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Genetic variability and heritability of pod and seed characteristics in green beans (*Phaseolus vulgaris*)

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Abstract

Thirty-nine green bean (*Phaseolus vulgaris*) genotypes were evaluated to determine the level of genetic variability and identify pod and seed traits that could be used as selection criteria for yield improvement. The evaluation was conducted at three out-stations of the Institute of Agricultural Research and Training, Nigeria, in 2023 using a 3 x 13 alpha lattice design in two replications. Data were collected on pod and seed parameters. Descriptive statistics, analysis of variance (ANOVA), genotypic (GCV) and phenotypic coefficient of variation (PCV), and correlation analysis were conducted. Genetic variances were estimated from mean squares of ANOVA. PCV estimates were higher than corresponding GCV. Range was high for some of the traits. Mean square of environment was significant for pod length, seed width and seeds/pod indicating the strong influence of environment on these traits. Mean square of genotypes was significant for seed length and seeds/pod. Estimate of environmental variance was slightly higher than genotypic variance estimate for all the traits. The value of genotypic variance was however high for 100 seed weight which also had high broad-sense heritability and high percentage expected gains. Broad-sense heritability and percentage expected gains were also high for pod length, seed length and number of seeds/pod indicating that these traits are under genetic control. Number of pods/peduncle had strong genotypic and phenotypic correlations with pod length, seed length and width, and number of seeds/pod, and strong phenotypic correlation with 100 seed weight. These traits also had strong correlations among themselves. This study revealed substantial genetic variability in the green bean collections for possible yield improvement. It also identified pod length, seed length, seeds/pod and 100-seed weight as reliable selection criteria for yield improvement in green bean under tropical environment.

Introduction

Green bean (*Phaseolus vulgaris*) is classified under the order *Fabales*, family *Fabaceae* and genus *Phaseolus* (Cichy *et al.*, 2015). It has chromosome number $2n = 2x = 22$. It is an erect or twinning, annual, herbaceous plant with various growth habits, morphological traits, and seed and pod characteristics. It is one of the most important legume crops cultivated primarily for its immature pods, which are consumed as fresh or processed vegetable (Ketema and Geleta, 2022). Its mature seeds are low in fat, rich in vitamins and also known as the second most important source of human dietary protein (Kimani, 1999). Protein content of green beans ranges from 20 to 30 %. This protein content significantly exceeds that of cereals, which typically range from 6 to 15 %, making green beans approximately 2.5-3.0 times more protein-dense than cereals (Chhetri *et al.*, 2025). Green beans are also rich in phenolic compounds, including flavonoids and tannins, that are valuable source of nutrients (Duenas *et al.*, 2016). The consumption of green beans presents several health benefits, such as antioxidant, anti-inflammatory, anticarcinogenic, antihyperglycemic, and antihypertensive properties (Graziani *et al.*, 2021).

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Despite its nutritional qualities, green bean remains constrained by its narrow genetic base and inadequate understanding of the genetic architecture controlling pod and seed traits which has led to its limited genetic improvement. To achieve genetic improvement in green beans, it is essential to understand the genetic variability within the germplasm. Genetic variability forms the cornerstone of any crop improvement program as the evaluation of phenotypic and genotypic variation within a germplasm provides opportunities to identify superior parental lines and to exploit heterosis and segregation in breeding. The values of genetic parameters such as heritability, genotypic variances and genetic gains give clearer picture of the gene action controlling a trait and the progress that could be made from selection in advanced generation.

Previous studies have reported high heritability estimates and genetic advance for pod length, pod width, and seed weight in diverse green bean genotypes indicating that these traits are predominantly controlled by additive gene action and can be effectively improved through phenotypic selection (Bagheri *et al.,* 2017; Singh *et al.,* 2018; Noopur *et al.,* 2019; Chhetri *et al.,* 2025). However, most previous studies have focused primarily on dry-bean and have assessed limited subset of genotypes. Studies on genetic variability of pod and seed traits in green bean germplasms is relatively limited, particularly under tropical environments where environmental factors significantly influence traits expression.

The present study was therefore conducted to determine the genetic variability for pod and seed traits in a diverse collections of green beans for possible yield improvement.

Materials and Methods

The study was conducted at three out-stations of the Institute of Agricultural Research and Training (IAR&T), Nigeria, namely Ikenne (Rain Forest zone), Kishi (Northern Guinea Savanna), and Ibadan (Derived Savanna) in 2023 cropping season. A total of 39 green bean genotypes sourced from the International Centre for Tropical Agriculture, Uganda (18 accessions); International Institute of Tropical Agriculture, Nigeria (10 accessions); The University of Zambia, (5 accessions); and from open markets in Abeokuta (2 accessions), Jos (3 accessions), and Abuja (1 accession), Nigeria, were used for the study.

The experimental design was a 3 x 13 alpha lattice design in two replications. Two replications were used due to insufficient quantity of seeds for the trial. A 2-row plot of 3 m long was used. Plant spacing was 60 cm within row and 60 cm between rows with a spacing of 1m between plots. Pre-emergence herbicide (Metolachlor 960 g EC. at 1.44 kg ai ha^{-1}) was applied at planting, while insects were controlled using Cypermethrin 30g/L + Dimethoate 250 g/L EC.

Data collection

The following traits were assessed during the evaluation- number of pods/peduncle, pod length, pod width, seed length, seed width, number of seeds/pod, and 100-seed weight. Pods/peduncle was taken by counting the number of pods on selected peduncles in five tagged plants and the average estimated. Pod length and pod width in centimeter (cm) were estimated from average of 10 randomly selected pods among the harvested pods/plot using tape rule. Seed length and seed width (in cm) were measured on average of 10 seeds per plot using small ruler. Number of seeds/pod was estimated by getting the average number of seeds in 10 selected pods. 100 seed weight was taken by weighing 100 seeds per plot in grammes (g).

Data analyses

Means, standard error and ranges were estimated. Combined analysis of variance (ANOVA) across environments was conducted. Values of genetic variances, environmental variance, genotype by environment interaction variance and phenotypic variance were obtained from mean squares from ANOVA according to Hallauer *et al*. (2010). Phenotypic (PCV) and genotypic coefficient of variation (GCV) were also computed.

Broad-sense heritability (H^2) was estimated as genetic variance value over phenotypic variance value and expressed in percentage as:

$$H^2 = \sigma^2 g/(\sigma^2 g + \sigma^2 ge/e + \sigma^2/er)$$

where $\sigma^2 g$ = component of variance estimate due to genotype;

$\sigma^2 ge$ = variance estimate due to genotype x environment interaction;

σ^2 = experimental error variance;

e = environments and r = replicates.

Expected genetic gains from selection (ΔG) was calculated according to Hallauer *et al.* (2010) as:

$\Delta G = k.\ \sigma ph.\ H^2$

where k is selection differential expressed in standard form (=1.216 at 25 % selection intensity); σph = phenotypic standard deviation, and H^2 = heritability (in broad-sense) of the trait under consideration. The values then expressed as a percentage of the means of each trait (ΔG%).

Phenotypic and genotypic correlation coefficients among traits were computed using variance-covariance matrix and estimates of genotypic and phenotypic variances as described by Falconer (1996).

Results and Discussion

Mean and estimates of variability

Means and variability estimates (Table 1) revealed substantial phenotypic and genotypic variations among the 39 green bean genotypes. The mean number of pods/peduncle was 2, with range of 1.0-4.0, suggesting limited variation for this trait. The observed higher phenotypic coefficient of variation (PCV) compared to the genotypic coefficient of variation (GCV) is expected since phenotypic variation is the combination of genotypic and environmental variation. It indicated that environmental factors contributed substantially to the observed variations. The high GCV value for 100 seed weight (24.79 %) and wide range (10.0- 38.5) suggest that selection for the trait would be effective, especially if combined with selection for correlated traits (Yohannes *et al.*, 2020). Deshmukh *et al.* (1986) classified PCV and GCV above 20 % as high, between 10-20 % as moderate and less than 10 % as low.

The wide range observed for pod length (4.3–13.8 cm) indicates appreciable variation in pod-related traits, which are key yield components in green bean. Pod length is an important market trait in green beans and it is often targeted in breeding programs. Similar levels of variability for pod length was reported in common bean by Chhetri *et al.* (2025). The moderate GCV values obtained for pod length (17.31 %) further suggests substantial genetic variability for the trait. The low range (0.4-1.2) and relatively low GCV values (11.76 %) for pod width indicated limited genetic variation for the trait.

Number of seeds/pod is a key yield component and reflects reproductive efficiency. Seeds/pod exhibited broad range (2-12) and moderate GCV (13.57 %) indicating substantial genetic variability for the trait.

Table 1. Mean±S.E, range and estimates of variability for pod and seed traits of 39 green beans genotypes evaluated at three locations in 2023.

Traits	Mean±S.E	Range	GCV (%)	PCV (%)
Pods/peduncle	2.13±0.28	1.0 -4.0	7.98	15.36
Pod length (cm)	9.57±0.86	4.3 -13.8	17.31	28.08
Pod width (cm)	0.73±0.07	0.4 -1.2	11.76	24.83
Seed length (cm)	0.88±0.06	0.5 -1.4	13.3	20.60
Seed width (cm)	0.53±0.05	0.35 -1.2	5.36	21.62
Seeds/pod	6.14±1.00	2.0 -12.0	13.57	23.38
100 Seed weight (g)	18.33±2.10	10.0 -38.5	24.79	37.44

S.E: Standard error; GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; g: gram; cm: centimeter

This also suggests that number of seeds/pod is amenable to genetic improvement through selection. Similar observation has been reported in green bean by Singh *et al.* (1991) and Ketema and Geleta (2022).

PCV values exceeding corresponding GCV values for all the traits, demonstrates the influence of environmental factors on the expression of the traits and possible genotype × environment interactions. This pattern is common in multi-location trials of legumes, where traits related to reproduction and yield are particularly sensitive to variations in rainfall, temperature, and soil conditions (Acquaah, 2012; Singh *et al.*, 2018 and Noopur *et al.*, 2019).

Mean squares from combined ANOVA

Mean squares from combined analysis of variance for pod traits (Table 2) showed a significant effect of environment on pod length, indicating that this trait is strongly influenced by differences among locations. This suggests that environmental factors such as rainfall, temperature, soil fertility, and management practices played a major role in determining pod morphology in green bean. Similar response to environmental conditions by pod traits has been reported in green bean and other legumes (Singh *et al.*, 2013). The mean squares for genotype × environment interaction was significant for only pod length, indicating differential genotypic response across environments, and emphasizes need for multi-location testing when selecting for this trait to identify stable performance (Yan and Kang, 2003; Gauch *et al.*, 2008).

Table 2. Mean squares from combined analysis of variance (ANOVA) for pod traits of 39 green beans genotypes evaluated at three locations in 2023.

Source	d.f	Pods/ peduncle	Pod length (cm)	Pod width (cm)
Env.	2	0.02	31. 85**	0.10
Rep/Env	3	0.14**	4.72	0.13*
Block/Env/Rep	12	0.07*	2.00	0.02
Gen.	38	0.05	6.42	0.03
Gen x Env.	76	0.03	4.18*	0.02
Error	114	0.03	1.88	0.03

Rep.: Replications; Env.: Environment; Gen.: Genotypes; **: Significant at 1% level of probability; *: Significant at 5% level of probability; cm: centimeter

The absence of significant environmental effects on pod width and number of pods/peduncle suggests a comparatively stable expression of these traits across the different locations. Also, the lack of significant genotypic effects for pod length and width, may imply a narrow genetic base for these traits among the evaluated genotypes.

For seed traits (Table 3), the environment had a highly significant effect on seed width and number of seeds/pod, demonstrating strong environmental influence on seed development in green bean. Seed traits are often affected by environmental factors during flowering and grain filling stages, hence their sensitivity to varying environmental conditions (Teng *et al.*, 2023). Similar observations have been documented in other legumes, where environmental variability significantly affected several seed traits (Segers *et al.*, 2022).

However, the non-significant environmental effects observed for seed length and 100 seed weight suggest greater stability of these traits across different environments. The significant mean squares of genotype for seed length and number of seeds/pod indicate substantial genetic variability among genotypes and highlight opportunities for genetic improvement of these traits through selection. Comparable results have been reported in green bean and Okra (Raffi and Nath, 2004; Nwangburuka *et al.*, 2012). In contrast, the absence of significant genotype × environment interaction for seed length, seed width, number of seeds/pod, and 100 seed weight indicates stable genotypic performance across locations.

Table 3. Mean squares from combined analysis of variance (ANOVA) for seed traits of 39 green beans genotypes evaluated at three locations in 2023

Source	d.f	Seed length (cm)	Seed width (cm)	Seeds/pod	100 Seed weight (g)
Env.	2	0.03	0.10**	2.20**	14.55
Rep (Env)	3	0.04	0.06*	0.74*	46.76
Block/Env/Rep	12	0.01	0.02	0.28	66.44
Gen.	38	0.05**	0.01	0.34*	51.20
Gen x Env.	76	0.02	0.01	0.17	26. 80
Error	114	0.02	0.02	0.24	13.17

Rep.: Replications; Env.: Environment; Gen.: Genotypes; **: Significant at 1% level of probability; *: Significant at 5% level of probability; g: gram; cm: centimeter

Variance estimates of the traits measured

The variance component analysis showed that environmental variance was higher than genotypic variance for the traits studied (Table 4), indicating that environmental factors strongly influenced trait expression in green beans. This pattern is in contrast to the previous report of Ketema and Geleta (2022) who reported that genotypic variance for most of the traits examined was higher than the environmental variance. This also highlights the importance of evaluating genotypes across multiple environments to accurately identify genetically superior lines.

Table 4. Variance component estimates, broad-sense heritability (H^2) and genetic gains for 11 traits of 39 green beans genotypes evaluated at three locations in 2023

Traits	σ^2e	σ^2g	σ^2ph	H^2 (%)	ΔG	ΔG (%)
Pods/peduncle	0.04	0.02	0.06	26.94	0.14	8.53
Pod length (cm)	4.47	2.74	7.22	38.01	2.10	21.98
Pod width (cm)	0.03	0.007	0.03	22.42	0.08	11.47
Seed length (cm)	0.02	0.01	0.03	41.69	0.16	17.69
Seed width (cm)	0.01	0.001	0.01	6.15	0.01	2.75
Seeds/pod	0.23	0.12	0.34	33.66	0.41	16.21
100 Seed weight (g)	26.44	20.64	47.08	43.84	6.20	33.81

σ^2e - Environmental variance; σ^2g - genotypic variance; σ^2ph -phenotypic variance; H^2 - broad-sense heritability; ΔG- genetic gain; ΔG%- genetic gain expressed as percentage of the means; cm- centimeter; g- gram

Broad-sense heritability estimates varied markedly among traits ranging from 6.15 % for seed width to 43.84 % for 100 seed weight. Dabholkar (1992) considered heritability values less than 10 % as low, between 10-30 % as moderate and those above 30 % as high. Seed width exhibited very low genotypic variance relative to environmental variance, resulting in low heritability estimates and minimal expected genetic gains. The low genetic gain indicates that selection for this trait within the evaluated population would be inefficient. Such traits are often controlled by non-additive gene effects or are highly sensitive to environmental variation (Acquaah, 2012), and so, selection could be more on correlated traits. Similar low heritability values have been reported for such qualitative and semi-qualitative traits in Bambara groundnut (Onwubiko *et al.*, 2019).

High heritability for pod length (38.01 %), seed length (41.69 %), seeds/pod (33.66 %) and 100 seed weight (47.08 %) suggests that these traits are predominantly under genetic control. The particularly high heritability and genetic gain (33.81 %) observed for 100 seed weight, indicate the predominance of additive gene action, making this trait a reliable selection criterion for yield improvement. Similar finding has been reported by Ketema and Geleta (2022). According to Johnson *et al.* (1955), expected gain is high when greater than 20 %, low when less than 10 % and moderate when it falls in between 10-20 %. Number of pods/peduncle and pod width showed moderate heritability (26.94 % and 22.42 %, respectively) and low to moderate expected genetic gains (8.53 % and 11.47 %, respectively). Although genetic improvement for these traits is possible, progress through direct selection would be slow. Consequently, improvement of the traits may be achieved more effectively through indirect selection of other traits, provided they are highly correlated and are of higher heritability.

Correlation among pod and seed traits

The correlation analysis revealed strong and consistent associations among pod and seed traits in green bean (Table 5), indicating coordinated genetic control of key yield components. At the genotypic level, the strong positive correlations of number of pods/peduncle with pod length (rg = 0.74**) and number of seeds/pod (rg = 0.99**) suggest that genotypes with higher pod-bearing capacity also possess superior pod morphology and enhanced seed set. This implies that selection for increased pods/peduncle could indirectly improve yield-related traits. Similar relationships have been reported in green

bean and other grain legumes, reflecting shared developmental pathways governing reproductive sink strength (Mofokeng *et al.,* 2020; Karavidas *et al.,* 2022). The negative genotypic correlations between number of pods/peduncle and seed length (rg = -0.37*) and width (rg= -0.90**) indicate a trade-off between seed number and seed size. This inverse relationship is widely reported in legumes and is attributed to competition for assimilates during seed filling, where increased seed number limits individual seed growth (Gambín and Borras, 2010). This pattern was also observed in winged bean (Bhadmus *et al.,* 2023).

Pod length showed strong positive genotypic associations with number of seeds/pod (rg = 0.82**), suggesting that longer pods tend to possess more seeds. This finding agrees with previous reports in common bean by Fatima *et al.* (2024). However, its negative correlation with pod width (rg = -0.53**) and seed width (rg = -0.79**) indicates that pod elongation may occur at the expense of pod and seed thickness, highlighting the need for balanced selection. Pod width exhibited strong positive genotypic correlations with seed width (rg = 0.99**) confirming that wider pods favour big seeds. Additionally, the strong negative correlation between number of seeds/pod.

Table 5. Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficients among pod and seed traits of the 39 green beans genotypes

Traits	PP	PL	PW	SL	SW	SP	100SW
PP		0.74**	-0.52*	-0.37*	-0.90**	0.99**	-0.16
PL	0.38**		-0.53**	-0.16	-0.79**	0.82**	0.02
PW	-0.35**	-0.23*		0.11	0.99**	-0.44**	0.75**
SL	-0.32**	-0.11	0.47**		0.94**	-0.43**	0.55**
SW	-0.30**	-0.12	0.29**	0.31**		-0.99**	0.50**
SP	0.46**	0.69**	-0.49**	-0.40**	-0.16		-0.41*
100SW	-0.31**	0.05	0.23	0.24*	0.11	-0.05	

PP: Pods/peduncle; PL: Pod length (cm); PW: Pod width (cm); SL: Seed length (cm); SW: Seed width (cm); SP: Seeds/pod; 100SW: 100- Seed weight (g)

and 100 seed weight (rg = -0.41*) confirms the compensatory effect between seed number and seed mass, a common feature in yield component interactions of legumes (Gambín and Borras, 2010).

Seed length and width were also negatively correlated with number of seeds/pod, but positively correlated with 100 seed weight at the genotypic level. This indicates that larger seeds contribute more to individual seed weight but with fewer numbers of seeds/pod. This negative relationship has been previously reported in common beans by Geravandi *et al.,* (2020).

Phenotypic correlations generally mirrored genotypic trends, but had lower values in some cases as also observed by Ketema and Geleta (2022). The positive phenotypic association of number of pods/peduncle with pod length (rp = 0.38**), and number of seeds/pod (rp = 0.46**) suggests that these traits are jointly expressed under field conditions. However, the negative phenotypic correlations with pod width (rp = - 0.35*), seed length (rp = -0.32*), seed width (rp = -0.30*) and 100 seed weight (rp = -0.31*) reflects the compensatory effect of number of pods and seed size, since yield is a function of number and weight. For plant breeders, genotypic correlations are more informative for selection decisions, as they reflect heritable relationships rather than environmentally-induced associations in phenotypic correlation.

Conclusion

The study revealed substantial genetic variability among the 39 green beans genotypes for key pod and seed traits across environments. High heritability and genetic gain estimates for pod length, seed length, number of seeds/pod and particularly 100 seed weight demonstrate that these traits are predominantly under genetic control and can be effectively improved through phenotypic selection. The predominance of

stronger genotypic over phenotypic correlations confirmed stable genetic associations among yield components, particularly among pod number, pod length, and seeds/pod, although trade-offs between seed number and seed size were evident. Traits such as pod length, seed length, seeds/pod, and 100 seed weight are reliable selection criteria for yield improvement in green beans under tropical environments.

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