

# Study on genetic variability parameters in soybean [*Glycine max* (L.) Merrill] genotypes



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## Summary

Thirty-two soybean genotypes were assessed to estimate genetic variability parameters in RBD design with three replications during 2021. The results of the Analysis of Variance (ANOVA) revealed significant variation across the genotypes for each trait studied which showed high variability in experimental material. The higher magnitude (>20%) of GCV and PCV were exhibited by seed yield per plant (33.71% and 35.60%) followed by biological yield per plant (26.64% and 28.47%), number of pods per plant (24.56% and 25.13%) and number of branches per plant (20.24% and 20.75%), respectively. High heritability coupled with high genetic advance showed by seed yield, biological yield, number of pods, number of branches per plant, harvest index, 100-seed weight and plant height, indicating additive gene action and provides the chance for selection-based development of these traits. In this study, higher yield was reported for AUKS 213 (12.44 g) followed by AUKS 259 (11.14 g), AUKS 263 (10.82 g), AUKS 262 (10.44 g) and AUKS 264 (9.99 g) genotypes as per their mean values.

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**Keywords:** Soybean; genetic variability; heritability; genetic advance; ANOVA

## INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is renowned as the "Golden Bean" and "Miracle Crop" of the 21st century. It plays significant role to fulfill the world's current and prospective protein and edible oil demands. It consists of 37-42% high quality protein, 6% ash, 29% carbohydrate and 17 to 24% oil. In India, soybean crop is occupied 12.92 m ha area with the production of 12.61 m tonnes and productivity of 976 kg/ha during 2020-21. Madhya Pradesh, Maharashtra and Rajasthan are the major soybean producing states. In Rajasthan, area under soybean production is about 1.1 m ha with the production and productivity of 0.86 m tonnes and 780 kg/ha, respectively during 2020-21 (Anonymous, 2021).<sup>4</sup> The primary goal of breeding programmes is to boost productivity of crops in emerging nations such as India. Usually, breeding for production must be used to complete this task of raising the yield level. Production breeding basically tries to increase the plants' inherent productivity by choosing the positive genes or gene

complexes that contribute to a higher expression of yield. A breeding program must have the existence and extent of genetic variation in its gene pool because genetic variation is necessary for population heterogeneity.<sup>10, 18</sup> The wide genetic variation enables selection on more genetic components to produce a genotype with desirable traits. Selection could not produce diversity since it could only be used to improve desirable traits that can be inherited and only on those that already exist. Because the observed variability represents a combined estimate of genetic and environmental causes, heritability is a reliable indicator of how quantitative traits are passed on from parents to offspring. However, estimations of heritability alone do not give an idea about the projected gain in the following generation and must be taken into account in conjunction with estimates of genetic advance which show the genetic advancement of the progeny possible through selection over the original population. The current study was conducted to investigate the genetic variability, heritability and genetic advance of soybean genotypes for crop improvement.

## Materials and Methods

The present investigation was conducted during 2021 at Research farm, College of Agriculture Ummendganj, Agriculture University, Kota, Rajasthan, India. The College

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of Agriculture, Ummadganj, Kota is situated at 25.11° North latitude and 75.50° East longitude at an altitude of 258 meters above mean sea level (MSL). In Rajasthan, this region falls under the Agro-Climatic Zone-V (Humid South Eastern Plain Zone). The observations were recorded on five randomly selected plants in each replication and in each genotype for following traits viz., plant height (cm), pod length (cm),<sup>3</sup> number of branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g), harvest index (%). Days to flowering, days to maturity, protein content (%) and oil content (%) observations were noted on plot basis. The analysis of variance (ANOVA) was computed as per Panse and Sukhatme (1985).<sup>15</sup> The values of genotypic coefficient of variation and phenotypic coefficient of variation were estimated according to the formula suggested by Burton (1952).<sup>6</sup> Heritability ( $h^2$ ) in broad sense and genetic advance as % of mean (GA%) were calculated as per the formula suggested by Allard (1960)<sup>3</sup> and Johnson *et al.* (1955),<sup>12</sup> respectively.

## Results and Discussion

Analysis of variance showed highly significant differences for all the traits studied which indicating a large amount of genetic variability among the genotypes (Table 1).

The values of genetic variability parameters viz., range, mean, GCV, PCV, heritability and genetic advance expressed as % of mean are presented in Table 2. The higher values for genotypic and phenotypic coefficient of variation (>20%) were reported for seed yield per plant (33.71% and 35.60%) followed by biological yield per plant (26.64% and 28.47%), number of pods per plant (24.56% and 25.13%) and number of branches per plant (20.24% and 20.75%), respectively. Similar conclusions on soybean for most of the traits were also reported by Suresh Rao *et al.* (2014),<sup>19</sup> Chandrawat *et al.* (2017),<sup>7</sup> Bhuva and Babariya (2020)<sup>5</sup> and Jandong *et al.* (2020),<sup>17</sup> while high values for branches per plant were earlier obtained by Chandrawat *et al.* (2017)<sup>7</sup> and Dangi and Sharma (2021).<sup>8</sup> Moderate estimates of genotypic and phenotypic coefficient of variation (10-20%) of soybean crop were obtained for harvest index (18.82% and 19.28%), 100-seed weight (17.61% and 18.44%), plant height (16.56%

and 16.97%) and pod length (11.09% and 11.49%), respectively, while remaining traits exhibited the lower values of genotypic and phenotypic coefficient of variation (<10%). Similar results on soybean were found earlier by Patil *et al.* (2011).<sup>16</sup>

Table 2 showed that most of the characters under study exhibited high heritability (>60%). Estimates of heritability were higher for the traits viz., number of pods per plant (95.50%), harvest index (95.20%), plant height (95.20%), number of branches per plant (95.1%), pod length (93.30%), days to maturity (93.10%), 100-seed weight (91.30%), days to 50% flowering (90.80%), seed yield per plant (89.60%), biological yield per plant (87.50%), oil content (86.10%) and protein content (72.90%). Such high heritability estimates for most of these characters had previously reported by Ali *et al.* (2016),<sup>2</sup> Getnet (2018)<sup>9</sup> and Neelima *et al.* (2018),<sup>14</sup> whereas moderate estimate (30-60%) of heritability was recorded for number of seeds per pod (44%) and Akram *et al.* (2016)<sup>1</sup> was also found similar results.

The expected genetic advance expressed as % of mean ranged from 4.46% (protein content) to 65.75% (seed yield per plant). The higher estimates of genetic advance as % of mean (>20%) recorded highest for the character seed yield per plant (65.75%) followed by biological yield per plant (51.33%), number of pods per plant (49.43%), number of branches per plant (40.66%), harvest index (37.82%), 100-seed weight (34.65%), plant height (33.28%) and pod length (22.07%). Moderate estimates of genetic advance as % of mean (10-20%) recorded for the characters viz., days to 50% flowering (18.56%) and oil content (15.85%). Low values of genetic advance as % of mean (<10%) were recorded for the characters viz., days to maturity (9.83%), number of seeds per pods (5.31%) and protein content (4.46%). The high heritability estimates coupled with high genetic advance were observed for seed yield per plant, biological yield per plant, number of pods per plant, number of branches per plant, harvest index, 100-seed weight and plant height. It indicates that direct selection of these traits for genetic improvement may be effective due to additive gene effect. Similar results on soybean crop were previously reported by Reni and Rao (2013),<sup>17</sup> Neelima *et al.* (2018)<sup>14</sup> and Koraddi and Basavaraja (2019).<sup>13</sup>

**Table 1: Analysis of variance for yield and its contributing traits in soybean genotypes**

Source of variation	df (degree of freedom)	Mean sum squares												
		Days to 50% flowering	Days to maturity	Plant height(cm)	Pod length(cm)	No. of branches per plant	No. of pods per plant	No. of seeds per pod	100-seed weight (g)	Biological yield per plant(g)	Harvest index (%)	Protein content (%)	Oil content (%)	Seed yield per plant(g)
Replications	2	1.167	2.542	1.559	0.021	0.016	0.642	0.018	0.121	5.755	0.311	0.417	0.150	0.908
Genotypes	31	46.591 **	72.317 **	83.935 **	0.487 **	0.799 **	547.870 **	0.040 **	12.129 **	60.237 **	194.145 **	3.369 **	6.371 **	17.046 **
Error	62	1.522	1.735	1.389	0.011	0.013	8.509	0.012	0.375	2.734	3.203	0.371	0.324	0.632

\*\* Significant at 1% level

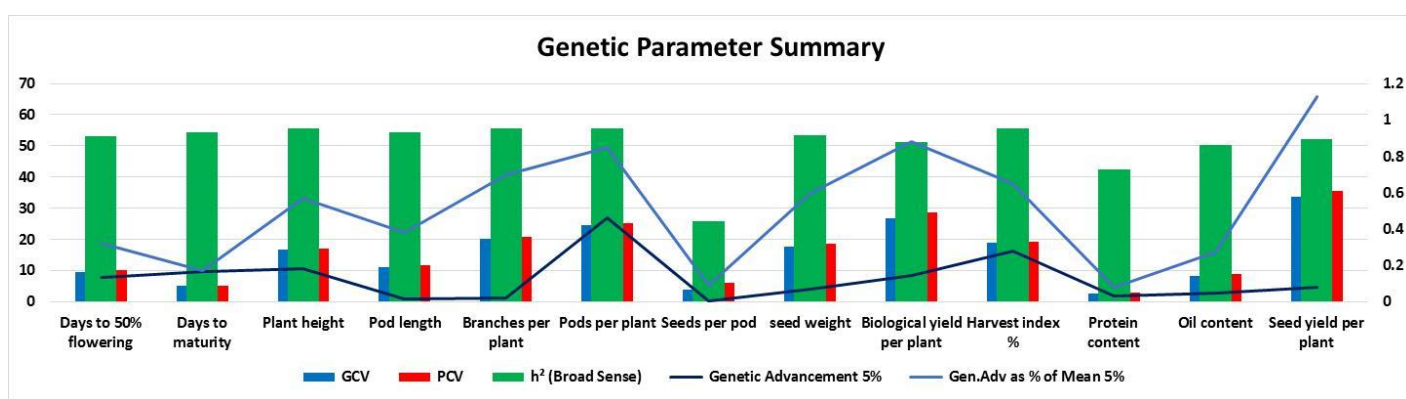
**Table 2: Genetic variability parameters for seed yield and its contributing traits in soybean**

S. No.	Characters	Range		Mean	GCV (%)	PCV (%)	Heritability % (broad sense)	Genetic Advance	Genetic Advance as % of Mean
		Min.	Max.						
1	Days to 50% flowering	34.00	46.00	40.99	9.46	9.92	90.80	7.61	18.56
2	Days to maturity	85.00	104.00	98.07	4.95	5.13	93.10	9.64	9.83
3	Plant height (cm)	23.65	41.99	31.67	16.56	16.97	95.20	10.54	33.28
4	Pod length (cm)	3.01	4.71	3.59	11.09	11.49	93.30	0.79	22.07
5	No. of branches per plant	1.20	3.50	2.53	20.24	20.75	95.10	1.03	40.66
6	No. of pods per plant	23.54	79.53	54.60	24.56	25.13	95.50	26.99	49.43
7	No. of seeds per pod	2.33	3.00	2.49	3.89	5.87	44.00	0.13	5.31
8	100-seed weight (g)	7.67	17.90	11.24	17.61	18.44	91.30	3.90	34.66
9	Seed yield per plant (g)	3.75	12.44	6.94	33.71	35.60	89.60	4.56	65.75
10	Biological yield per plant (g)	8.96	25.73	16.44	26.64	28.47	87.50	8.44	51.33
11	Harvest index (%)	22.09	54.29	42.40	18.82	19.28	95.20	16.04	37.82
12	Protein content (%)	36.86	42.12	39.41	2.54	2.97	72.90	1.76	4.46
13	Oil content (%)	14.57	20.30	17.12	8.29	8.94	86.10	2.71	15.86

High heritability estimates accompanied with moderate genetic advance were observed for pod length, days to 50% flowering and oil content. It indicates less environmental influence but was controlled by both additive and non-additive gene action. High heritability but low genetic advance as % of mean was found for days to maturity, revealing non-additive gene action. Similar findings of soybean crop were earlier documented by Getnet (2018).<sup>9</sup> Remaining traits showed non-additive gene effects.

Five high yielder genotypes including, AUKS 213 (12.44 g), AUKS 259 (11.14 g), AUKS 263 (10.82 g), AUKS 262 (10.44 g) and AUKS 264 (9.99 g) were found in this study and these genotypes were also exhibited higher mean

performance for some other important yield contributing traits. AUKS 213 had the higher number of branches per plant (3.00), number of pods per plant (79.53), biological yield per plant (25.75 g), harvest index (48.43%) and oil content (18.30%). AUKS 259 exhibited higher number of pods per plant (66.53), biological yield per plant (20.49 g) and harvest index (54.29%). AUKS 263 and AUKS 262 were found early maturing (94.33 and 93.67), dwarf (26.70 cm and 25.10 cm), higher number of primary branches per plant (3.07 and 2.80), 100-seed weight (13.60 g and 13.37 g) and biological yield per plant (20.20 g and 20.57 g). AUKS 264 showed short height (25.36 cm), high number of pods per plant (59.47), 100-seed weight (13.37 g) and biological yield per plant (20.78 g).



## Conclusion

High amount of genetic variability was found for most of the traits including seed yield per plant. The higher values of genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance were observed for seed yield per plant, biological yield per plant, number of pods per plant and number of branches per plant. These features might be utilized in crop improvement program since they were regulated by additive gene action. The genotypes viz., AUKS 213, AUKS 259, AUKS 263, AUKS 262 and AUKS 264 were found high yielding based on their mean performance for seed yield per plant. Additionally, they performed better in terms of other attributes like harvest index, number of pods per plant, number of branches per plant and biological yield per plant. Thus, these genotypes may be employed in future crop improvement program to develop high yielding soybean varieties with desirable yield contributing traits.

## Declaration of interests

The authors have no conflict of interest to declare.

## Data sharing

All relevant data are within the manuscript.

## Acknowledgments

## References

- 1 Akram S, Hussain BN, Bari MA, Burritt DJ & Hossain MA. 2016. Genetic variability and association analysis of soybean (*Glycine max* (L.) Merrill) for yield and yield attributing traits. *Plant Gene and Trait*, 7 (13): 1-11.
- 2 Ali A, Khan SA, Ulla E, Ali N & Hussain I. 2016. Estimation of genetic parameters in soybean for yield and morphological characters. *Pakistan Journal of Agriculture, Agricultural Engineering and Veterinary Sciences*, 32 (2): 162-168.
- 3 Allard RW. 1960. "Principles of Plant Breeding". John Willey and Sons, Inc., New York. 89-93.
- 4 Anonymous. 2021. Annual Report, AICRP on Soybean, Indian Council of Agricultural Research, Indian Institute of Soybean Research, Indore. 1-2.
- 5 Bhuva RB & Babariya CA. 2020. Genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. *International Journal of Agriculture and Plant Science*, 2 (4): 14-18.
- 6 Burton GW. 1952. Quantitative inheritance in grasses. *Proceedings of 6th International Grassland Congress*. 1: 227-283.
- 7 Chandrawat KS, Baig KS, Hashmi S, Sarang DH, Kumar A & Dumai K. 2017. Study on genetic variability,

- heritability and genetic advance in soybean. *International Journal of Pure and Applied Bioscience*, 5 (1): 57-63.
- 8 Dangi V & Sharma KK. 2021. Genetic variability, correlation and path analysis for grain yield and its components in soybean. *International Journal of Current Microbiology and Applied Science*, 10 (3): 1776-1782.
  - 9 Getnet BE. 2018. Genetic variability, heritability and expected genetic advance as indices for selection in soybean [*Glycine max* (L.) Merrill] varieties. *American Journal of Life Sciences*, 6 (4): 52-56.
  - 10 Jain RK, Joshi A, Chaudhary HR, Dashora A & Khatik CL. 2018. Study on genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. *Legume Research*, 41 (4): 532-536.
  - 11 Jandong EA, Uguru MI & Okechukwu EC. 2020. Estimates of genetic variability, heritability and genetic advance for agronomic and yield traits in soybean [*Glycine max* (L.)]. *African Journal of Biotechnology*, 19 (4): 201-206.
  - 12 Johnson HW, Robinson HF & Comstock RE. 1955. Genotypic and phenotypic Correlation in soybean and their implication in selection. *Agronomy Journal*, 47 (10): 477-483.
  - 13 Koraddi S & Basavaraja GT. 2019. Genetic variability studies on yield and yield component traits of soybean. *International Journal of Current Microbiology and Applied Sciences*, 8 (2): 1269-1274.
  - 14 Neelima G, Mehtre SP & Narkhede GW. 2018. Genetic variability, heritability and genetic advance in soybean. *International Journal of Pure and Applied Bioscience*, 6 (2): 1011-1017.
  - 15 Panse VG & Sukhatme PV. 1985. "Statistical Methods for Agriculture Workers." ICAR, New Delhi.
  - 16 Patil SS, Naik MR, Patil PP & Shinde DA. 2011. Genetic variability, correlation and path analysis in soybean. *Legume Research-An International Journal*, 34 (1): 36-40.
  - 17 Reni YP & Rao YK. 2013. Genetic variability in soybean [*Glycine max* (L.) Merrill]. *International Journal of Plant, Animal and Environmental Sciences*, 3 (4): 35-38.
  - 18 Singh U, Kumar S, Archana, Yadav K, Chaman & Sidharth. 2022. Genetic variability and correlation studies in various genotypes of watermelon [*Citrullus lanatus* (Thunb.) Mansf.]. *Journal of Agriculture and Ecology*, 13: 65-78.
  - 19 Sureshrao SS, Singh VJ, Gampala S and Rangare NR. 2014. Assessment of genetic variability of the main yield related characters in soybean. *International Journal of Food, Agriculture and Veterinary Sciences*, 4 (2): 69-74.