

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

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 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. MATERIAL AND METHOD

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.

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)

$$\text{Since, } \sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

$$\text{PCV} = \left(\frac{\sigma_p}{\bar{x}} \right) \times 100$$

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

Genotypic coefficient of variation (GCV)

$$\text{GCV} = \left(\frac{\sigma_g}{\bar{x}} \right) \times 100$$

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

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:

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

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).

$$GA = K \cdot \sigma_p \cdot h^2 \text{ (b)}$$

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):

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

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. RESULT 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	D F	Mean Sum of Squares												
		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
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

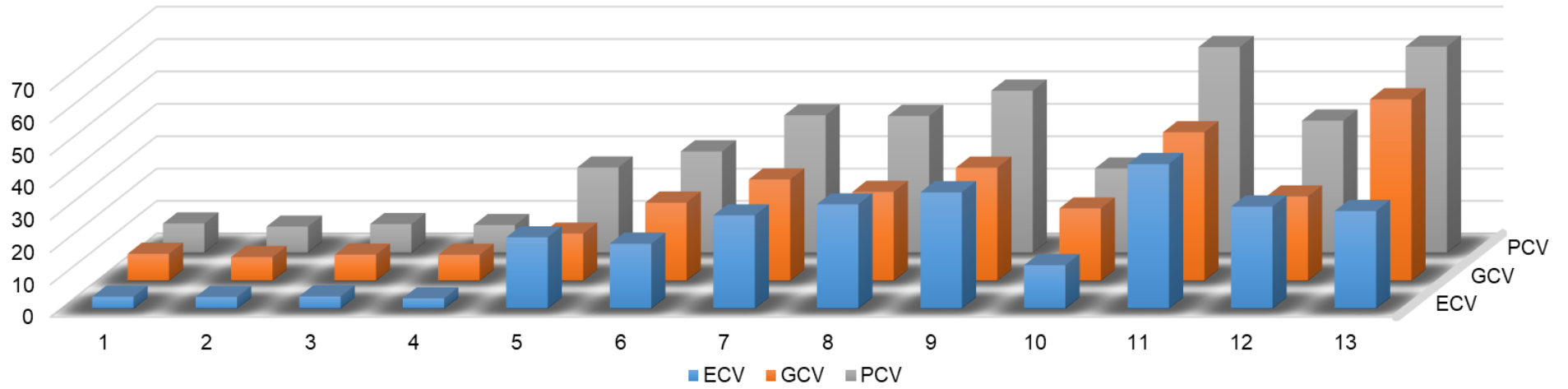
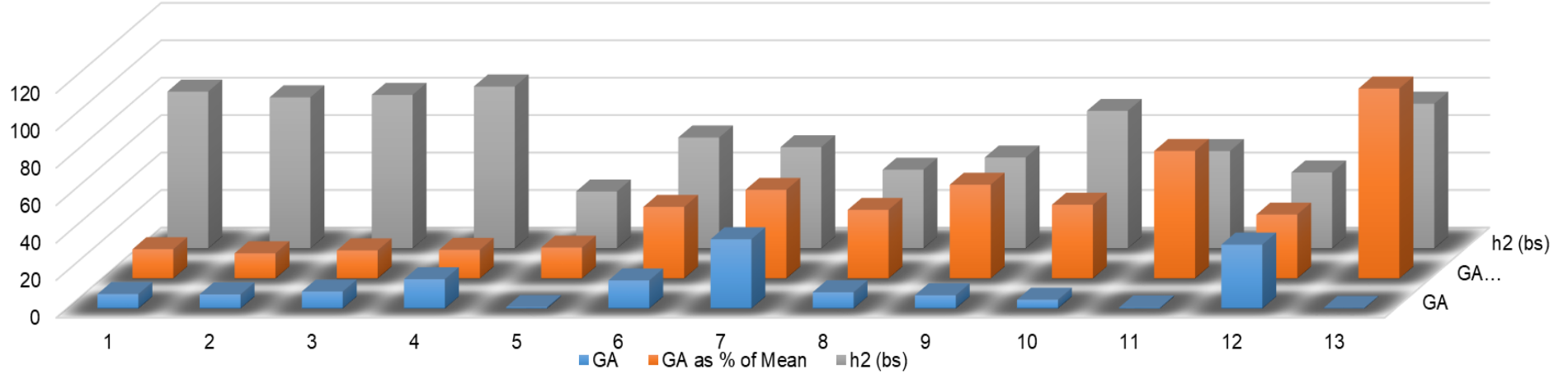


Fig 2 : Visual Analysis of Heritability, Genetic Advance, and Relative Genetic Advance in Yield-Related Traits of Soybean Genotypes



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.

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