.Similar trend of results was observed in the present investigation.

High heritability estimates coupled with high expected genetic advance were observed for the characters viz., seed yield per plant, number of pods per plant, number of branches per plant and plant height indicating the presence of additive gene action on the expression of these characters. Similar trends of results were reported by Rajarathinam *et al.*, (1996), Dhillon *et al.* (2005), Yadav *et al.* (2007), Islam *et al.* (2015) and Kushwantoro (2017).The selection of characters with high heritability with expected high expected genetic advance will be more

useful than the character with low genetic gain. High heritability estimates coupled with insufficient genetic advance were observed for characters viz., oil content, days to 50 % flowering, days to maturity and 100 seed weight. Similar type of findings were reported by Dhillon *et al.* (2005), Sahay *et al.* (2005), Karad *et al.* (2005), Chettri *et al.* (2005), Baraskar *et al.* (2014) and Promin *et al.*, (2014) indicating the presence of poor genetic variance in the material for these characters.

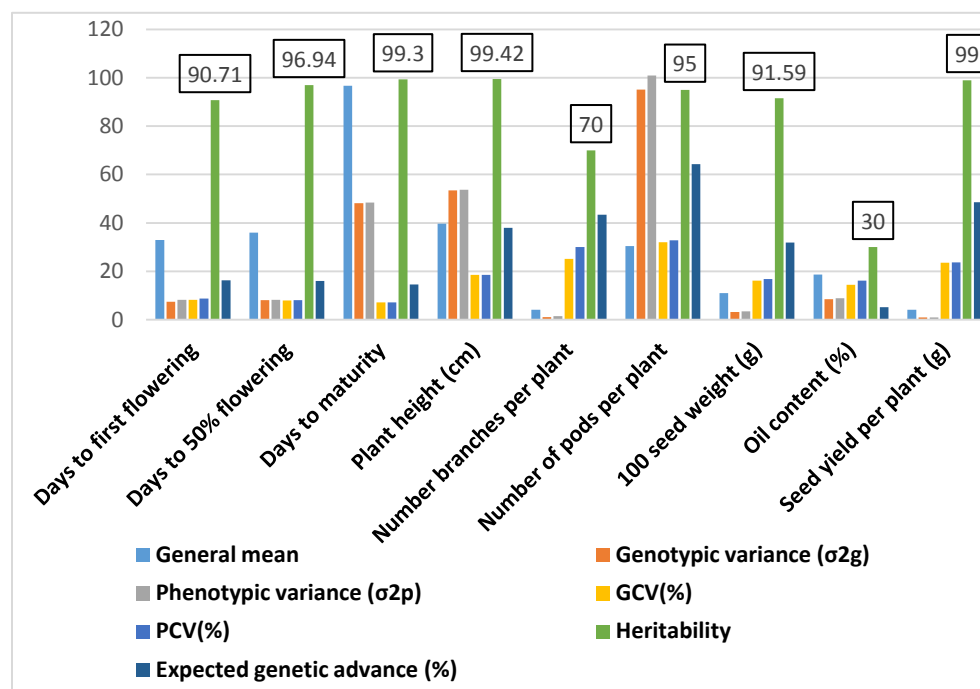


Fig.1. Parameters of Genetic Variability for yield, yield contributing and morphological characters in Soybean

4. Conclusion

Research findings of the present investigation revealed considerable presence of high genetic heterogeneity among genotypes, both genotypic and phenotypic variation. Six out of nine traits viz., seed yield per plant, number of days for first and 50 % flowering, number of branches per plant, number of pods per plant and plant height recorded high heritability with high expected genetic advance indicating the presence of additive gene action and phenotypic selection will be more effective for these traits. Therefore, in genetic enhancement program of soybean, more emphasis should be given for improvement these traits during selection.

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