ENVIRONMENTAL REPORTS

Original Research Article
ISSN: 3041-556X
Journal homepage: https://er.researchfloor.org/

Studies on Character Expression for yield Components in Soybean

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Citation: Osekita, O. S., Ajayi, A. T., Atimokhale, D. and Adeniyi, B. C. (2025). Studies on Character Expression for yield Components in Soybean. *Environmental Reports; an International Journal.* **DOI: https://doi.org/10.51470/ER.2025.7.2.159**

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Received 24 July 2025 | Revised 17 August 2025 | Accepted September 18 2025 | Available Online October 15 2025

ABSTRACT

Soybean (Glycine max (L.) Merrill), a leguminous crop of East Asian origin, is globally cultivated for its protein and oil-rich seeds. Understanding yield-related traits is vital for improving productivity and ensuring food security. This study assessed the variability, heritability, and genetic control of yield and its component traits in five soybean accessions. The accessions were evaluated using a randomized complete block design with three replications, and data on ten quantitative traits were analyzed statistically. Results revealed that the number of pods per plant (81.78%, 98.80%), seed yield per plant (76.14%, 87.83%), and 100-seed weight (69.73%, 63.45%) exhibited high heritability and high genetic advance as a percentage of the mean (GAM), indicating additive gene effects and strong potential for selection. Plant height correlated positively with the number of leaves (r= 0.83), branches (r= 0.79), pods per plant (r= 0.66), and seed yield (r= 0.69) suggesting that taller plants with greater foliage and branching potential tend to produce more pods and higher seed yield, making plant height a valuable indirect selection criterion for yield improvement. Traits showing high variability and favorable associations can therefore serve as key selection indices for enhancing soybean yield in breeding programs.

Keywords: *Genetic advance, genetic variability, heritability, trait correlation.*

1. Introduction

Soybean (*Glycine max* (L.) Merrill) is a globally cultivated legume believed to have originated from East Asia, particularly the northern and central regions of China [15]. It is a diploidized allotetraploid species (2n = 40), predominantly self-pollinated [18], and valued for its edible seeds, which serve as major sources of vegetable oil and high-quality protein. Morphologically, soybean is an erect, bushy plant that thrives across tropical, subtropical, and temperate regions. Its exceptional nutritional composition—rich in protein, oil, and bioactive compounds such as isoflavones—enhances its importance in food, feed, and industrial applications [16, 17]. Globally, soybean occupies about 124.9 million hectares, yielding approximately 348.7 million tonnes in 2018 (ref). The United States, Brazil, and Argentina accounted for most of this output, contributing about 87.2% of global production, followed by Asia (9.3%), Europe (2.7%), and Africa (0.8%). In Africa, total production was estimated at 3.56 million tonnes across 2.61 million hectares, with Nigeria leading in West Africa at about 393,860 metric tonnes [8, 9].

Yield in soybean is a complex quantitative trait influenced by multiple genes and strongly modulated by environmental factors [4]. The variability observed in yield and its related components arises from the combined effects of genetic constitution and environmental conditions, making the evaluation of genetic variability essential for effective selection in breeding programs. Estimates of heritability and genetic advance provide critical information on the extent of genetic control over a trait and the potential for improvement through selection [14]. Key yield components such as the number of pods per plant, seeds per pod, and total number of seeds are important determinants of productivity and are relatively simple to assess [19]. Several studies have reported significant genetic variation among soybean genotypes for yield and associated traits. For instance, [6] and [24] quantified heritability, as well as phenotypic and genotypic coefficients of variation and genetic advance for major yield components, while [21] analyzed genetic variability, heritability, and genetic advance across 124 soybean germplasm accessions. Biometric parameters—including the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance (GA)—remain indispensable tools for quantifying genetic variability and predicting potential genetic gains in soybean breeding [1, 2].

Understanding the genetic expression of yield-related traits in soybean is crucial for improving productivity and enhancing its contribution to food security. Such insights can guide the development of superior cultivars, support sustainable agricultural practices, and strengthen breeding programs under changing environmental conditions. The present study was therefore undertaken to evaluate the variability in yield-related traits of soybean and to analyze the interactions between genetic and environmental factors influencing these characteristics.

2. Materials and Methods

Five soybean (*Glycine max* L.) accessions used in this study were obtained from the National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan, Nigeria (Table 1). The field experiment was conducted at the Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba-Akoko, Ondo State, Nigeria. The experimental site is located at latitude 7.20°N, longitude 5.44°E, and an altitude of 423 meters above sea level. A randomized complete block design (RCBD) with three replications was employed to ensure statistical precision and minimize environmental variation among treatments [22]. For each accession, three seeds were sown per planting hole. Each plot consisted of rows measuring 4 m in length, with a spacing of 60 cm between rows and 30 cm between plants within a row [22]. Irrigation commenced immediately after sowing and was applied twice daily during the early growth stages, then reduced to once daily approximately 45 days after planting. Weeding was carried out manually at regular intervals to minimize competition from weeds. A 10% cypermethrin solution was applied by spraying to control insect infestations.

Table 1: List of Soybean accessions evaluated for quantitative traits performance under field conditions

S/N	Accessions
1	NGB03547
2	NGB03536
3	NGB03579
4	NGB03556
5	NGB02653

2.1 Data collection

Data were collected on ten quantitative traits: plant height (cm), internode length (cm), number of leaves, number of branches, days to flowering, number of pods per plant, seed yield per plant, pod weight (g), days to maturity, and 100-seed weight (g). Data were collected from three randomly selected plants from each accession in every plot, 14 days after the application of insecticide (cypermethrin). Measurements were taken using a ruler (cm), weighing balance, field notebook, and pen.

2.2 Statistical Analysis

Data obtained from the experiment were subjected to analysis of variance (ANOVA) to determine significant differences among treatments. Duncan's Multiple Range Test (DMRT) was employed to separate the means at a 5% probability level ($P \leq 0.05$). All statistical analyses were performed using SPSS software (version 20).

The phenotypic coefficient of variation (PCV%) and genotypic coefficient of variation (GCV%) were estimated using the method suggested by [3]

$$PCV = \frac{\sqrt{Vp}}{x} \times 100$$

$$GCV = \frac{\sqrt{Vg}}{x} \times 100$$

Where,

Vp: Phenotypic variance

Vg: Genotypic variance

x: Grand mean

The genetic advance as a percentage of mean (GAM) was determined by using the formula provided by [13]

$$GAM = \frac{GA}{GM} \times 100$$

Where,

GA: Genetic advance

GM: Grand mean

Genetic advance (GA) was calculated according to [10] as:

$$GA = H^2B \times K \times \sqrt{Vp}$$

Where,

H^2B: Broad sense heritability

K: Constant also known as intensity of selection (2.06)

3. Result and Discussion

3.1 Analysis of variance

The analysis of variance (ANOVA) results (Table 2) revealed significant differences among the soybean accessions for all evaluated traits, indicating substantial genetic variability among them. These findings align with those of [12], who reported similar variability patterns among soybean lines, as well as with studies by [7], [20], and [23]. The highest coefficient of variation (CV) was observed for the number of leaves (29.33%), suggesting a greater environmental influence on this trait, while days to maturity recorded the lowest CV (7.15%), consistent with the findings of [11] and [5].

Table 2: Mean square values from analysis of variance (ANOVA) for quantitative traits among soybean accessions evaluated under field conditions

Source of variation	Df	PH (cm)	INL (cm)	NL	NB	DTF	NPP
Accession	4	178.00*	1.97*	1152.93*	94.77*	9.50*	1981.10*
Replication	2	128.22*	0.110	444.20*	58.40*	0.467	328.87*
Error	8	48.83	0.388	258.283	32.067	7.800	136.950
CV		21.93	28.97	29.33	28.03	4.63	19.88

Source of variation	Df	SYP (g)	PWT (g)	SW (g)	NDM
Accession	4	10652.60*	0.28*	14.56*	119.07*
Replication	2	992.60*	0.11*	4.64*	7.800
Error	8	1007.600	0.115	1.841	49.467
CV		20.59	15.97	13.21	7.15

**: significant at $P \leq 0.05$; ns: not significant.*

Df: Degree of freedom; CV: Coefficient of variation; PH: Plant height: INL: Internode length; NL: Number of leaves; NB: Number of branches; DTF: Days to flowering; NPP: Number of pods per plant; SYP: Seed yield per plant; PWT: Pod weight; NDM: Days to maturity; SW:100-Seed weight.

3.2 Mean performance for quantitative traits among soybean accessions evaluated under field conditions

Table 3 presents the mean performance of the evaluated soybean accessions for quantitative traits.

Plant height ranged from 22.53 cm in NGBO3579 to 42.33 cm in NGBO3547, with NGBO2653 recording 34.40 cm. Internode length varied from 1.33 cm in NGBO3536 to 3.17 cm in NGBO3556. The number of leaves ranged from 35.67 in NGBO3579 to 54.33 in NGBO3556, while the number of branches varied between 14.67 in NGBO3579 and 29.67 in NGBO3547. The number of days to flowering ranged from 57.67 days in NGBO3547 (earliest) to 62.33 days in NGBO3536 (latest). The number of pods per plant ranged from 29.67 in NGBO3536 to 85.67 in NGBO3556. Seed yield per plant ranged from 87.33 g in NGBO3536 to 213.33 g in NGBO3579, while pod weight ranged from 1.80 g in NGBO3579 to 2.57 g in NGBO3556. The 100-seed weight varied from 7.00 g in NGBO3547 to 12.70 g in NGBO3556. The number of days to maturity ranged from 97.67 days in NGBO3536 (earliest) to 106.33 days in NGBO3579 (latest).

Table 3. Mean performance for quantitative traits among soybean accessions evaluated under field conditions

Accession	PH (cm)	INL (cm)	NL	NB	DTF	NPP	SYP (g)	PWT (g)	SW (g)	NDM
NGBO3547	42.33±1.59$_{b}$	1.87±0.27$_{ab}$	87.67±12.17$_{b}$	29.67±4.33$_{b}$	57.67±1.45$_{a}$	62.33±7.21$_{b}$	172.00±26.91$_{b}$	2.10±0.21$_{ab}$	7.00±0.12$_{a}$	89.00±3.61$_{a}$
NGBO3536	26.33±3.93$_{a}$	1.33±0.09$_{a}$	47.00±8.72$_{a}$	18.67±1.76$_{ab}$	62.33±1.45$_{a}$	29.67±5.61$_{a}$	87.33±15.07$_{a}$	1.90±0.15$_{a}$	10.60±0.72$_{bc}$	97.67±2.51$_{ab}$
NGBO3579	22.53±5.63$_{a}$	1.53±0.24$_{a}$	35.67±4.41$_{a}$	14.67±0.88$_{a}$	60.67±12.33$_{a}$	35.33±8.51$_{a}$	95.00±15.31$_{a}$	1.80±0.12$_{a}$	9.40±1.71$_{ab}$	106.33±5.51$_{b}$
NGBO3556	33.63±6.31$_{ab}$	3.17±0.61$_{c}$	54.33±14.11$_{a}$	18.33±5.54$_{ab}$	61.33±0.88$_{a}$	85.67±8.09$_{b}$	213.33±18.56$_{b}$	2.57±0.09$_{b}$	12.70±0.38$_{c}$	98.00±7.94$_{ab}$
NGBO2653	34.50±4.29$_{ab}$	2.83±0.20$_{bc}$	49.33±7.06$_{a}$	19.67±2.96$_{ab}$	59.67±0.33$_{a}$	81.33±8.41$_{b}$	203.33±12.02$_{b}$	2.27±0.19$_{ab}$	11.67±0.63$_{bc}$	101.00±9.64$_{ab}$
GM	31.87±2.54	2.15±0.23	54.80±6.00	20.2±1.89	60.33±0.69	58.87±6.79	154.20±15.83	2.12±0.09	10.27±0.63	98.40±7.96

Mean values followed by similar superscripts letter(s) within a column do not significantly different from one another at P≤ 0.05 according to Duncan's Multiple Range Test (DMRT). GM: Grand mean; PH: Plant height: INL: Internode length; NL: Number of leaves; NB: Number of branches; DTF: Days to flowering; NPP: Number of pods per plant; SYP: Seed yield per plant; PWT: Pod weight; NDM: Days to maturity; SW:100-Seed weight.

3.3 Estimate of Genetic Parameters

Table 4 presents the estimates of genotypic and phenotypic variances, genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (H^2B), and genetic advance as a percentage of the mean (GAM) for the traits evaluated. The results revealed high GAM values for most of the studied traits, indicating substantial potential for genetic improvement through selection. However, days to flowering and days to maturity exhibited moderate GAM values of 10.11% and 18.51%, respectively, suggesting that these traits are relatively less influenced by additive gene effects and may respond more slowly to selection. Traits such as plant height (20.59%, 30.08%), internode length (33.78%, 44.50%), number of leaves (31.51%, 43.05%), number of branches (22.63%, 36.03%), number of pods per plant (42.12%, 46.57%), seed yield per plant (36.77%, 42.14%), and 100-seed weight (20.05%, 24.01%) exhibited high GCV and PCV values (>20%), indicating substantial genetic variability among accessions. Pod weight showed moderate GCV and PCV (11.07%, 19.44%), while days to flowering (1.25%, 4.79%) and days to maturity (4.90%, 8.66%) displayed relatively low values, suggesting limited variability for these traits.

Table 4: Estimates of genetic parameters of quantitative traits among soybean accessions evaluated under field conditions

Traits	GM	GV	PV	GCV (%)	PCV (%)	H^2B (%)	GA	GAM (%)
PH	31.87	43.06	91.89	20.59	30.08	46.86	20.71	64.99
INL	2.15	0.53	0.92	33.78	44.50	57.61	3.16	146.87
NL	54.80	298.22	556.50	31.51	43.05	53.59	49.70	90.69
NB	20.20	20.90	52.97	22.63	36.03	39.46	15.81	78.24
DTF	60.33	0.57	8.37	1.25	4.79	6.77	6.10	10.11
NPP	58.87	614.72	751.67	42.12	46.57	81.78	58.16	98.80
SYP	154.20	3215.00	4222.60	36.77	42.14	76.14	135.43	87.83
PWT	2.12	0.06	0.17	11.07	19.44	32.46	1.52	71.58
SW	10.27	4.24	6.08	20.05	24.01	69.73	6.52	63.45
NDM	98.40	23.20	72.67	4.90	8.66	31.93	18.22	18.51

GM: General mean; GV: Genotypic variance; PV: Phenotypic variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; H^2B: Heritability; GA: Genetic advance; GAM: Genetic advance as percent over mean.
PH: Plant height: INL: Internode length; NL: Number of leaf; NB: Number of branches; DTF: Days to flowering; NPP: Number of pods per plant; SYP: Seed yield per plant; PWT: Pod weight; NDM: Days to maturity; SW: 100-Seed weight.

According to [26], the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are classified as low (0–10%), moderate (10–20%), and high (above 20%). The genetic parameter estimates from this study revealed considerable variability across all traits, with PCV values consistently higher than GCV, indicating environmental influence on phenotypic expression. Similar observations were made by [27]. The largest difference between PCV and GCV occurred in internode length, suggesting a strong environmental effect on this trait, while pod weight showed moderate variability and days to flowering exhibited the lowest values for both parameters, in agreement with [6].

Heritability in the broad sense (H^2B) quantifies the proportion of total phenotypic variance attributable to genetic factors, thereby indicating the degree of genetic control over a given trait. It serves as a critical parameter for identifying and selecting superior genotypes, particularly among homozygous lines. According to [25], heritability can be classified as low (0–30%), moderate (30–60%), and high (>60%), while [13] categorized genetic advance as a percentage of the mean (GAM) as low (0–10%), moderate (10–20%), and high (>20%). In the present study, number of pods per plant, seed yield per plant, and 100-seed weight exhibited high heritability coupled with high GAM, suggesting that these traits are largely governed by additive gene action and can be effectively improved through simple selection methods. Conversely, days to flowering exhibited the lowest heritability and GAM, indicating a stronger environmental influence on its phenotypic expression and limited genetic gain through selection.

3.4. Pearson's Correlation Analysis

The Pearson correlation coefficients among the quantitative traits are presented in Table 5. Plant height exhibited highly significant positive correlations with the number of leaves (r = 0.83**), number of branches (r = 0.80**), number of pods per plant (r = 0.66**), and seed yield per plant (r = 0.69**), as well as a significant positive correlation with pod weight (r = 0.57*). In contrast, plant height showed a significant negative correlation with days to maturity (r = –0.53*).

Internode length was positively and significantly correlated with the number of pods per plant (r = 0.87**), seed yield per plant (r = 0.86**), and pod weight (r = 0.77**). The number of leaves also exhibited a strong positive correlation with the number of branches (r = 0.94**), while both traits were negatively associated with days to maturity (r = –0.65**). Furthermore, the number of pods per plant showed very strong positive associations with both seed yield per plant (r = 0.98**) and 100-seed weight (r = 0.88**), indicating that these traits are reliable predictors of yield performance among the soybean accessions.The Pearson correlation coefficients among the quantitative traits are presented in Table 5. Plant height exhibited highly significant positive correlations with the number of leaves (r = 0.83**), number of branches (r = 0.80**), number of pods per plant (r = 0.66**), and seed yield per plant (r = 0.69**), as well as a significant positive correlation with pod weight (r = 0.57*). In contrast, plant height showed a significant negative correlation with days to maturity (r = –0.53*).

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Similarly, internode length exhibited strong positive and significant correlations with number of pods per plant (r = 0.87**), seed yield per plant (r = 0.86**), and pod weight (r = 0.77**), indicating its importance as a yield-contributing trait. The number of leaves was strongly and positively correlated with the number of branches (r = 0.94**), whereas both traits were negatively associated with days to maturity (r = –0.65**), implying that vigorous vegetative growth may shorten the crop's maturation period.

Furthermore, the number of pods per plant displayed exceptionally strong positive associations with both seed yield per plant (r = 0.98**) and 100-seed weight (r = 0.88**). These relationships highlight that pod number, seed yield, and seed weight are reliable indicators of yield potential and can serve as effective selection criteria in soybean breeding programs.

Table 5: Pearson's correlation for quantitative traits among soybean accessions evaluated under field conditions

Traits	PH	INL	NL	NB	DTF	NPP	SYP	PWT	SW	NDM
PH	1	0.501	0.830**	0.795**	-0.366	0.662**	0.691**	0.568*	0.077	-0.533*
INL		1	0.246	0.161	-0.197	0.868**	0.859**	0.769**	0.611*	-0.112
NL			1	0.943**	-0.335	0.470	0.538*	0.461	-0.231	-0.654**
NB				1	-0.395	0.407	0.472	0.365	-0.269	-0.648**
DTF					1	-0.251	-0.254	0.078	0.240	0.160
NPP						1	0.981**	0.876**	0.483	-0.180
SYP							1	0.875**	0.398	-0.274
PWT								1	0.582*	-0.308
SW									1	0.276
NDM										1.000

***: Significant at P ≤ 0.05; **: Significant at P ≤ 0.01.**

PH: Plant height: INL: Internode length; NL: Number of leaves; NB: Number of branches; DTF: Days to first flowering; NPP: Number of pods per plant; SYP: Seed yield per plant; PWT: Pod weight; NDM: Days to maturity; SW: 100-Seed weight.

Correlation analysis reveals the nature and magnitude of associations among traits and serves as a valuable tool in breeding programs, as noted by [3]. Selection for positively correlated traits can result in simultaneous improvement of related traits, whereas selection for negatively correlated traits may hinder progress. In this study, plant height exhibited strong positive associations with the number of leaves, branches, and pods per plant, suggesting that taller plants generally produce more foliage and pods. Additionally, the number of pods per plant showed a strong positive correlation with seed yield per plant, indicating that increased pod production directly contributes to higher seed yield. Conversely, a negative correlation between the number of branches and days to flowering suggests that genotypes with more branches tend to flower earlier.

5.0 Conclusion

The results of this study revealed that the number of pods per plant, seed yield per plant, and 100-seed weight exhibited high heritability coupled with high genetic advance as a percentage of the mean (GAM). This combination suggests that these traits are predominantly governed by additive gene effects, making them highly responsive to selection in breeding programs. The strong genetic control further implies minimal environmental influence, thereby enhancing the reliability of selection based on phenotypic performance, the positive and significant correlation between the number of pods per plant and seed yield per plant underscores their importance as key selection criteria for yield improvement. Their responsiveness to selection provides soybean breeders with strategic opportunities to enhance productivity efficiently. Strengthening these yield-related traits could improve overall soybean performance and contribute to sustainable production systems, particularly amid the challenges of climate change and increasing global food demand.

References

1. Aditya J.P., Pushpendra B. and Anuradha B. (2011). Genetic variability, heritability and character association for yield and component characters in soybean (*Glycine max* (L.) Merrill). *Journal of Central European Agriculture*, 12(1):27-34.

2. Agong, S.G., Ayiecho, P.O. and Arap Sang, W.K. (2001). Genetic variability and correlation studies in soybean (*Glycine max* (L.) Merrill) germplasm. *African Crop Science Journal, 9*(4): 599-605.
3. Ajayi, A.T., Adesoye, A.I. and Adekoya, A.E. (2014). Genetic variability, heritability and genetic advance estimates in cowpea breeding lines (*Vigna unguiculata* L. Walp). *Journal of Agricultural Sciences*, 62(4): 279-293.
4. Aravin, A.A. (2006). Variability assessment in quantitative traits of soybean. *Plant Breeding Review*, 26(2): 89-107.
5. Azevedo, R.A., Lima, V.A. and Rombola, A.D. (2019). Variability and correlations among agronomic traits of soybean. *Plant Breeding Journal*, 150(1): 112-120.
6. Baraska, V.S., Reddy, K.R.B. and Ghosh, M.K. (2014). Genetic variability, heritability, and genetic advance in soybean. *Journal of Agronomy and Crop Science*, 200(4): 249-258.
7. Danshiell, F. (1993). Genetic variability in soybean lines: A review. *Soybean Research Journal*, 15(3): 234-248.
8. FAO. (2012). The state of food and agriculture: Investing in food security. Food and Agriculture Organization of the United Nations. http://www.fao.org/docrep/016/i3028e/i3028e.pdf.
9. FAO. (2020). Food and Agriculture Organization. Soybean production statistics 2018.
10. Fehr, W. R., Caviness, C. E., Burmood, D. T., & Pennington, J. S. (1987). Stage of development descriptions for soybeans, *Glycine max* (L.) Merrill. *Crop Science, 17*(6): 913-915.
11. Govindaraj, M., Vetriventhan, M. and Srinivasan, M. (2010). Nutritional and genetic variability in soybean varieties. *Journal of Food Legumes*, 23(2): 106-111.
12. IITA. (2010). Annual report on soybean research. *International Institute of Tropical Agriculture*.
13. Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimate of genetic and environmental variability in soybean. *Agronomy Journal*, 47(7): 314-318.
14. Jandong, E. A., Uguru, M. I. and Okechukwu, E. C. (2020). Genetic variability, heritability and expected genetic advance in soybean (*Glycine max* (L.) Merrill) accessions. *Journal of Plant Breeding and Crop Science, 12*(2), 45-53.
15. Laswai, H.S., Fuchs, J. and Manya, A. (2005). Soybean: Seed composition and its prospects in Tanzania. *African Journal of Agricultural Research*, 1(1): 20-26.
16. Liu, K. (2017). Nutritional composition of soybeans: A comprehensive review. *Journal of Nutritional Science*, 6: 1-18.
17. Mahamood, Y., Adetunji, M.O. and Daramola, O.A. (2009). Soybean as a strategic crop for food security in developing countries: A review. *African Journal of Food Science*, 3(9): 234-239.
18. Maletsema Alina Mofokeng 2021. Genetic variability, heritability and genetic advance of soybean (Glycine max) genotypes based on yield and yield-related traits. *Australian Journal of Crop Science*, 15(12):1427-1434.
19. Malik M.F.A., Ashraf M., Qureshi A.S. and Khan, M.R 2011. Investigation and comparison of some morphological traits of the soybean populations using cluster analysis. *Pakistan Journal of Botany*, 43(2):1249-1255.
20. Maestri, M., Salerno, G.L. and Melchiorre, C. (1998). Agronomic performance and genetic variability in soybean. *Field Crops Research*, 57(1): 157-165.
21. Neelima G., Mehtre S.P, Narkhede G.W (2018) Genetic Variability, heritability and genetic advance in soybean. *International Journal of Pure Applied Bioscience*, 6(2):1011-1017.
22. Osekita, O.S. and Atimokhale D. Genetic diversity studies for assessment of variability in okra (*Abelmoschus esculentus*). *International Journal of Science Letters*. 6:2, 1-14.
23. Rao, P.S., Reddy, K. R. B. and Naik, B. (1998). Genetic assessment of soybean accessions. *Journal of Oilseed Research*, 15(1): 7-11.
24. Ravindra KJ, Arunabh J, Hem RC, Abhay D, Champa LK (2017) Study on genetic variability, heritability and genetic advance in soybean [Glycine max (L.) Merrill]. *Legume Resources*, (41):532-536
25. Robinson, H.F., Comstock, R.E. and Harvey, G.F. (1949). Estimation of heritability and the degrees of dominance in corn. *Agronomy Journal*, 41(7): 353-359.
26. Sivasubramanian, S. and Menon, M. (1973). Genetic variability in rice varieties. *Indian Journal of Genetics and Plant Breeding*, 33(2): 241-249.
27. Zida, A., Bognounou, F. and Gahouma, H. (2021). Evaluation of genetic variability in soybean genotypes. *African Journal of Agricultural Research*, 16(3): 243-250.