Original Research Article

Study on genetic variability and heritability in F_3 population of yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) for yield and its components

Abstract

Yardlong bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt), is significant among legume vegetable crops. Global warming and climate change can significantly impact its cultivation, yield, and production. This study examined the F_3 population of five yardlong bean families: F_3-1, F_3-2, F_3-3, F_3-4, and F_3-5. The findings revealed that all five families exhibited high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for yield per plant, indicating substantial variability for these traits in their progenies. For all the characters under consideration, the genotypic variation coefficient was lower than the phenotypic coefficient of variation. High heritability, along with high genetic advance per mean (GAM), was observed in pod weight, pods per plant, yield per plant, and vine length. This indicates significant potential for selecting these traits within ~~these~~ specific populations due to the wide range of variation and the influence of additive gene action. The study will help in selecting traits for further crop improvement programs.

Keywords: Heritability, Yardlong bean, Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Genetic Advance as Percent Mean (GAM)

Introduction

“The yardlong bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt; YB) is a significant legume crop belonging to the Fabaceae family, a chromosome number of 2n = 2x = 22. It is widely grown in tropical and subtropical regions across the globe. Renowned for its long, tender pods, this crop is a staple in many diets and plays a crucial role in sustainable agriculture due to its nitrogen-fixing ability” [1,2]. The cultivation of yard long bean is particularly significant in regions where soil fertility and crop productivity are major concerns [3,4]. Globally, Brazil is the leading producer of yard long beans. In India, which contributes about 28.12% of the world's grain legume production, the annual yield is approximately 23.37 million tonnes from around 29 million hectares of cultivated land [5]. “In India, yardlong beans are predominantly grown in Kerala, Karnataka, and Maharashtra. The primary constraints of YB cultivation under low rainfall conditions are low fertile lands, frequent dry spells, poor availability of quality seeds, lack of improved varieties, and a narrow genetic base”[40-42]. There is an urgent need to enhance the genetic potential of yard long bean for yield.

“The genetic improvement of yard long bean has become a priority to meet the growing demand and to enhance yield potential, resilience to biotic and abiotic stresses, and nutritional quality. One of the critical approaches to achieving these goals is studying genetic variability and heritability within breeding populations” [6]. Understanding the genetic architecture of yield and its contributing traits can provide valuable insights for breeders aiming to develop superior cultivars.

“To increase yield through selection, it's vital to thoroughly grasp the genetic variability within the germplasm and the heritability of desirable traits. This requires a detailed examination of ancillary characters to facilitate better selection. Hence, this study aimed to explore the natural extent of genetic variability in segregating populations of YB, with a focus on pod yield and other yield component traits for future breeding efforts” [7,8].

Genetic parameters like the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are valuable for assessing the variability within germplasm. Burton [9] suggested that considering both GCV and heritability estimates can provide a more accurate estimation of the progress expected from phenotypic selection. Values for heritability and genetic advances are more dependable for predicting gains under selection compared to heritability estimates alone. Thus, this study was conducted to enhance YB genetically by assessing genetic variability and heritability in selected F_3 families.

Materials and methods

Plant material

The material for investigation was collected at the Department of Genetics and Plant Breeding (GPB), College of Agriculture (COA), Vellayani, Kerala, India. The experimental material consisted of five families., F_3-1, F_3-2, F_3-3, F_3-4, and F_3-5. The F_3 populations were grown as families, and the F_3 populations were sown following a spacing of 1.5m between the rows and 0.45m between the plants within a row. Agronomic practices were done as per the Package of Practices Recommendations Crops 2016 of Kerala Agricultural University [10].

Experimental design

The experiment was conducted at the GPB, COA, Vellayani, from February to May 2024. Five replications of each family with five progenies per replication were laid out in a compact family block design. Data were recorded for yield and yield attributing traits *viz.*, days to 50% flowering, pod length, pod width, pod weight, pods per plant, yield per plant, vine length, harvest index, and crop duration. The data thus generated were subjected to statistical analysis.

Statistical analyses

The data were subjected to analysis of variance (ANOVA). The mean values were compared at a $p < 0.05$ significance level. The study was done using the GRAPES (General R-based Analysis Platform Empowered by Statistics, (www.kaugrapes.com) software V:1.10 [11].

The mean values obtained for each character were subjected to analysis of variance using a compact family block design according to the model described by Chandel [12]. The study was carried out in two stages as families. The analysis variance (ANOVA) of families was analyzed in compact family block design with r replications, as shown in Table 1.

Table 1. Analysis of variance in Compact Family Block Design with r replication

Source	Degrees of freedom	Mean Squares	Expected mean squares
Replications	(r-1)	M_1	$\sigma^{2}{}_{e}{}^{1} + \sigma^{2}\ r$
Families	(f-1)	M_2	$\sigma^{2}{}_{e}{}^{1} + \sigma^{2}\ f$
Error	(r-1) (f-1)	M_3	$\sigma^{2}{}_{e}{}^{1}$

The progenies under each family were analyzed separately for each character. The ANOVA for progenies was conducted, as shown in Table 2.

Table 2. Analysis of variance for progenies

Source	Degrees of freedom	Mean Squares	Expected mean squares
Replications	(r-1)	M_4	$\sigma^{2}{}_{e}{}^{2} + p\sigma^{2}{}_{r}$
Progenies within families	(p-1)	M_5	$\sigma^{2}{}_{e}{}^{2} + r\ \sigma^{2}{}_{p}$
Error	(r-1) (p-1)	M_6	$\sigma^{2}{}_{e}{}^{2}$

Where,

r = Number of replications

f = Number of families

p = Number of progenies within each family

M_4 = Mean sum of squares due to replications

M_5 = Mean sum of squares due to families

M_6 = Mean sum of squares due to main plot error

$\sigma^{2}{}_{e}{}^{1}$= Error variance for families

$\sigma^{2}{}_{e}{}^{2}$= Error variance for progenies

$\sigma^{2}r$ = Variance between replications

$\sigma^{2}p$ = Variance between progenies

Before comparing, a homogeneity test of error variance for progenies was carried out for each character by applying Bartlett's homogeneity test described by Panse and Sukhatme [12].

From Table 2, the following statistics were computed.

(1) Standard error of the mean (S.Em) = $\sqrt{M6/r}$

(2) Critical difference (C.D.) = $\sqrt{2}$ S.Em x x t (0.05) at error degree of freedom

(3) Coefficient of variation (C.V.) % = $\frac{\sqrt{M6}}{Mean\ of\ progenies}$ x 100

Phenotypic and genotypic coefficients of variation (PCV and GCV) were calculated following equations 1 and 2. Broad-sense heritability (h^2 (bs)) was determined using the equation 3 provided by Lush [14]. The genetic advance was estimated from the heritability estimates using equation 4 proposed by Johnson [15]. Genetic advance per mean is computed by using equation 5.

$$\text{Phenotypic coefficient of variation, PCV} = \frac{\sqrt{VP}}{\bar{X}} \times 100 \qquad \text{(Equation 1)}$$

$$\text{Genotypic coefficient of variation, GCV} = \frac{\sqrt{VG}}{\bar{X}} \times 100 \qquad \text{(Equation 2)}$$

$$\text{Heritability, H2} = \frac{VG}{VP} \times 100 \qquad \text{(Equation 3)}$$

$$\text{Genetic Advance, GA} = k.\ \text{H2}.\sqrt{VP} \qquad \text{(Equation 4)}$$

$$\text{Genetic advance as percent mean, GAM} = \frac{GA}{\bar{X}} \times 100 \qquad \text{(Equation 5)}$$

Results and discussion

Analysis of variance

Analysis of variance (ANOVA) was done to know the variations among the progenies based on the nine morphological traits. The analysis of variance for all the characters studied in five families of YB was presented in Table 3. The analysis of variance between families revealed that the mean squares due to crosses were significant for pods per plant.

Bartlett's test for error variances for five families indicated that the error variances were homogeneous for the characters pod width, vine length, and harvest index and other characters like days to 50% flowering, pod length, pod weight, pods per plant, yield per plant and crop duration are not homogenous between families and all characters are homogenous within each family.

Before comparing, a homogeneity test of error variance for progenies was carried out for each character by applying Bartlett's homogeneity test described by Panse and Sukhatme[13]. Between families, Bartlett's test for error variances for five families indicated that the error variances were homogeneous for the characters pod width, vine length, and harvest index and other characters like days to 50% flowering, pod length, pod weight, pods per plant, yield per plant and crop duration are not homogenous between families. However, all progeny error variances within the families are homogenous because these are F_3 segregation populations [7,8,38,39].

Between families, all characters except pod width, vine length, and harvest index, all five families were significantly different. The ANOVA among progenies within each family indicated a significant difference between progeny means for characters days to 50% flowering, pods per plant, yield per plant, and crop duration in F_3-1, in F_3-2 for pods per plant and vine length, in F_3-3 for vine length. While in F3-4 and F3-5, no progeny means were significantly different.

Genetic parameters

Segregation, by allowing allelic recombination, increases the variability among the population. The estimates of genetic parameters viz., phenotypic and genotypic coefficient of variation (PCV and GCV), heritability in a broad sense, genetic advance, and genetic advance as percent of mean were computed for nine characters in five families of yard long bean (Table 4). The PCV, GCV, heritability, and GAM ranged from 1.54 to 50.30, 1.22 to 37.69, 47.23 to 88.21%, and 6.40 to 49.75%, respectively.

Different genotypes exhibit a broad spectrum of variability across various traits. The presence of extensive variability in quantitative traits has been documented in yardlong beans [16,17,18,19,31]. Genetic Coefficient of Variation (GCV) provides essential information for evaluating and analyzing these traits' genetic variability range. In contrast, the Phenotypic Coefficient of Variation (PCV) assesses the extent of total variation present [34,35].

Phenotypic and Genotypic coefficient of variation (PCV and GCV)

High PCV and GCV were observed in yield per plant for all five families (Figure 1). Moderate PCV was observed for days to 50% flowering by F_3-5, pods per plant by F_3-1, F_3-4, and both moderate PCV and GCV were observed in F_3-5, crop duration by F3-$_3$. All five families showed low PCV and GCV in pod length, pod weight, vine length, and harvest index. The analysis showed that the phenotypic coefficient of variation (PCV) was slightly greater than the genotypic coefficient of variation (GCV) for all traits. This suggests that the characteristics are primarily influenced by the genotypes with minimal environmental impact.

High PCV and GCV values were recorded for yield per plant across all five families, consistent with the results reported for cowpea and vegetable cowpea yield (kg/plant) [16,26]. Moderate PCV was noted for days to 50% flowering in F3-5 and pods per plant in F3-1 and F3-4, while moderate PCV and GCV were observed in crop duration for F3-5 and F3-3. These observations align with the findings of vegetable cowpeas and cowpeas [16,20,30]. Conversely, all five families exhibited low PCV and GCV in traits such as pod length, pod weight, vine length, and harvest index, which agrees with the studies on bush cowpeas [18, 21,29].

Heritability (H^2) and genetic advance as percent mean (GAM)

For all characters, moderate to high heritability was observed for all five families. In F_3-1, the highest heritability was observed in days to 50% flowering, pod width, pod weight, pods per plant, and crop duration. Moderate heritability was observed in pod length, yield per plant, vine length, and harvest index.

In F_3-2, the highest heritability was observed in days to 50% flowering, pod width, pod weight, pods per plant, yield per plant, and vine length. Moderate heritability was observed in pod length, harvest index, and crop duration. Highest heritability in yield per plant, vine length, and crop duration. Moderate heritability was observed in days to 50% flowering, pod length, pod width, pod weight, harvest index, and pods per plant in F_3-3.F_3-4. The highest heritability was observed in pod weight and crop duration. Moderate heritability in days to 50% flowering, pod length, pod width, yield per plant, pods per plant, vine length, and harvest index.Highest heritability in pod width, crop duration, pods per plant, and yield per plant. Moderate heritability was observed in days to 50 % flowering, pod length, pod weight, vine length, and harvest index in F_3-5. The highest heritability and genetic advance as per mean observed in yield per plant was depicted in Figure 2.

High heritability suggests a significant influence of additive and additive x additive gene action, which can be harnessed through simple selection methods [37,38,39]. Similar findings have been reported for yield (kg/plant) in yardlong bean, plant height at final harvest and the pods per plant in cowpea, pod length in yardlong bean, vegetable cowpea, the number of pods per plant in bush cowpea, and in vegetable cowpea [16,21,22,23,24,25]. Additionally, high heritability in yardlong bean and cowpea for traits such as pod length, vine length, and the number of pods per plant, pods per plant, and yield per plant [22,26,27,28].

The highest GAM was observed in F_3-1 for pod weight, pods per plant, and yield per plant. In F_3-2, pods, yield per plant, and vine length were shown. F_3-3 for yield per plant and vine length F_3-4 and F_3-5 showed the highest GAM for pods per plant and yield per plant.

Moderate GAM was observed in days to 50% flowering and vine length by F_3-1. In F_3-2, days to 50% flowering, pod width, pod weight, pods per plant, harvest index, and crop duration[32,33]. In F_3-3, observed, moderate GAM in days to 50% flowering, pod width, pod weight, pods per plant, harvest index, crop duration, and vine length. In F_3-4, days to 50% flowering, pod length, harvest index, crop duration, and vine length showed moderate GAM. F3-5 a moderate GAM was observed in days to 50% flowering, pod length, harvest index, and vine length.

Low GAM was observed in pod width, harvest index, and crop duration (F_3-1). –Crop duration (in F_3-2).pod weight (in F_3-4). Pod weight and crop duration (in F_3-5).

High heritability with high GAM for pods per plant, yield per plant, pod weight, and vine length suggest additive gene action. These traits can be used for effective selection in further breeding programs to improve the yield.

Table 3. Analysis of variance (mean squares) between families and between progenies within families of five F_3 families for yield contributing attributes in the yardlong bean.

Source of variation	Degrees of freedom	Days to 50 % flowering	Pod length (cm)	Pod width (mm)	Pod weight(g)	Pods per plant	Yield per plant (g)	Vine length (m)	Harvest index (%)	Crop duration (days)
Analysis of variances between families										
Replications	4	57.12	18.57	1.09	5.9**	32.85	326.03	1.80	389.12**	48.73
Families	4	148.70**	43156**	0.95	51.81**	943.77**	3347429.29**	2.42	41.95	938.87**
Error	16	23.19	6.71	0.49	1.00	16.91	10227.22	1.80	11.75	23.66
Bartlett's test		S	S	NS	S	S	S	NS	NS	S
Analysis of variances between progenies of different families										
			F_3-1							
Replication	4	25.36**	4.27	0.13	4.16	20.34*	21317.30*	0.63**	4.93	6.46
Progenies	4	22.96**	7.40	0.14	4.39	27.74**	8294.47	0.13	6.11	10.66*
Error	16	3.16	5.66	0.08	2.24	4.99	5603.48	0.10	5.19	3.41
Bartlett's test		NS	NS	NS	NS	NS	NS	NS	NS	NS
			F_3-2							
Replication	4	36.76**	14.48	1.75*	1.48*	27.54*	15637.69**	0.81**	7.29	33.64
Progenies	4	15.76	5.49	0.82	0.50	32.24*	2804.25*	0.61**	12.38	42.64
Error	16	6.78	5.01	0.45	0.28	7.12	921.55	0.08	7.36	32.54
Bartlett's test		NS	NS	NS	NS	NS	NS	NS	NS	NS
			F_3-3							
Replication	4	14.74	3.45	0.08	3.67*	9.74	3124.59	0.43*	32.79	45.44
Progenies	4	10.34	21.85	0.39	1.34	11.44	3973.93	0.57**	15.46	79.74
Error	16	6.32	13.94	0.32	1.04	7.69	1803.36	0.11	11.48	31.77
Bartlett's test		NS	NS	NS	NS	NS	NS	NS	NS	NS
			F_3-4							
Replication	4	36.26	2.74	0.11	0.03	10.84	1154.23	0.55**	6.51	37.16
Progenies	4	19.66	6.05	0.48	0.22	31.34	1616.44	0.08	7.85	68.66
Error	16	12.61	4.70	0.32	0.11	22.49	1005.05	0.06	7.02	38.06
Bartlett's test		NS	NS	NS	NS	NS	NS	NS	NS	NS
			F_3-5							
Replication	4	31.94	18.37	0.96*	1.10**	32.04	1630.14	0.33	6.42	20.66
Progenies	4	26.74	19.32	0.59	0.30	33.54	2714.75	0.21	10.67	34.46

Error	16	24.17	16.37	0.24	0.19	11.42	1019.36	0.15	6.30	25.68
Bartlett's test		NS	NS	NS	NS	NS	NS	NS	NS	NS

*significant at 1%   ** significant at 5%

S-significant   NS-non significant

Table 4. Genetic variability and selection parameters estimated for yield and its components in F_3 populations of five families of yardlong bean

Character	Family	Mean	PV	GV	PCV	GCV	H^2(bs) (%)	GA	GAM
Days to 50% flowering	F_3-1	42.92	21.19	14.40	6.80	5.60	67.98	6.45	15.02
	F_3-2	45.88	21.18	14.40	6.89	5.68	67.97	6.44	14.05
	F_3-3	40.84	15.39	9.07	6.13	4.71	58.97	4.77	11.67
	F_3-4	47.68	29.74	17.13	7.89	5.99	57.61	6.47	13.57
	F_3-5	44.84	46.07	21.90	10.13	6.98	47.54	6.65	14.82
Pod length(cm)	F_3-1	39.13	11.92	6.26	5.52	4.10	52.55	3.74	9.55
	F_3-2	32.96	9.49	4.48	5.36	3.68	47.23	3.00	9.09
	F_3-3	39.12	32.99	19.06	9.18	6.98	57.76	6.83	17.47
	F_3-4	29.55	9.81	5.11	5.76	4.15	52.09	3.36	11.37
	F_3-5	33.83	32.41	16.04	9.78	6.88	49.50	5.81	17.16
Pod width (mm)	F_3-1	8.42	0.20	0.12	1.54	1.22	62.36	0.57	6.82
	F_3-2	8.39	1.18	0.73	3.75	2.95	61.78	1.38	16.48
	F_3-3	7.95	0.64	0.32	2.84	2.01	50.26	0.83	10.42
	F_3-4	8.13	0.72	0.41	2.99	2.25	56.46	0.99	12.14
	F_3-5	8.17	0.77	0.54	3.08	2.57	69.36	1.25	15.35
Pod weight (g)	F_3-1	12.25	6.18	3.94	7.10	5.67	63.83	3.27	26.68
	F_3-2	10.18	0.73	0.44	2.67	2.09	61.21	1.08	10.58
	F_3-3	11.17	2.17	1.13	4.40	3.18	52.18	1.58	14.18
	F_3-4	8.79	0.30	0.19	1.87	1.50	64.26	0.73	8.25
	F_3-5	9.24	0.45	0.26	2.20	1.68	57.90	0.80	8.66
Pods per plant	F_3-1	41.56	31.73	26.74	8.74	8.02	84.27	9.78	23.53
	F_3-2	35.96	37.93	30.82	10.27	9.26	81.25	10.31	28.67
	F_3-3	32.36	17.59	9.90	7.37	5.53	56.29	4.86	15.03
	F_3-4	27.24	49.33	26.84	13.46	9.93	54.41	7.87	28.90
	F_3-5	27.04	42.67	31.26	12.56	10.75	73.25	9.86	36.45
Vine length (m)	F_3-1	3.97	0.21	0.12	2.32	1.70	53.69	0.51	12.77
	F_3-2	2.99	0.67	0.59	4.73	4.44	88.21	1.49	49.75
	F_3-3	3.64	0.66	0.55	4.26	3.89	83.41	1.40	38.35
	F_3-4	2.63	0.13	0.07	2.19	1.61	54.48	0.40	15.39
	F_3-5	3.37	0.32	0.18	3.09	2.29	54.88	0.64	18.98
Harvest index (%)	F_3-1	37.86	10.26	5.07	5.21	3.66	49.43	3.26	8.61
	F_3-2	35.58	18.27	10.91	7.17	5.54	59.70	5.26	14.77
	F_3-3	37.43	24.64	13.17	8.11	5.93	53.43	5.46	14.60
	F_3-4	35.64	13.46	6.44	6.15	4.25	47.85	3.62	10.15
	F_3-5	34.86	15.70	9.41	6.71	5.19	59.90	4.89	14.03
Crop duration (days)	F_3-1	87.72	13.39	9.98	3.91	3.37	74.53	5.62	6.40
	F_3-2	99.64	68.67	36.13	8.30	6.02	52.62	8.98	9.02
	F_3-3	95.96	105.15	73.39	10.47	8.75	69.79	14.74	15.36

	F_3-4	104.48	99.11	61.05	9.74	7.64	61.60	12.63	12.09
	F_3-5	97.32	55.01	29.32	7.52	5.49	53.31	8.15	8.37

PV-Phenotypic variation PCV- Phenotypic coefficient of variation

GV-Genotypic variation GCV- Genotypic coefficient of variation

H^2(bs) (%)-Heritability (broad sense) GA- Genetic advance GAM-Genetic advance per mean

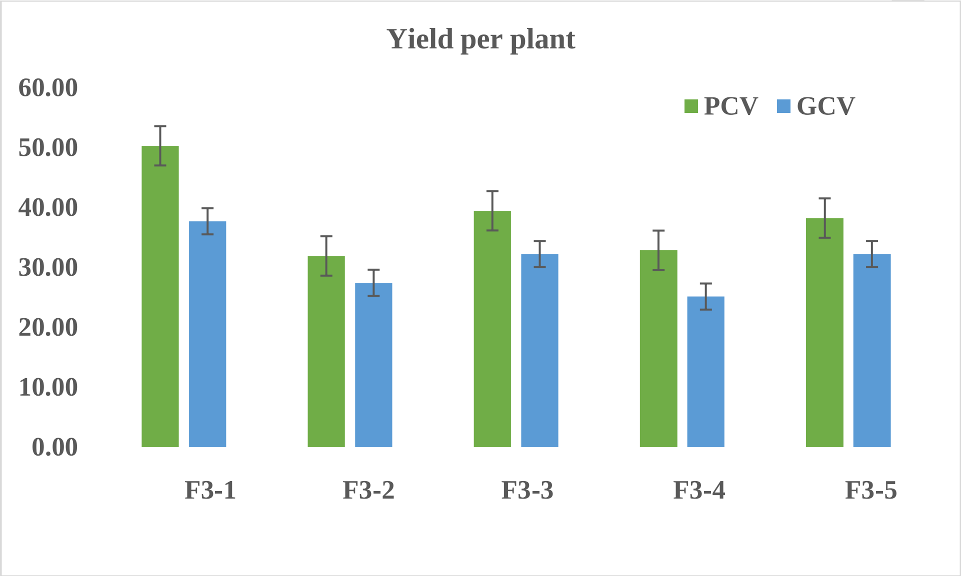

Figure 1. Phenotypic and genotypic coefficient of variation (PCV & GCV) of yield per plant in all five families

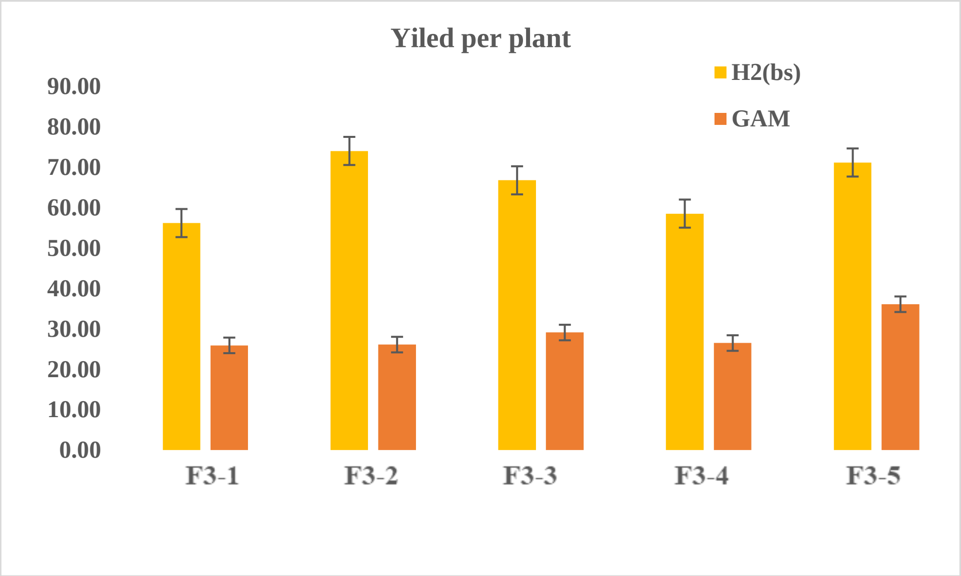

Figure 2. Heritability (bs)% and genetic advance per mean(%) of yield per plant in all five families

Conclusion

The phenotypic coefficient of variation (PCV) for all traits exceeds the genotypic coefficient of variation (GCV), indicating that environmental factors influence these traits. However, the minimal differences between PCV and GCV suggest negligible environmental impact on trait expression. Traits such as the number of pods per plant, yield per plant, pod weight, and vine length exhibit high values of both PCV and GCV. These traits show substantial variability, heritability, and genetic progress as a percentage of the mean, indicating that they possess sufficient genetic variability and are influenced primarily by additive genetic factors with minimal environmental interference. Therefore, direct selection for these traits will likely enhance crop yield. The observed variability among the F3 progenies of yard long bean from five different families indicates that progeny selection is an effective strategy to increase yield.

Statements and declarations

Data availability

Data is provided in the manuscript

Disclaimer (Artificial intelligence)

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