International Journal of Plant & Soil Science

Volume 35, Issue 22, Page 9-17, 2023; Article no.IJPSS.108908
ISSN: 2320-7035

Comprehensive Genetic Analysis of Yield and Yield-Related Traits in Soybean Germplasms for Enhanced Crop Improvement

Bhumika Singh Lodhi [a*], Pramod Kumar [b], Monika Chouhan [b], Alok Rajpoot [c] and Amit Jha [b*]

[a] *Department of Genetics and Plant Breeding, College of Agriculture, JNKVV, Jabalpur- 482004 (M.P.), India.*
[b] *Department of Agronomy, College of Agriculture, JNKVV, Jabalpur- 482004 (M.P.), India.*
[c] *Department of Maths & Agriculture Statistics, College of Agriculture, JNKVV, Jabalpur- 482004 (M.P.), India.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJPSS/2023/v35i224109

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/108908

Original Research Article

Received: 12/09/2023
Accepted: 15/11/2023
Published: 15/11/2023

ABSTRACT

In the context of escalating global food demands, this study provides a comprehensive genetic analysis of soybean (*Glycine max* (L.) Merrill), focusing on 13 distinct traits that contribute to yield and quality. We investigated four phenological traits marking critical growth phases and nine quantitative traits, utilizing an analysis of variance to highlight the significant genetic influences on these variables. The study reveals that phenotypic and genotypic variances, when measured through the coefficient of variability, present a deeper understanding of soybean variability than

---

*Corresponding author: E-mail: bhumikasinghlodhi16@gmail.com, amitagcrewa@rediffmail.com;

variance analysis alone. This is underscored by our findings where phenotypic coefficient of variance (PCV) values consistently exceeded genotypic coefficient of variance (GCV) across all traits, indicating the substantial effect of genotype-environment interactions. The highest GCV was observed in seed yield and biological yield, indicating these traits' potential for genetic improvement. Heritability studies showed days to physiological maturity as the trait with the highest inheritability, suggesting its stability across environmental conditions. Moreover, the significant genetic advance as a percentage of the mean for grain yield and biological yield underscores the potential for considerable gains through selective breeding. By identifying traits governed by additive genes, such as the weight of a hundred seeds and grain yield, our study indicates promising avenues for future soybean breeding programs to enhance these characteristics.

Keywords: Glycine max (L.) merrill; Genetic variability; heritability; yield traits; genotypic coefficient of variance; phenotypic coefficient of variance.

1. INTRODUCTION

Soybean scientifically referred to as Glycine max (L.) Merrill, has been a subject of extensive research over the years due to its immense agricultural and nutritional significance. Widely cultivated in diverse regions ranging from East and South East Asia to parts of North America, this legume stands out not only as a major source of protein and oil but also for its versatile applications in food, feed, and medicinal products [1,2]. The genetic foundations of soybean have piqued the interest of researchers, aiming to understand the intricate mechanisms that dictate its growth, yield, and adaptability [3,4].

Recent studies have emphasized the importance of examining the genetic parameters of soybean germplasm, focusing on yield-contributing traits to optimize its cultivation and harness its full potential [5]. Variability, both phenotypic and genotypic, serves as a bedrock for breeding programs, offering insights into the inherent differences within and between the populations. Factors such as the coefficient of variance, heritability in a broad sense, and genetic advance play pivotal roles in steering breeding strategies and predicting the success of selection methods [6].

In this research endeavor, we delve deep into the genetic realm of soybean by scrutinizing 13 distinct traits. These encompass four phenological attributes, marking key growth phases, and nine quantitative characteristics, which collectively influence the overall yield and quality of the crop. By understanding the genetic interplay behind these traits, we aim to pave the way for informed agricultural practices and innovative breeding techniques that can cater to the ever-evolving global food demands.

2. MATERIALS AND METHODS

During the 2022 kharif season, research was conducted at the Dryland Agriculture Research Center, part of the College of Agriculture in Indore, Madhya Pradesh. This study rigorously evaluated 63 genotypes, juxtaposing them with three local benchmarks: JS 20 98, JS 20 116, and JS 20 34.

For the methodology, a randomized design was chosen with two replications for every genotype. Each was planted arranged in two rows, with plant to plant and row to row spacings of 10 cm and 45 cm, respectively. To ensure unbiased results, data were taken from five randomly picked plants in each section, examining attributes such as the number of primary branches, height, pod quantity and weight, yield, and the weight of a batch of 100 seeds. Comprehensive analyses were also performed on the entire plot, aiming to capture essential metrics. These included the timeline to achieve 50% flowering, onset of pod formation, the midpoint of podding, the point of physiological maturity, and key yield figures (both biological and grain) in kg/ha. Additionally, the harvest index was assessed to provide a holistic view of the yield efficiency.

2.1 Statistical Analysis

In examining quantitative attributes, we employed a statistical approach rooted in the Randomized Complete Block design, as introduced by Cochran and Cox in 1950. The assessment of treatment significance involved computing a meaningful distinction, following the methodology outlined by Fisher and Yates in 1963. This process is encapsulated by the formula:

$$Y_{ij} = \mu + a_i + b_j + e_{ij}$$

Parameters of genetic variability: Genotypic and phenotypic coefficients of variation (GCV and PCV) were computed using Burton's method from 1952. The formulas for PCV and GCV are as follows:

Phenotypic coefficient of variation (PCV)

Since, $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

$$\mathrm{PCV} = \left(\frac{\sigma_p}{\bar{X}}\right) \times 100$$

Where, $\sigma_p = \sqrt{\sigma_p^2}$

Genotypic coefficient of variation (GCV)

$$\mathrm{GCV} = \left(\frac{\sigma_g}{\bar{X}}\right) \times 100$$

Where, $\sigma_g = \sqrt{\sigma_g^2}$

Where,
σ_p^2 = Phenotypic variance
σ_p = Phenotypic standard deviation
σ_g^2 = Genotypic variance
σ_g = Genotypic standard deviation
σ_e^2 = Environmental variance
$\bar{X}$ = General Mean

Heritability: Heritability, a measure of genotypic variance in relation to total phenotypic variance, is calculated using Hanson et al.'s (1956) formula:

$$\text{Heritability } (h^2 bs\ \%) = \frac{\sigma_g^2}{\sigma_g^2} \times 100$$

Where,
h^2 = Heritability in broad sense

Genetic advance: Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Expected genetic advance was calculated by the method suggested by Johnson *et al*. (1955).

$$\mathrm{GA} = K.\sigma_p.h^2\ (b)$$

Where, GA = Genetic advance

K = Constant (Standard selection differential) having the value of 2.06 at 5% of selection intensity.

Genetic advance as percent of mean: Genetic Advance, indicating the improvement in mean genotypic value over the parental population, was calculated using the method suggested by Johnson et al. (1955):

$$\frac{\mathrm{GA}}{\text{Grand mean}} \times 100$$

The range of genetic advance as a percentage of mean was categorized as low (<10%), moderate (10-20%), and high (>20%) following Johnson et al. (1955).

The comparison between PCV and GCV often reveals a greater PCV, indicating environmental influence on soybean genotype performance. The PCV and GCV estimates were classified as low (<10%), moderate (10-20%), or high (>20%) based on the criteria suggested by Sivasubramanian S. and Madhavamenon P. (1973). Additionally, Heritability in broad sense was calculated and classified into three groups: high (>60%), medium (30% to 60%), and low (<30%), as recommended by Robinson et al. (1949).

3. RESULTS AND DISCUSSION

The analysis of variance (refer to table no 1.) highlights the significant impact of genetic factors on all the variables under investigation. These variables include critical parameters such as the time to reach 50% flowering, days to initiate pod development, days to achieve 50% podding, days to physiological maturity, the count of primary branches per plant, plant height (measured in centimeters), pods per plant, pod weight per plant (in grams), grain yield per plant (in grams), 100-seed weight, biological yield (measured in kilograms per hectare), harvest index, and grain yield (in kilograms per hectare) [7,8].

In 1950, Vavilov argued that the extent of variation is directly linked to improvements achieved through selective breeding, particularly in relation to specific traits. Given the evident diversity within the current population being studied, there is a compelling opportunity for continuous advancements in crop development.

The analysis of variance might not fully capture the existing variability, so to assess this more effectively, one should consider examining both phenotypic and genotypic variances via the coefficient of variability.

Table 1. Analysis of Variance for yield and its component traits in Soybean genotypes

Source of Variation	DF	Mean Sum of Squares												
		Days to 50% Flowering	**Days to Pod Initiation**	**Days to 50% Podding**	**Days to Physio-Logical Maturity**	**No. of Primary Branches per Plant**	**Plant Height**	**No. of Pods per Plant**	**Pod Weight per Plant**	**Grain Yield per Plant**	**Hundred Seed Weight**	**Biological Yield (kg/ ha)**	**Harvest Index**	**Grain Yield (kg/ ha)**
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
Replication	1	95.03	44.92	96.73	114.61	16.31	366.86	19442.45	1374.56	406.70	0.55	1555.6	163.82	66.67
Genotype	65	37.03**	37.44**	52.58**	144.42**	1.85*	240.82**	1697.57**	143.65**	74.87**	16.70**	1777.8**	355.16**	262.9**
Error	65	3.26	3.99	5.18	10.43	0.99	61.63	505.33	58.61	25.91	2.55	555.6	150.14	33.33
SEm±		1.27	1.41	1.61	2.28	0.70	5.551	15.89	5.41	3.59	1.13	999.9	8.66	248.14
CD at 0.05		3.61	3.99	4.54	6.45	1.98	15.68	44.89	15.28	10.16	3.18	2888.8	24.47	703.7

** Significant at 5% level and ** Significant at 1% level of probability respectively.*

Table 2. Genetic Parameters for yield trait and contributing traits in soybean genotypes

Traits	**Days to 50% Flowering**	**Days to Pod Initiation**	**Days to 50% Podding**	**Days to Physiological Maturity**	**No. of Primary Branches per Plant**	**Plant Height**	**No. of Pods per Plant**	**Pod Weight per Plant**	**Grain Yield per Plant**	**Hundred Seed Weight**	**Biological Yield (kg/ha)**	**Harvest Index**	**Grain Yield (kg/ha)**
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
Mean	49.591	56.219	60.598	102.583	4.527	39.251	78.142	23.783	14.178	11.921	3363.12	36.64	1168.61
Max.	67.5	73	77.5	119.5	7.3	71.115	170.3	50.6	30.2	22	8870.4	56.59	3925.9
Min.	41	46.5	50.5	88	2.6	23.49	22.5	8.0	3.2	6.5	962.96	17.29	333.3
GCV %	8.286	7.275	8.034	7.979	14.539	24.115	31.245	27.418	34.899	22.313	45.839	26.022	56.018
PCV %	9.051	8.097	8.869	8.577	26.355	31.329	42.471	42.283	50.068	26.027	63.545	40.852	63.689
h^2 (bs)	83.81	80.73	82.06	86.53	30.44	59.25	54.12	42.05	48.59	73.5	52.04	40.57	77.36
GA	7.75	7.57	9.08	15.68	0.75	15.01	37.00	8.71	7.10	4.69	0.604	34.14	0.32
GA as % of Mean	15.626	13.465	14.993	15.289	16.524	38.237	47.351	36.626	50.111	39.406	68.124	34.145	101.489

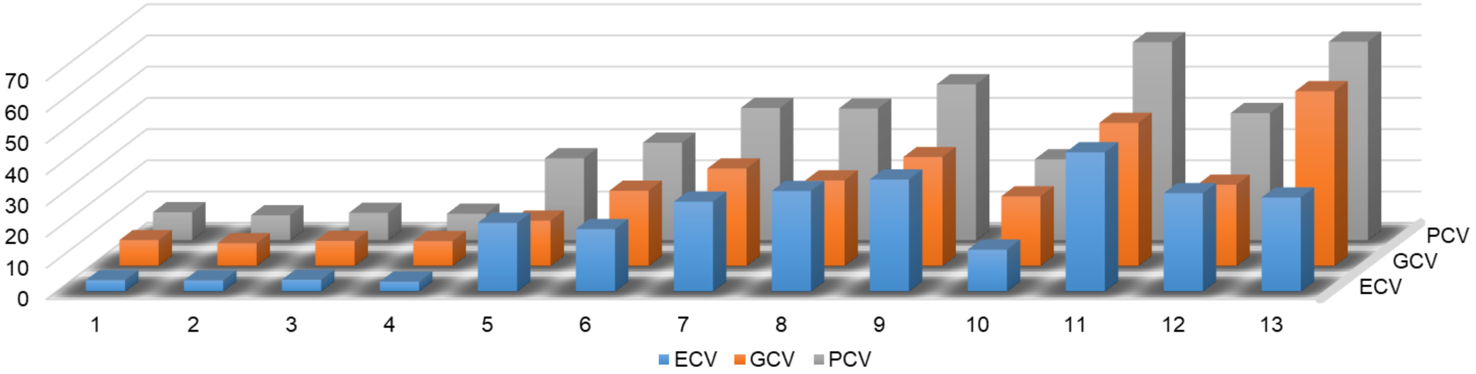

Fig. 1. Visual Analysis of PCV, GCV, and ECV in Yield-Related Traits of Soybean Genotypes

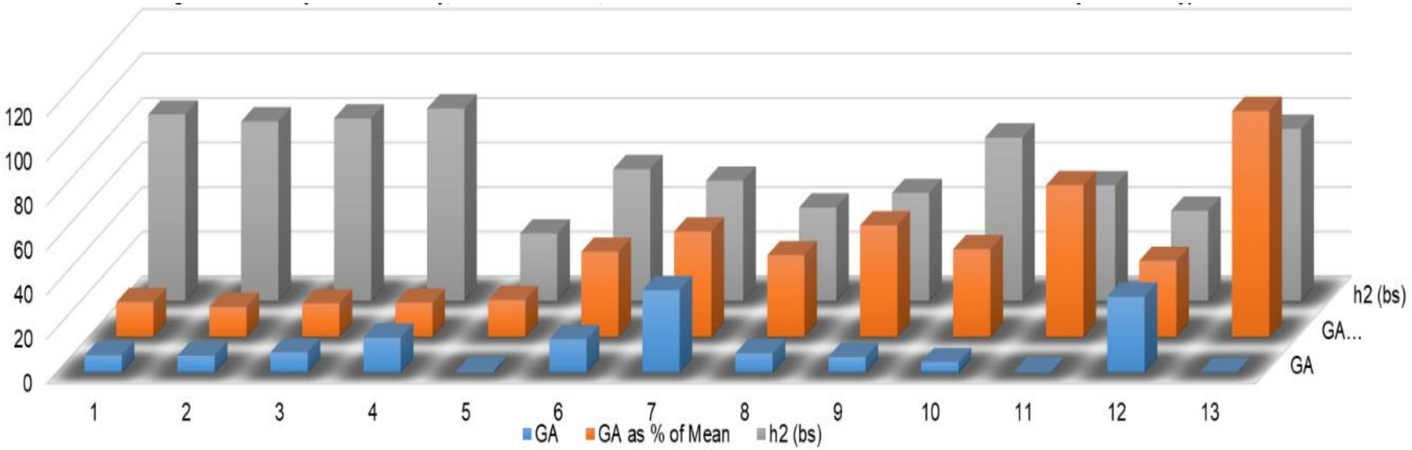

Fig. 2. Visual Analysis of Heritability, Genetic Advance, and Relative Genetic Advance in Yield-Related Traits of Soybean Genotypes

Genotypic, environmental and phenotypic coefficient of variance (Table no.2): The comparison between genotypic (GCV) and phenotypic (PCV) variability coefficients revealed that PCV values consistently exceeded GCV for all observed traits (Fig. 1). This disparity can be attributed to the combined effects of genotype-environment interactions and other external factors that influence trait expression, however the fact that there was a smaller difference between these two estimations for all the characters indicates that they were less affected by environmental influences.

The GCV estimates revealed the highest values for seed yield (kg/ha) at 56.02%, followed by biological yield (kg/ha) at 45.84%. Other notable traits included seed yield per plant (34.89%), number of pods per plant (31.24%), weight of pods per plant (27.42%), harvest index (26.02%), plant height (24.11%), and weight of a hundred seeds (22.31%). Only the number of primary branches per plant registered a moderate GCV value of 14.54%. Meanwhile, traits such as days to 50% flowering (8.28%), days to reach 50% podding (8.03%), days until physiological maturity (7.97%), and days to initiate podding (7.27%) showed the lowest GCV values. In comparison, [9] also observed a high value for the number of pods per plant. [10] documented high values for seed yield, harvest index, and number of pods per plant. On the other hand, [11,12] reported low GCV values for days to 50% flowering and days to physiological maturity, respectively.

The data revealed that the ECV values were generally lower than GCV for the primary traits, suggesting a minimal environmental impact on the expression of the observed traits. The highest ECV was noted for biological yield (kg/ha) at 44.60%, followed by metrics such as seed yield per plant (35.90%), weight of pods per plant (32.18%), harvest index (31.49%), seed yield (kg/ha) (30.11%), and number of pods per plant (28.76%), including the number of primary branches. Intermediate ECV levels were found for traits like plant height (20%) and weight of a hundred seeds (13.39%). Conversely, the lowest ECV values were seen for attributes like days to reach podding (3.75%), days to achieve days to 50% flowering (3.64%), days until pod formation begins (3.55%), and days to reach physiological maturity (3.14%).

The trend observed in PCV estimates largely mirrors that of GCV. Elevated PCV values were identified for seed yield (kg/ha) at 63.56%, closely followed by biological yield (kg/ha) at 63.54%, seed yield per individual plant (50.06%), pod count per plant (42.47%), weight of pods for each plant (42.28%), the harvest index (40.85%), the stature of the plant (31.32%), primary branch count per plant (26.35%), and weight for a set of a hundred seeds (26.02%). On the other hand, diminished PCV values were associated with attributes like the span to days to 50% flowering (9.05%), duration until days to 50% podding (8.86%), time to physiological maturation (8.57%), and the interval leading to pod emergence (8.09%). Comparable observations have been noted in studies by [13,14], which highlighted metrics such as plant height, pod count, and grain yield. [15] also drew parallels for attributes like biological yield, grain yield per plant, pod count, and primary branch quantity. Similar results were reported by [16,17].

Heritability and Genetic Advance as percentage of mean (Fig 2): Among the traits studied, days to physiological maturity topped the list with a heritability of 86.53%. This was closely followed by durations to achieve days to 50% flowering (83.81%), days to 50% pod initiation (82.06%), pod emergence (80.73%), grain yield (kg/ha) at 77.36%, and weight of a hundred seeds at 73.5%. In terms of moderate heritability, the height of the plant stood out with a value of 59.25%. Other traits in this bracket included pod count per plant (54.12%), overall biological yield (52.04%), grain yield for individual plants (48.59%), weight of pods on a single plant (42.05%), the harvest index (40.57%), and the primary branch count on each plant (30.44%). These findings align with those of [18,19].

Broad-sense heritability encompasses the entire genetic variation, factoring in both additive and non-additive variances. Consequently, while traits with high heritability remain largely uninfluenced by external environmental factors, the pursuit of enhancing such characteristics might not always yield beneficial results.

Past research, including work by [20], documented the highest heritability for traits such as days to 50 percent flowering and days to physiological maturity, while moderate heritability was observed for hundred seed weight and plant height. Similarly, [21’22], and [23] also reported heritability observations for days to reach 50 percent flowering.

The most significant genetic advance, relative to the mean, was evident in grain yield (kg/ha), with a notable 101.489% increase. This was succeeded by enhancements in biological yield (68.124%), yield per individual plant (50.111%), pod count per plant (47.351%), weight of a set of a hundred seeds (39.406%), plant stature (38.237%), pod weight for each plant (36.626%), and the harvest index (34.145%).

Genetic advance of a moderate scale, relative to the mean, was observed in traits such as primary branch count per plant (16.52%), span to days to 50% flowering (15.62%), time until physiological maturity (15.28%), duration to 50 percent podding (14.99%), and the interval leading to pod emergence (13.46%). Traits exhibiting substantial genetic progression in relation to their mean are typically governed by additive genes. The refinement of such traits, as delineated above, through selection would be productive.

Forecasts of potential gains from selection are often better informed by heritability estimates that consider genetic progression relative to the average. The enhancement of characteristics, specifically the weight of a hundred seeds and grain yield (kg/ha), which both show high heritability and significant genetic advance, points to the influence of additive genes. Thus, the focused selection for these traits promises fruitful improvements.

The current observations resonate with previous studies. Specifically, the findings related to the weight of a hundred seeds have been echoed by researchers like [24, 25] and [26]. Similarly, [27] found parallels in grain yield (kg/ha). Both [28,29] highlighted congruent results for the weight of a hundred seeds and grain yield (kg/ha), suggesting the influence of additive gene action.

4. CONCLUSION

In this comprehensive study, significant genetic influences on a variety of soybean traits were observed, reinforcing the critical role of genetics in crop yield and development. The genetic variations, encapsulated through metrics like GCV, PCV, and ECV, highlighted the potential for targeted breeding, especially for traits exhibiting high heritability and substantial genetic advancement relative to their mean. Notably, days to physiological maturity, grain yield, and the weight of a hundred seeds emerged as prominent traits governed by additive genes, underpinning their potential for targeted enhancement. Our findings align with previous research, underscoring the consistency of these genetic influences across different studies. The observed genetic diversity in the studied population offers promising avenues for soybean crop enhancement through selective breeding. Harnessing this genetic potential can drive future advancements, paving the way for more resilient and productive soybean varieties.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Jha AK, Soni M. Weed management by sowing methods and herbicides in soybean. Indian Journal of Weed Science. 2013;45(4):250-252.
2. Yadav PS, Kewat ML, Jha AK, Hemalatha K, Verma B. Effect of sowing management and herbicides on the weed dynamics of berseem (*Trifolium alexandrinum*). Pharma Innovation. 2023;12(2):2845-2848.
3. Pahade S, Jha AK, Verma B, Meshram RK, Toppo O, Shrivastava A. Efficacy of sulfentrazone 39.6% and pendimethalin as a pre emergence application against weed spectrum of soybean (*Glycine max* L. Merrill). International Journal of Plant & Soil Science. 2023;35(12):51-58.
4. Yadav PS, Kewat ML, Jha AK, Sahu MP, Verma B and Toppo Oscar. Floristic composition of weeds as influence by sowing time and herbicides in berseem. Eco. Env. & Cons. 2023; 29 (3): 64-68.
5. Jha AK, Yadav PS, Shrivastava A, Upadhyay AK, Sekhawat LS, Verma B, Sahu MP. Effect of nutrient management practices on productivity of perennial grasses under high moisture condition. AMA, Agricultural Mechanization in Asia, Africa and Latin America. 2023;54(3): 12283-12288.
6. Yadav PK, Sikarwar RS, Verma B, Tiwari S, Shrivastava DK. Genetic divergence for grain yield and its components in bread wheat (*Triticum aestivum* L.): Experimental investigation. International Journal of Environment and Climate Change. 2023;13(5):340-348.
7. Verma Badal, Bhan Manish, Jha AK and Porwal Muskan. Influence of weed management practices on direct-seeded rice grown under rainfed and irrigated

agroecosystems. Environment Conservation Journal. 2023;24(3):240-248.

8. Patel R, Jha AK, Verma B, Porwal M, Toppo O, Raghuwanshi S. Performance of pinoxaden herbicide against complex weed flora in wheat (*Triticum aestivum* L.). International Journal of Environment and Climate Change. 2023; 13(7): 339-345.
9. Chauhan A, Singh K, Kandwal N, Singh P, Reddy BS. Genetic variability studies in early generation lines of Soyabean (*Glycine max* (L.) Merrill.) For yield and its contributing traits. The Pharma Innovation Journal. 2023;12(1):168-172.
10. Joshi D, Pushpendra SK, Adhikari S. Study of genetic parameters in soybean germplasm based on yield and yield contributing traits. International Journal of Current Microbiology and Applied Sciences. 2018;7(1):700-709.
11. Bisht M, Singh K, Bhatt P, Kunduru B, Chourasia K. Studies on variability parameters in early generation of soybean [*Glycine max* (L.) Merrill]. International Journal of Chemical Studies. 2018;6: 208-211.
12. Guleria H, Kumar P, Jyoti B, Kumar A, Paliwal A, Paliwal A. Genetic variability and correlation analysis in soybean (*Glycine max* (L.) Merrill) genotypes. Int. J. Chem. Stud. 2019;7:1928-32.
13. Akram S, Hussain BN, Al Bari MA, Burritt DJ, Hossain MA. Genetic Variability and Association Analysis of Soybean (*Glycine max* (L.) Merrill) for Yield and Yield Attributing Traits. Plant Gene. 2016;7(13):1-11.
14. Aditya JP, Bhartiya P, Bhartiya A. Genetic variability, heritability and character association for yield and component characters in soybean (*G. max* (L.) Merrill). Journal of Central European Agriculture 2011;12(1): 27-34.
15. Kumari S, Meena BL, Sharma SC, Koli NR, Tak Y, Fozdar P. Study on genetic variability parameters in soybean [*Glycine max* (L.) Merrill] genotypes. Journal of Agriculture and Ecology. 2022;14:72-76.
16. Verma Badal, Bhan Manish, Jha AK, Khatoon Shahiba, Raghuwanshi Monika, Bhayal Lalita, Sahu MP, Patel Rajendra and Singh Vikash. Weeds of direct-seeded rice influenced by herbicide mixture. Pharma Innovation. 2022;11(2):1080-1082.
17. Tomar DS, Jha AK, Verma B, Meshram RK, Porwal M, Chouhan M, Rajpoot A. Comparative Efficacy of Different Herbicidal Combinations on Weed Growth and Yield Attributes of Wheat. International Journal of Environment and Climate Change. 2023;13(8): 889-898.
18. Verma Badal, Bhan Manish, Jha AK, Singh Vikash, Patel Rajendra, Sahu MP and Kumar Vijay. Weed management in direct-seeded rice through herbicidal mixtures under diverse agroecosystems. AMA, Agricultural Mechanization in Asia, Africa and Latin America. 2022;53(4): 7299-7306.
19. Yadav PS, Jha AK, Pachauri V, Verma B, Shrivastava A, Chouhan M, Rajpoot A. Oat genotypes response to different nitrogen levels under agro-climatic condition of Kymore Plateau zone of Madhya Pradesh. The Pharma Innovation Journal. 2023;12(4): 2371-2374.
20. Banerjee J, Shrivastava MK, Amrate PK, Singh Y, Upadhyay A, Soni M. Genetic variability and association of yield contributing traits in advanced breeding lines of soybean. Electronic Journal of Plant Breeding. 2022;13(2): 597-607.
21. Reni YP, Rao YK. Genetic variability in soybean [*Glycine max* (L) Merrill]. International Journal of Plant, Animal and Environmental Sciences. 2013;3(4):35-38.
22. Mahbub MM, Rahman MM, Hossain MS, Mahmud F, Kabir MM. Genetic variability, correlation and path analysis for yield and yield components in soybean. American-Eurasian Journal of Agricultural & Environmental Sciences. 2015;15(2): 231-236.
23. Kuswantoro H, Artari R, Rahajeng W, Ginting E, Supeno A. Genetic Variability, Heritability, and Correlation of Some Agronomical Characters of Soybean Varieties. Biosaintifika: Journal of Biology & Biology Education. 2018;10(1):9-15.
24. Baria AR, Akabari VR, Gohil VN. Variability studies for seed yield and its components in soybean. Journal of Genetics, Genomics & Plant Breeding. 2022;6(2):54-59.
25. Kumar S, Kumari V, Kumar V. Genetic variability and character association studies for seed yield and component characters in soybean [*Glycine max* (L.) Merrill] under North-western Himalayas. Legume Research-An International Journal. 2018;43(4).
26. Sonkamble P, Nandanwar RS, Sakhare SB, Jadhav PV, Varghese P. Genetic variability for yield and its component traits in grain and vegetable type soybean. IJCS. 2020;8(6):2287-2290.

27. Sureshrao SS, Singh VJ, Gampala S, Rangare NR. Assessment of genetic variability of the main yield related characters in soybean. International Journal of Food, Agriculture and Veterinary Sciences. 2014;4(2):69-74.
28. Berhanu H, Tesso B, Lule D. Genetic variability and traits associations among soybean Genotypes. Adaptation and Generation of Agricultural Technologie. 2019;26:104.
29. Shruthi K, Siddaraju R, Naveena K, Ramanappa TM, Vishwanath K. Assessment of variability based on morphometric characteristics in the core set of soybean germplasm accessions. Legume Research-An International Journal. 2021;1: 7.

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/108908