



Assessment of genetic variability among soybean genotypes (*Glycine max* (L.) Merrill)

Ronika Thakur* and Vedna Kumari

Department of Genetics and Plant Breeding, College of Agriculture, Chaudhary Sarwan Kumar Himachal Pradesh
Krishi Vishvavidyalaya, Palampur-176 062, India

*Corresponding author e-mail: ronikathakur7@gmail.com

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Abstract

An experiment was conducted to evaluate genetic variability among 247 genotypes of soybean during *kharif* 2021 and 2022 at Palampur. Analysis of variance showed significant variability for all traits. PCV (%) and GCV (%) were higher for biological yield, pods per plant and harvest index indicating the presence of high genetic variation for the traits. High heritability coupled with high genetic advance was observed for most of the traits indicated the presence of additive gene action suggesting the selection of these traits for substantial genetic gains in the subsequent generations. Based on mean performance over the environments, the genotypes GW59, GW6, GW222 and GW376 were found suitable for yield trait improvement in soybean. Hence, these genotypes can be effectively utilized in soybean breeding programs to develop high-yielding varieties and thus would be helpful in mitigating the existing yield gap.

Keywords: Genetic parameters, GCV, heritability, PCV, Soybean

Soybean (*Glycine max* (L.) Merrill) stands as a paramount legume crop, not only for its economic significance but also for its pivotal role in global food security and nutrition. Soybean is a high-yield cash crop and a vital component of the cereal-based Indian diet due to its high protein (40%) and oil (20%) content. Rich in amino acids, unsaturated fats, vitamins, and minerals, it serves as a nutritional substitute to combat hunger and malnutrition, especially in India and other Asian countries (Shah and Kataria 2019). Globally, soybean covers 133.79 mha, producing 348.86 mt with a productivity of 26.07 q/ha. India, the fifth-largest producer, has 12.15 mha area, producing 12.99 mt with a productivity of 10.69 q/ha (Anonymous 2022a). In Himachal Pradesh, it is grown on 400 ha, yielding 310 tons at 7.69 q/ha (Anonymous 2022b). The yield gap is attributed to erratic monsoons, abiotic and biotic stress, high input costs, poor crop management and lack of high-yield varieties at right time. To fulfil the increasing need of the changing production ecology, phenotypic and genotypic dissection of current germplasm is required on a regular basis in order to identify genetically varied

lines with desirable features (Srishti *et al.* 2023). The quest for improving soybean varieties necessitates a deep understanding of its genetic architecture, particularly genetic diversity and the components of genetic variability, heritability and genetic advance.

Genetic diversity is crucial for breeding success as it enables the creation of productive recombinants and enhances variability during generational segregation for genetic improvement (Priyanka *et al.* 2023). Such insights are fundamental for designing effective breeding strategies aimed at enhancing yield, nutritional quality and resilience to biotic and abiotic stresses. Genetic variability, the basis for evolution and selection, encompasses phenotypic variation attributable to both genetic and environmental factors (Sekhon *et al.* 2019). Partitioning this variability into different components, namely phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), elucidates the relative contributions of genetic and environmental factors to phenotypic expression. PCV measures the total variability observed in a population, while GCV represents the genetic variability free from environmental influences.

Understanding these components is crucial for discerning the extent to which phenotypic traits are influenced by genetic factors, guiding breeding efforts towards traits with higher heritability (Sharma *et al.* 2016; Sharma *et al.* 2020). Heritability (h^2_{bs}) is another indispensable parameter in breeding programmes, quantifying the proportion of phenotypic variation attributable to genetic factors. It serves as a predictive measure for the response of traits to selection, thereby guiding breeders in identifying the most promising genotypes for further improvement. Moreover, knowledge of heritability aids in deciding the breeding method most suitable for a given trait, whether it be conventional selection, hybridization, or advanced molecular techniques like marker-assisted selection and genomic selection. Accompanying heritability, genetic advance (GA) expressed as percent of mean provides an estimate of the expected gain from selection, facilitating the identification of superior genotypes with precision. By considering both heritability and genetic advance, breeders can prioritize traits with high heritability and substantial genetic advance, accelerating the breeding process towards desired outcomes. Considering the above facts, the present experiment was carried out to assess the genetic variability among 247 soybean genotypes for various yield-attributing traits, which could lead to the development of high yielding soybean genotypes in future breeding programmes.

Materials and Methods

The present investigation was undertaken during *kharif* 2021 and *kharif* 2022 at the experimental farm of CSK HPKV, Palampur. Agro-climatically, Palampur falls under the sub-temperate humid zone of Himachal Pradesh, with mild summers, harsh winters, and annual rainfall of 1500-2500 mm, 80% of which occurs from June to September, creating humid conditions during the *kharif* season. All the standard agronomical practices for soybean were applied to ensure good crop growth. The experimental material comprised of 247 soybean genotypes. Observations were recorded on five randomly selected plants per treatment for thirteen quantitative characters *viz.*, days to 50% flowering, days to 75% maturity, plant height,

nodes on main shoot, internode length, branches per plant, pods per plant, seeds per pod, pod length, 100-seed weight, biological yield per plant, harvest index and seed yield per plant. To establish the homogeneity of error variance over the seasons, Bartlett's Chi-square test was utilized which indicated homogeneous error variances for all the traits studied. The analysis of variance was done as suggested by Panse and Sukhatme (1989). The PCV, GCV and genetic advance expressed as percent of mean were worked out according to the method given by Burton and De Vane (1953) and Johnson *et al.* (1955) and categorized as Low <10%; Moderate 10-20%; high >20%. Heritability in broad sense was also worked out according to the method given by Burton and De Vane (1953) and Johnson *et al.* (1955) and categorized as Low <30%; Moderate 30-60%; high >60%.

Results and Discussion

The results of analysis of variance for *kharif* 2021 and *kharif* 2022 revealed that mean sum of squares due to genotypes were significant ($P \leq 0.05$) for all the traits except for the seeds per pod during *kharif* 2021 (Table 1). Significant differences within 247 soybean genotypes across both the seasons highlighted substantial magnitude of variation among the genotypes for different yield attributing traits. The result of present investigation is in accordance with Kumar *et al.* (2015), Naik *et al.* (2016), Sareo *et al.* (2018), Kachare *et al.* (2020), Ullah *et al.* (2021) and Thakur *et al.* (2022).

To establish the homogeneity of error variance over the seasons, Bartlett's Chi-square test was utilized which indicated homogeneous error variances for all the traits studied over two seasons *i.e.* *kharif* 2021 and *kharif* 2022 at Palampur (Table 2). Further, pooled analysis of variance reported significant differences ($P \leq 0.05$) between the seasons for all the traits except for seeds per pod. Similarly, all 247 soybean genotypes under consideration were significantly different for various traits studied except for internode length and seeds per pod which indicated differences in the genetic makeup of the materials used. This finding agreed with Shrestha *et al.* (2023) who also found that soybean genotypes differed significantly for yield

Table 1. Mean sum of squares from the analysis of variance of 247 soybean genotypes evaluated for morphological traits in two environments

Traits	Environment	Replications	Source	
	df	1	Genotypes	Error
			246	246
Days to 50% flowering	<i>Kharif</i> 2021	162.12	46.85*	1.80
	<i>Kharif</i> 2022	2,160.10	86.85*	7.06
Days to 75% maturity	<i>Kharif</i> 2021	19.84	8.61*	1.09
	<i>Kharif</i> 2022	20.65	20.25*	3.08
Plant height (cm)	<i>Kharif</i> 2021	115.24	578.92*	15.67
	<i>Kharif</i> 2022	315.90	313.68*	23.40
Nodes on main stem	<i>Kharif</i> 2021	2.63	2.10*	1.24
	<i>Kharif</i> 2022	10.72	8.30*	2.25
Internode length (cm)	<i>Kharif</i> 2021	77.37	9.37*	1.25
	<i>Kharif</i> 2022	100.03	4.57*	2.95
Branches per plant	<i>Kharif</i> 2021	25.44	2.21*	0.72
	<i>Kharif</i> 2022	2.50	1.55*	0.23
Pods per plant	<i>Kharif</i> 2021	80.00	475.64*	53.86
	<i>Kharif</i> 2022	246.86	363.55*	26.77
Seeds per pod	<i>Kharif</i> 2021	0.74	0.07	0.08
	<i>Kharif</i> 2022	2.02	0.04*	0.02
Pod length (cm)	<i>Kharif</i> 2021	1.82	0.16*	0.07
	<i>Kharif</i> 2022	0.85	0.10*	0.06
100-seed weight (g)	<i>Kharif</i> 2021	0.79	9.89*	0.13
	<i>Kharif</i> 2022	0.30	13.64*	0.27
Biological yield per plant (g)	<i>Kharif</i> 2021	1645.66	327.09*	46.36
	<i>Kharif</i> 2022	186.84	198.79*	20.17
Seed yield per plant (g)	<i>Kharif</i> 2021	0.81	15.89*	0.99
	<i>Kharif</i> 2022	0.98	7.46*	0.36
Harvest index (%)	<i>Kharif</i> 2021	146.93	35.13*	5.25
	<i>Kharif</i> 2022	4.84	57.42*	10.33

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

Table 2. Mean sum of squares from pooled analysis of variance of 247 soybean genotypes evaluated for morphological traits over two seasons

Source of variation	Mean squares			
	Seasons	Genotypes	Genotypes $\times$ Seasons	Pooled error
Degree of freedom (df)	1	246	246	492
Days to 50% flowering	32,013.54*	68.31*	65.38*	4.43
Days to 75% maturity	2,098.79*	13.54*	15.31*	2.08
Plant height (cm)	8,833.28*	603.80*	288.79*	19.55
Nodes on main stem	3,902.43*	12.20*	5.47*	1.75
Internode length (cm)	8,892.88*	3.09	3.58	2.10
Branches per plant	220.63*	2.26*	1.50*	0.48
Pods per plant	45,359.77*	470.08*	369.10*	40.32
Seeds per pod	0.12	0.06	0.05	0.05
Pod length (cm)	6.52*	0.16*	0.10	0.07
100-seed weight (g)	6.07*	12.20*	11.58*	0.34
Biological yield per plant (g)	7,692.56*	226.36*	176.73*	25.07
Seed yield per plant (g)	5,940.13*	11.32*	12.03*	0.67
Harvest index (%)	13,436.22*	99.42*	85.41*	13.94

*Significance at ≤ 0.05

component traits. Moreover, the genotypes $\times$ seasons interaction was also found to be significant for most of the yield and component traits and non-significant for internode length, seeds per pod and pod length. Krisnawati and Adie (2018) found significant interactions for seven soybean genotypes for all the traits except for branches per plant. In contrast to this, Milioli *et al.* (2018) reported significant genotypes $\times$ seasons interaction for all the soybean yield and related traits.

The mean performance of 247 soybean genotypes based on pooled analysis over years showed that none of the genotypes were found superior to check for days to 50% flowering (check NRC 128=56.50 days); days to 75% maturity, (check NRC 128=123.75 days); plant height (check JS 20-116=108 cm); nodes on main stem (check JS 71-05=16.15); internode length (check AMS 2014-1=11.80 cm); branches per plant (check JS 97-52=6.40); pod length (check JS 97-52=4.35cm); pods per plant (check JS 97-52=77.15) and harvest index (check NRC 128=33.19%), however most of the genotypes were statistically at par with the respective best checks for these traits.

In contrary, seeds per pod revealed that the genotype GW59 (3.51) exhibited significant superiority over the best check NRC 37 (2.59) while 231 genotypes revealed statistically similar performance. For 100-seed weight, GW6 (19.95g) showed significant and superior performance than the best check AMS 2014-1 (14.75g) with 235 genotypes performed statistically at par with check variety. Moreover, for biological yield per plant, two genotypes namely, GW222 (64.11g) and GW376 (62.58 g) were found to be significant and superior over the best check AMS 2014-1 (41.73g) along with 237 genotypes being statistically at par with it.

For the most economic trait, 33 genotypes recorded significantly higher seed yield than the best check AMS 2014-1 (15.60g) with GW51 (17.60g), GW74 (20.20g), GW105 (19.40g), GW142 (20.50g) as top ranked five genotypes during *khariif*, 2021 while during *khariif* 2022, only 18 genotypes observed to be significantly superior to the best checks NRC 128 and AMS 2014-1 (11.30g each) with GW7 (12.75g), GW17 (12.80g), GW49 (12.60g), GW117 (12.75g)

and GW186 (13.40g) placed among the top ranked genotypes. In contrast, all the genotypes were statistically at par with the best check AMS 2014-1 (13.45 g) for seed yield per plant in pooled analysis.

In general, the PCV was higher than GCV for all the studied characters which indicated the effect of environmental variation. Moderate GCV and PCV were observed for traits *viz.*, plant height, nodes on main shoot, branches per plant, pods per plant, 100-seed weight, biological yield per plant, harvest index and seed yield per plant and the traits *viz.*, days to 50% flowering, days to 75% maturity, seeds per pod and pod length exhibited low GCV and PCV values whereas internode length showed moderate PCV coupled with low GCV (Table 3). The GCV measures the amount of variation present in a particular character but it doesn't provide an idea about the proportion of heritable variation present in the total variation therefore, heritability estimates were calculated in the present study.

Genetic advance under screening is the improvement in genotypic traits passed to the next generation at a given selection intensity. Combining heritability with genetic gain offers better prediction of selection effectiveness than heritability alone (Bhardwaj *et al.* 2020). High heritability coupled with high genetic advance expressed as percent of mean was observed for the traits *viz.*, plant height, nodes on main shoot, pods per plant, 100-seed weight, biological yield per plant, harvest index and seed yield per plant which indicated the presence of additive gene action and offers the best possibility for improvement of these traits by selection methods. These results were in accordance with Soharu *et al.* (2022) and Thakur *et al.* (2022). High heritability coupled with moderate genetic advance was observed for characters *viz.*, days to 50% flowering and branches per plant indicating the presence of both additive and non-additive gene action for these traits. High heritability coupled with low genetic advance found for only days to 75% maturity indicating the presence of non-additive gene action and therefore, selection is not rewarding for this trait (Sharma *et al.* 2007). Similar results were estimated by Kumar *et al.* (2015) and Sareo *et al.* (2018).

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

Traits	Season	Mean± SE(m)	Range		PCV(%)	GCV(%)	Heritability h ² bs (%)	GA (%)	GAM(as % mean)
			Min.	Max.					
Days to 50% flowering	<i>Kharif</i> , 2021	55.00±0.95	43.00	63.50	8.96	8.62	92.61	9.41	17.11
	<i>Kharif</i> , 2022	66.39±1.88	47.00	84.50	10.32	9.51	84.97	11.99	18.06
	Pooled	60.69±1.03	45.25	70.50	7.01	6.59	88.25	7.74	12.76
Days to 75% maturity	<i>Kharif</i> , 2021	124.07±0.74	113.50	129.00	1.77	1.56	77.55	3.52	2.83
	<i>Kharif</i> , 2022	126.99±1.24	120.50	132.50	2.69	2.30	73.59	5.18	4.08
	Pooled	125.53±0.77	121.25	129.50	1.59	1.33	70.15	2.88	2.30
Plant height (cm)	<i>Kharif</i> , 2021	97.71±2.80	52.90	145.40	17.64	17.17	94.73	33.65	34.44
	<i>Kharif</i> , 2022	91.73±3.42	57.30	122.00	14.15	13.13	86.11	23.03	25.11
	Pooled	94.72±2.17	58.35	123.40	13.17	12.76	93.97	24.15	25.50
Nodes on main stem	<i>Kharif</i> , 2021	12.00±0.79	5.50	17.60	19.17	9.70	25.64	0.68	10.12
	<i>Kharif</i> , 2022	15.98±1.06	11.00	21.90	14.37	10.88	57.33	2.71	16.97
	Pooled	13.99±0.69	8.85	17.85	13.41	11.47	73.17	2.83	20.22
Internode length (cm)	<i>Kharif</i> , 2021	6.74±0.79	4.30	12.30	19.20	16.79	76.48	3.63	30.25
	<i>Kharif</i> , 2022	12.74±1.22	8.00	18.50	15.20	7.06	21.52	0.86	6.74
	Pooled	9.74±0.75	7.00	13.10	11.86	4.69	15.62	0.37	3.82
Branches per plant	<i>Kharif</i> , 2021	6.13±0.60	3.60	8.80	19.75	14.06	50.73	1.26	20.64
	<i>Kharif</i> , 2022	5.18±0.34	3.70	8.85	18.22	15.66	73.91	1.44	27.74
	Pooled	5.65±0.35	3.70	7.45	14.62	11.79	65.12	1.11	19.61
Pods per plant	<i>Kharif</i> , 2021	69.22±5.19	29.50	121.10	23.51	20.98	79.66	26.70	38.58
	<i>Kharif</i> , 2022	55.66±3.66	27.80	90.20	25.10	23.31	86.28	24.83	44.61
	Pooled	62.44±3.25	36.23	91.55	18.12	16.56	83.53	19.47	31.19

Cont./...

Cont./...

Traits	Season	Mean± SE(m)	Range		PCV (%)	GCV (%)	Heritability h ² bs (%)	GA (%)	GAM (as % mean)
			Min.	Max.					
Seeds per pod	<i>Khariif</i> , 2021	2.46±0.20	2.15	3.10	11.16	2.34	4.38	0.03	1.01
	<i>Khariif</i> , 2022	2.48±0.10	2.14	2.80	6.75	3.99	35.00	0.12	4.86
	Pooled	2.47±0.11	2.20	3.51	6.64	1.98	8.92	0.03	1.22
Pod length (cm)	<i>Khariif</i> , 2021	4.01±0.19	3.25	4.85	8.45	5.07	36.11	0.25	6.28
	<i>Khariif</i> , 2022	3.86±0.17	3.25	4.55	7.25	3.78	27.24	0.16	4.07
	Pooled	3.93±0.13	3.38	4.50	6.05	3.69	37.08	0.18	4.63
100-seed weight (g)	<i>Khariif</i> , 2021	13.55±0.25	9.05	20.60	16.50	16.30	97.50	4.50	33.15
	<i>Khariif</i> , 2022	13.41±0.52	7.50	20.27	20.06	19.27	92.30	5.11	38.14
	Pooled	13.47±0.29	9.05	19.95	13.13	12.77	94.67	3.45	25.61
Biological yield per plant (g)	<i>Khariif</i> , 2021	43.58±3.87	18.55	68.50	24.06	20.86	75.17	21.16	37.25
	<i>Khariif</i> , 2022	38.01±3.18	18.40	66.55	22.11	19.57	78.31	17.03	35.67
	Pooled	40.80±6.65	22.47	64.11	19.47	17.33	79.19	12.96	31.77
Seed yield per plant (g)	<i>Khariif</i> , 2021	14.39±0.71	6.70	22.30	20.19	18.97	88.30	5.28	36.73
	<i>Khariif</i> , 2022	9.48±0.42	5.40	16.35	20.85	19.88	90.91	3.70	39.05
	Pooled	11.94±0.42	6.83	16.85	14.50	13.65	88.50	3.16	26.47
Harvest index (%)	<i>Khariif</i> , 2021	33.96±1.62	17.60	48.13	15.85	13.63	73.97	6.85	24.15
	<i>Khariif</i> , 2022	26.58±2.27	13.83	48.80	21.11	17.60	69.51	8.33	30.22
	Pooled	30.27±1.90	17.34	44.44	17.62	15.22	74.54	8.19	27.06

Conclusion

The enormous phenotypic variability and significant differences were observed among the genotypes for majority of traits studied suggesting prevalence of wide range of genetic variation and scope of selection for these traits among the genotypes. The estimate of PCV was higher than corresponding GCV for all the characters studied which indicated that the apparent variation is not only due to genotypes but also due to the influence of environment. High heritability coupled with high genetic advance expressed as percent of mean was observed for various traits *viz.*, plant height, nodes on main shoot, pods per plant, 100-seed weight, biological yield per plant, harvest index and seed yield per plant indicate additive gene action of these traits.

Therefore, direct selection will be rewarding for improvement of such traits which could be profitable for soybean genetic improvement. The results indicate that the many of the evaluated genotypes are suitable for yield trait improvement and there is need to identify and utilize genetic variation for enhancing earliness in soybean.

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