

GENETIC VARIABILITY ANALYSIS FOR QUANTITATIVE TRAITS IN SOYBEAN (*Glycine max* (L.) Merrill)

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Abstract

An investigation was undertaken to assess the extent of genetic variability, heritability, and genetic advance for ten quantitative traits in twenty-three soybean (*Glycine max* (L.) Merrill) genotypes evaluated in a Randomized Block Design (RBD) with three replications. Analysis of variance revealed highly significant differences among genotypes for all the traits studied ($p < 0.01$), indicating the presence of substantial genetic variability in the experimental material. The genotypic coefficient of variation (GCV) ranged from 7.64% (days to maturity) to 114.42% (seed yield per plant), while the phenotypic coefficient of variation (PCV) ranged from 9.66% to 115.24% for the same traits. Phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all traits, though the difference was narrow for most characters, suggesting relatively low environmental influence on trait expression. Broad-sense heritability was high (>60%) for all ten traits, ranging from 62.52% (days to maturity) to 99.42% (number of pods per plant). High heritability coupled with high genetic advance as percent of mean (ranging up to 234.02% for seed yield per plant) was recorded for number of pods per plant, seed yield per plant, biological yield per plant, and harvest index, indicating that these traits are governed predominantly by additive gene action and would respond favourably to direct phenotypic selection. Days to maturity recorded the lowest estimates of GCV (7.64%), PCV (9.66%), and genetic advance as percent of mean (12.44%), indicating that this trait is less amenable to improvement through simple selection. These findings suggest that emphasis on pods per plant, seed yield per plant, biological yield, and harvest index would be rewarding in soybean improvement programmes aimed at enhancing seed yield.

1. INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is one of the most important oilseed and protein-rich legume crops cultivated worldwide, occupying a pivotal position in global agriculture owing to its high seed protein (approximately 40%) and oil (approximately 20%) content [1]. Often referred to as the "golden bean" or "miracle crop," soybean serves as a major source of vegetable oil, animal feed, and an increasingly important raw material for the food processing and biodiesel industries [1]. Given its economic and nutritional significance, continuous genetic improvement of soybean for higher and

more stable seed yield remains a central objective of crop breeding programmes [2].

Seed yield in soybean is a complex quantitative trait controlled by polygenes and is the cumulative expression of several interacting yield-contributing characters such as plant height, number of branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, biological yield, and harvest index [3,4]. Because yield itself is highly influenced by environmental fluctuations, direct selection for yield alone is often not very effective. Breeders therefore rely on the study of

genetic variability in yield-contributing component traits to identify heritable variation that can be exploited through selection [5].

The presence of genetic variability in a breeding population is the basic prerequisite for any successful crop improvement programme, as it provides breeders the scope to select genotypes with desirable trait combinations [6]. However, the phenotypic expression of a trait is a composite outcome of both genotypic and environmental effects, and the observable (phenotypic) variation does not always reflect true heritable (genotypic) variation. Partitioning of total phenotypic variance into its genotypic and environmental components, through the estimation of genotypic and phenotypic coefficients of variation (GCV and PCV), therefore becomes essential to correctly assess the magnitude and nature of variability present for a given trait [7].

Heritability estimates alone, however, may not always provide a reliable index of the expected genetic gain from selection, as they do not account for the type of gene action (additive versus non-additive) involved in the expression of a trait [8]. Heritability estimates in conjunction with genetic advance provide a more meaningful and reliable measure of the extent to which a trait can be improved through direct

phenotypic selection, since genetic advance reflects the actual expected gain under a given selection intensity [9]. Traits combining high heritability with high genetic advance as percent of mean are typically governed by additive gene action and are more responsive to simple selection, whereas high heritability with low genetic advance suggests the involvement of non-additive gene effects, in which case selection may not translate into proportionate genetic gain [9]. Several earlier studies in soybean have reported high heritability coupled with high genetic advance for pods per plant, branches per plant, plant height, and seed weight, identifying these as favourable traits for improvement through phenotypic selection [3,10].

Keeping this in view, the present investigation was undertaken with the objective of estimating the extent of genetic variability, genotypic and phenotypic coefficients of variation, heritability (broad sense), and genetic advance as percent of mean for ten economically important quantitative traits in a set of soybean genotypes, so as to identify traits amenable to improvement through phenotypic selection and to provide baseline information for future soybean breeding programmes.

2. MATERIALS AND METHODS

2.1 Experimental Material and Design

The experimental material for the present study comprised twenty-three (23) genotypes of soybean (*Glycine max* (L.) Merrill), obtained from the National Bureau of Plant Genetic Resources, NBM Mau.

The genotypes used in the present study are listed in Table 1. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Standard agronomic package of practices was followed to raise a healthy crop stand.

Table 1. List of soybean genotypes used in the present study (Source: ICAR-NISST, Mau)

Genotype Code	Genotype Name	Genotype Code	Genotype Name
G1	NRC 150	G12	GW 195 W
G2	GW 219 W	G13	GW 151 W
G3	GW 65 W	G14	GW 143 W
G4	GW 222 W	G15	GW 75 W
G5	GW 68 W	G16	GW 204 W
G6	GW 211 G	G17	GW 210 B
G7	JS 20 -116	G18	GW 208 W
G8	GW 117 W	G19	20 AGS-143 B
G9	GW 172 W	G20	GW 41 W
G10	GW 32 W	G21	GW49 W
G11	GW 127 W	G22	GW 134 W

Source: ICAR-National Institute of Seed Science & Technology, Mau.

2.2 Statistical Analysis

The mean values recorded for each genotype in each replication were subjected to analysis of variance (ANOVA) as per the standard procedure for Randomized Block Design to test the significance of differences among genotypes. Data were analysed using OPSTAT, the online statistical analysis package developed by CCS Haryana Agricultural University, Hisar.

Genotypic variance (σ^2g) and phenotypic variance (σ^2p) were computed following the standard method of Burton and de Vane [11], as:

$$\sigma^2g = (MSt - MSe) / r$$

$$\sigma^2p = \sigma^2g + \sigma^2e$$

where, MSt = Mean sum of squares due to genotypes/treatments, MSe ($= \sigma^2e$) = Mean sum of squares due to error, and r = number of replications ($r = 3$).

Genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated according to Burton [12]:

$$GCV (\%) = (\sqrt{\sigma^2g} / \bar{x}) \times 100$$

$$PCV (\%) = (\sqrt{\sigma^2p} / \bar{x}) \times 100$$

where, $\bar{x}$ = general/grand mean of the trait. The GCV and PCV estimates were

categorized as low (<10%), moderate (10–20%), and high (>20%) following the classification proposed by Sivasubramanian and Madhavamenon [7].

Broad-sense heritability ($h^2_{b.s.}$) was estimated as the ratio of genotypic variance to phenotypic variance, following Lush [8] and Hanson et al. [13]:

$$h^2 \text{ (broad sense) (\%)} = (\sigma^2_g / \sigma^2_p) \times 100$$

Heritability estimates were categorized as low (<30%), moderate (30–60%), and high (>60%), following Robinson et al. [14].

Genetic advance (GA) under selection, assuming a selection intensity of 5% ($K =$

2.06), was estimated using the formula of Johnson et al. [9]:

$$GA = K \times \sigma_p \times h^2(b.s.)$$

where, K = selection differential at 5% selection intensity (2.06), σ_p = phenotypic standard deviation ($\sqrt{\sigma^2_p}$), and h^2 = heritability in broad sense (as a proportion). Genetic advance as percent of mean (GAM) was computed as:

$$GAM (\%) = (GA / \bar{x}) \times 100$$

GAM estimates were categorized as low (<10%), moderate (10–20%), and high (>20%), following Johnson et al. [9].

Table 2. Analysis of variance (mean squares) for ten quantitative traits in soybean

Source of Variation	d.f.	DF	DM	PH	NPP	SPP	TB	TW	HI	BY	YPP
Replications (Mean Sq.)	2	0.6	10.03	18.63	2.81	0.1	0.16	2.51	8.53	0.38	0.99
Genotypes/Treatments (Mean Sq.)	22	606.68	214.13	1,925.39	1,463.66	13.26	7.57	38.19	765.93	1,221	43.37
Error (Mean Sq.)	44	9.48	35.67	15.54	2.83	0.16	0.24	1.53	20.22	31.7	0.21
F value (Genotypes)		64.01**	6.00**	123.86**	517.97**	81.45**	31.57**	24.90**	37.88**	38.52**	208.77**
C.V. (%)		6.86	5.92	4.04	5.87	10.96	5.98	11.69	17.52	21.99	13.75
C.D. at 5%		5.0795	9.8538	6.505	2.7735	0.6658	0.8077	2.0433	7.4196	9.289	0.752

**Significant at 1% level; *Significant at 5% level; NS = Non-significant

3. RESULTS

Observations were recorded on ten quantitative traits of breeding importance, namely Days to 50% Flowering (DF), Days to Maturity (DM), Plant Height (cm) (PH), Number of Pods per Plant (NPP), Number of Seeds per Pod (SPP), Number of Branches per Plant (TB), 100-Seed Weight (g) (TW), Harvest Index (%) (HI),

Biological Yield per Plant (g) (BY), and Seed Yield per Plant (g) (YPP).

3.1 Analysis of Variance

The analysis of variance (Table 2) revealed highly significant differences ($p < 0.01$) among the twenty-three genotypes for all ten quantitative traits studied, indicating the presence of ample genetic variability in the experimental material for all the characters under investigation. The replication (block)

effect was non-significant for all traits except seed yield per plant, where it was significant at the 5% level, suggesting that the blocking arrangement adequately controlled field variability for most traits. The coefficient of variation (C.V.) ranged from 4.04% (plant height) to 21.99% (biological yield per plant), indicating an acceptable level of experimental precision across traits.

Genotype G23 should be interpreted with caution for days to 50% flowering, as its recorded mean (106.6 days) was nearly double the range observed among the remaining twenty-two genotypes (35.3–50.5 days) and is most likely attributable to a data-recording anomaly rather than genuine biological variation; this value is flagged accordingly and its influence on the variability estimates for this particular trait should be interpreted with due caution. For all other traits, this genotype's performance fell within, or close to, the normal range recorded across the genotype panel.

3.2 Mean Performance, Range, and Precision of the Experiment

The mean values, range of genotypic means, coefficient of variation, critical difference at 5%, and standard errors (SEm and SEd) for all ten traits are presented in Table 3. Wide ranges were observed for number of pods per plant (2.68–79.30), biological yield per plant (2.72–63.26 g),

and harvest index (5.08–55.13%), reflecting substantial diversity among the genotypes for these yield-contributing traits. In contrast, comparatively narrower ranges were recorded for days to maturity (84.75–119.31 days) and number of seeds per pod (1.95–8.44). The standard error of mean (SEm) was lowest for number of seeds per pod (± 0.233) and highest for biological yield per plant (± 3.250), while the critical difference (C.D.) at 5% followed a similar pattern, being lowest for number of seeds per pod (0.67) and highest for biological yield per plant (9.29), reflecting the differing scales and inherent variability of these traits.

Table 3. Mean, range, coefficient of variation, critical difference (C.D.), and standard errors (SEm, SEd) for ten quantitative traits in soybean

Trait	Mean	Range (Min–Max)	C.V. (%)	C.D. (5%)	SEm(±)	SEd(±)
DF	44.88	35.30 – 106.63	6.86	5.08	1.777	2.514
DM	100.96	84.75 – 119.31	5.92	9.85	3.448	4.876
PH	97.53	26.78 – 120.15	4.04	6.50	2.276	3.219
NPP	28.63	2.68 – 79.30	5.87	2.77	0.971	1.373
SPP	3.68	1.95 – 8.44	10.96	0.67	0.233	0.330
TB	8.19	5.73 – 11.52	5.98	0.81	0.283	0.400
TW	10.60	6.54 – 21.81	11.69	2.04	0.715	1.011
HI	25.66	5.08 – 55.13	17.52	7.42	2.596	3.672
BY	25.60	2.72 – 63.26	21.99	9.29	3.250	4.597
YPP	3.31	0.00 – 12.88	13.75	0.75	0.263	0.372

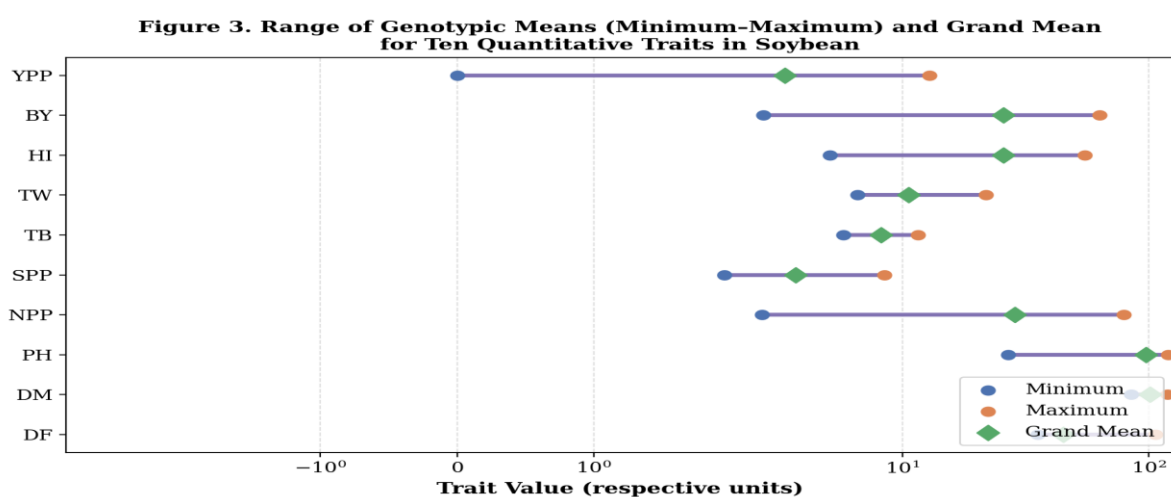


Figure 3. Range of genotypic means (minimum–maximum) and grand mean for ten quantitative traits in soybean (x-axis on symmetric log scale).

3.3 Genotypic and Phenotypic Coefficients of Variation

Estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for the ten traits studied are presented in Table 4. The PCV was higher than the corresponding GCV for all the traits studied, which is expected since phenotypic variance includes both genotypic and environmental components. However, the difference between PCV and GCV was narrow for most traits (e.g., plant height, number of pods per plant, harvest

index, seed yield per plant), indicating comparatively low environmental influence and a predominant contribution of genotypic factors towards the observed phenotypic variability for these characters.

High GCV and PCV estimates (>20%) were recorded for days to 50% flowering (31.44%, 32.18%), plant height (25.87%, 26.18%), number of pods per plant (77.07%, 77.29%), number of seeds per pod (56.74%, 57.79%), 100-seed weight (32.99%, 35%), harvest index (61.43%,

63.88%), biological yield per plant (77.77%, 80.82%), and seed yield per plant (114.42%, 115.24%). Number of branches per plant recorded a moderate GCV (19.09%) but a high PCV (20%). Days to maturity recorded the lowest GCV (7.64%) and PCV (9.66%) among all traits studied, both falling in the low category, indicating limited scope for improvement of this trait through direct selection.

The highest GCV and PCV were recorded for seed yield per plant (114.42% and 115.24% respectively), followed by biological yield per plant and number of pods per plant, indicating the presence of substantial exploitable genetic variability for these yield-related traits in the genotype panel evaluated.

3.4 Heritability (Broad Sense)

Broad-sense heritability estimates (Table 4) were high (>60%) for all ten traits studied, ranging from 62.52% for days to maturity to 99.42% for number of pods per plant. High heritability estimates for all the traits suggest that a major proportion of the observed phenotypic variability is attributable to genotypic differences, with

comparatively limited environmental influence on trait expression in the present set of genotypes.

3.5 Genetic Advance as Percent of Mean

Genetic advance as percent of mean (GAM) (Table 4) ranged from 12.44% for days to maturity (moderate category) to 234.02% for seed yield per plant (g) (high category). High GAM (>20%), coupled with high heritability, was recorded for days to 50% flowering, plant height, number of pods per plant, number of seeds per pod, number of branches per plant, 100-seed weight, harvest index, biological yield per plant, and seed yield per plant, suggesting that these traits are predominantly under the control of additive gene action and would respond favourably to direct phenotypic selection. Days to maturity was the only trait to show a moderate GAM (12.44%) despite high heritability, indicating that non-additive gene effects may also be contributing to the inheritance of this trait, and that selection gains for maturity duration are likely to be comparatively slower.

Figure 1. Genotypic (GCV) and Phenotypic (PCV) Coefficients of Variation for Ten Quantitative Traits in Soybean

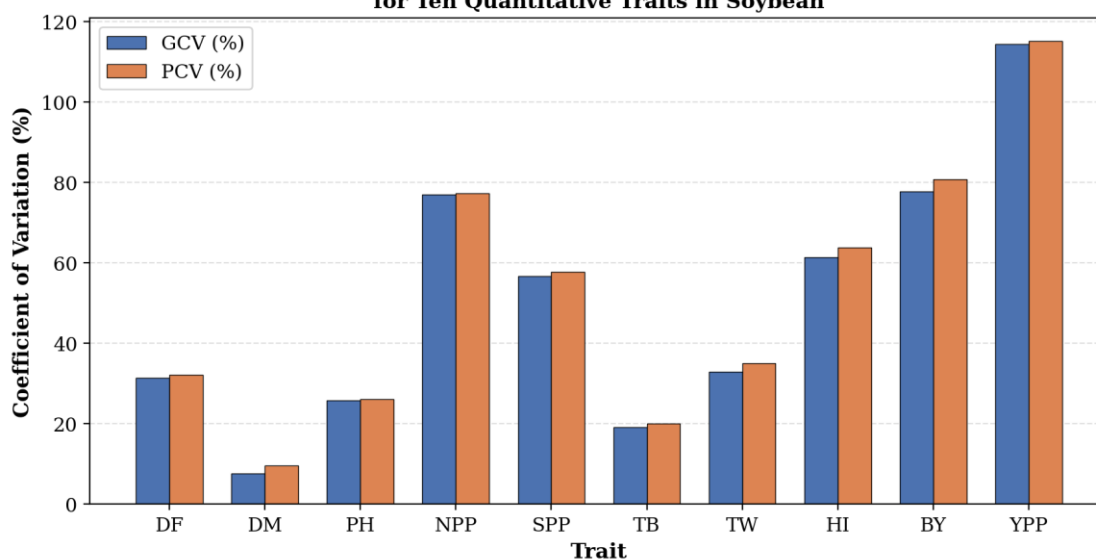


Figure 1. Genotypic (GCV) and phenotypic (PCV) coefficients of variation for ten quantitative traits in soybean.

Figure 2. Broad-Sense Heritability and Genetic Advance as Percent of Mean for Ten Quantitative Traits in Soybean

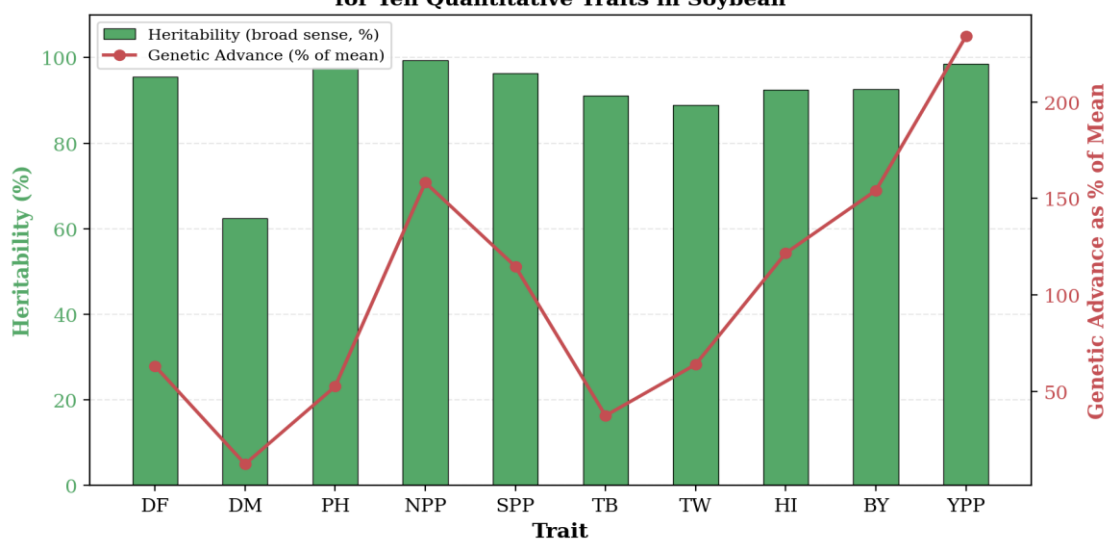


Figure 2. Broad-sense heritability and genetic advance as percent of mean for ten quantitative traits in soybean.

Table 4. Estimates of genetic parameters

Trait	σ^2g	σ^2p	GCV (%)	PCV (%)	h^2 (b.s.) (%)	GA	GAM (%)
DF	199.07	208.55	31.44	32.18	95.46	28.40	63.28
DM	59.49	95.15	7.64	9.66	62.52	12.56	12.44
PH	636.62	652.16	25.87	26.18	97.62	51.35	52.65
NPP	486.94	489.77	77.07	77.29	99.42	45.33	158.30
SPP	4.37	4.53	56.74	57.79	96.41	4.23	114.77
TB	2.44	2.68	19.09	20.00	91.07	3.07	37.52
TW	12.22	13.75	32.99	35.00	88.85	6.79	64.05
HI	248.57	268.79	61.43	63.88	92.48	31.23	121.70
BY	396.43	428.13	77.77	80.82	92.60	39.47	154.17
YPP	14.39	14.60	114.42	115.24	98.58	7.76	234.02

σ^2g = Genotypic variance; σ^2p = Phenotypic variance; GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; h^2 (b.s.) = Heritability in broad sense; GA = Genetic advance (at 5% selection intensity, $K = 2.06$); GAM = Genetic advance as percent of mean.

Table 5. Categorization of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance as percent of mean for ten quantitative traits in soybean

Trait	GCV Category	PCV Category	Heritability Category	GAM Category
DF	High	High	High	High
DM	Low	Low	High	Moderate
PH	High	High	High	High
NPP	High	High	High	High
SPP	High	High	High	High
TB	Moderate	High	High	High
TW	High	High	High	High
HI	High	High	High	High
BY	High	High	High	High
YPP	High	High	High	High

Classification of GCV and PCV following Sivasubramanian and Madhavamenon (1973): Low < 10%, Moderate 10–20%, High > 20%. Classification of heritability following Robinson *et al.* (1949): Low < 30%, Moderate 30–60%, High > 60%. Classification of GAM following Johnson *et al.* (1955): Low < 10%, Moderate 10–20%, High > 20%.

4. DISCUSSION

The significant differences observed among genotypes for all ten quantitative traits in the present study confirm the existence of considerable genetic variability in the soybean germplasm evaluated, providing a

sound basis for selection-based improvement. This finding agrees with several earlier reports of highly significant genotypic variation for yield and yield-contributing traits in soybean under randomized block designs [3,15,16].

In the present study, PCV was consistently higher than GCV for all traits, which is a well-established and expected pattern since phenotypic variance is the sum of genotypic and environmental variance components. However, the magnitude of difference between PCV and GCV was narrow for most of the traits studied, particularly plant height, number of pods per plant, harvest index, and seed yield per plant, indicating that environmental factors exerted comparatively limited influence on the expression of these traits and that the observed phenotypic variation largely reflects true genetic variation. This narrow GCV-PCV gap for yield and yield-component traits in soybean has similarly been reported by Malik et al. [16] and Verma et al. [17], lending support to the reliability of phenotypic selection for these characters in the present material.

Days to maturity showed the lowest GCV and PCV among the traits studied, a result consistent with the generally narrow range of variation typically observed for maturity duration in soybean, a trait that tends to be comparatively more stable and less responsive to selection pressure across environments. Comparably low coefficients of variation for maturity duration relative to yield-component traits have similarly been reported by Karad and Harer [18] and Hossain et al. [19].

High heritability estimates (>60%) were recorded for all ten traits in the present investigation, indicating that the genotypic component was the predominant contributor to the observed phenotypic variance. However, heritability estimates alone can be misleading when used in isolation to predict selection response, since heritability reflects only the relative magnitude of genetic and environmental variance and does not indicate whether the underlying gene action is additive or non-additive [8]. It is for this reason that heritability estimates are most meaningfully interpreted alongside genetic advance [9].

In the present study, high heritability was accompanied by high genetic advance as percent of mean for nine of the ten traits studied — namely days to 50% flowering, plant height, number of pods per plant, number of seeds per pod, number of branches per plant, 100-seed weight, harvest index, biological yield per plant, and seed yield per plant. This combination of high heritability with high genetic advance is generally attributed to the preponderance of additive gene action in the inheritance of these traits, implying that phenotypic selection would be effective and that appreciable genetic gains can be expected from even a single cycle of direct selection for these characters. Similar

combinations of high heritability coupled with high genetic advance for pods per plant, branches per plant, plant height and seed weight in soybean have been reported by Malek et al. [15], while Karad and Harer [18] similarly identified pods per plant, biological yield, and harvest index as favourable traits for phenotypic selection, reinforcing the consistency of the present findings with the broader body of evidence on soybean genetic architecture.

Days to maturity, in contrast, combined high heritability with only moderate genetic advance as percent of mean, suggesting that non-additive gene effects (dominance and/or epistasis) may also be contributing to the inheritance of this trait in the present genotype panel. In such cases, simple phenotypic selection may not translate proportionately into genetic gain, and breeding strategies that exploit non-additive gene action, such as biparental mating or recurrent selection, may be more appropriate for improving maturity duration.

The particularly high estimates of GCV, PCV, and GAM recorded for seed yield per plant and biological yield per plant in the present study warrant some caution in interpretation. Because seed yield and its component traits are inherently more sensitive to microenvironmental variation and to a wider genotype base than traits

such as days to maturity, unusually elevated coefficients of variation of the magnitude recorded here may, at least in part, reflect the wide genotypic range present in this particular panel (including near-zero yield in at least one genotype) rather than representing a universally generalizable feature of soybean genetic architecture. These estimates should therefore be treated as specific to the present set of genotypes and environment, and would benefit from validation across multiple locations and seasons before being used as a basis for broader breeding recommendations.

Taken together, the present results indicate that selection based on number of pods per plant, seed yield per plant, biological yield per plant, and harvest index — traits combining high GCV, high heritability, and high genetic advance — would be the most rewarding approach for improving seed yield in the soybean genotypes studied, consistent with the findings of Malik et al. [16] and Karad and Harer [18]. Plant height, 100-seed weight, and number of branches per plant, which also showed favourable combinations of these parameters, may serve as useful secondary selection criteria in a multi-trait selection index.

5. CONCLUSION

The present investigation revealed the presence of substantial genetic variability among the twenty-three soybean genotypes evaluated for all ten quantitative traits studied. High heritability coupled with high genetic advance as percent of mean was recorded for days to 50% flowering, plant height, number of pods per plant, number of seeds per pod, number of branches per plant, 100-seed weight, harvest index, biological yield per plant, and seed yield per plant, indicating that these traits are governed predominantly by additive gene action and offer good scope for improvement through direct phenotypic selection. Days to maturity, while highly heritable, showed only moderate genetic advance, suggesting a role for non-additive gene action and the need for alternative breeding strategies to improve this trait. Based on the magnitude of genetic parameters observed, selection emphasis on number of pods per plant, seed yield per plant, biological yield per plant, and harvest index is recommended for effective genetic improvement of seed yield in soybean. These findings, however, are based on a single season of evaluation at one location, and multi-environment testing is recommended to confirm the stability of the genetic parameters reported here before their use in large-scale breeding decisions.

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