






Genetic variance estimates and relationship among yield and yield components of mung bean (*Vigna radiata* L.)

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ABSTRACT

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Some mung bean genotypes were evaluated to estimate the level of genetic variability and identify traits that are closely linked to seed yield. The evaluation was conducted at three locations in 2022 and 2023. The experimental design was randomized complete block (RCBD) replicated three times. Parameters measured included flowering, pod and other yield parameters. Data were analyzed using SAS. Most of the parameters measured had significant mean squares of genotypes and high broad-sense heritability. Estimates of genotypic variance were significant and larger than environmental variance estimates for most of the parameters. Expected gains ranged from low (1.46%) in pod weight/plot, to high (23.49%) in pod length. Strong positive phenotypic and genotypic correlation existed between pod and seed weight per plot, and seeds per plot, as well as pod length. The study revealed substantial variability in the mung bean genotypes and presented number of seeds per plot and pod length as major components of mung bean grain yield. Progress will be made in the improvement of the crop for grain yield.

Contribution/Originality: This is one of the very few studies on mung bean improvement in Nigeria. It gave an insight into the appropriate breeding scheme to employ and the traits that could be used as selection criteria for yield improvement to make rapid progress.

1. INTRODUCTION

An underutilized legumes whose importance in food and nutrition security has not been exploited is mung bean (*Vigna radiata*). Mung bean had diploid chromosome number of $2n = 2x = 22$ and a genome size of 579 Mb [1]. Mung bean, though widely grown in India, has good adaptability varied environments, with short maturity time and can enrich soil with nitrogen. It is higher in some mineral components such as magnesium, sodium, sulphur, zinc and ash, than cowpea and its iron content is comparable to that of cowpea. Unlike other underutilized legumes with hard-to-cook problem, mung bean is easier to cook, with easy digestibility and less flatulence. Hence, mung bean has the ability to be a good substitute to cowpea in household diet.

The understanding of level of variation in crop germplasms for yield and other agronomic parameters is important in crop improvement. This enables plant breeders to decide on the right breeding method to employ and

the suitable selection strategy [2]. The values of genetic parameters such as heritability, genotypic variances and genetic gains give clearer picture of the gene action controlling a trait and progress that could be made from selection in advanced generation.

The role of heritability cannot be over-emphasized in plant breeding as it helps to understand the breeding value. Genetic advance helps to measure the progress in selection as it estimates the expected and the actual gain [3-5]. Estimation of genotypic and phenotypic coefficients of variation, are also as essential in crop improvement, as heritability and genetic advance [6, 7]. Reports on mung bean genetic variability is limited in the literature [8] though low genetic variability has been reported in some cases in the local collections.

This study therefore, aims at determining (1) the level of genetic variation of some mung bean accessions for grain yield and its components (2) the correlation among yield components of mung bean.

2. MATERIALS AND METHODS

2.1. The Mung Bean Genotypes and Field Evaluation

Twenty-one mung bean accessions obtained from the International Institute of Tropical Agriculture (IITA), Nigeria were used for this study. The accessions contains both green gram and black gram with varying seed colour ranging from green, orange, light brown and black. The accessions were evaluated in the cropping season of 2022 and 2023 at three out-stations of the Institute of Agricultural Research and Training (IAR&T), Nigeria - Ile-Ife, Ibadan and Kishi. Randomized complete block design in three replication was used to lay out the experiment. The plot size was 2.4 m x 2.4 m with a spacing of 0.6 m between rows and 0.6 m within rows. Three seeds were sown per hole and later thinned to two plants per hill to give a total of 50 plant stands per plot. Pre-emergence herbicide (Metolachlor 960 gE.C. at 1.44 kg/ha) was applied at planting. Weeding was done as and when due using hoe. Magic Force (Lambda-cyhalothrin 15 % + Dimethoate 300 g/L) insecticide was sprayed at the vegetative and reproductive stages against insect pests.

2.2. Parameters Assessed

Parameters assessed included number of days to 50 % flowering and podding, pod length, number of pods per plant, number of seeds per pod, 1000 seed weight, pod and seed weight per plot. Days to 50 % flowering was recorded by counting the number of days from planting to when the flowering reached 50 % per plot. Days to 50 % podding was recorded by counting the number of days from planting to when the pods reached 50 % per plot. Pod length (in centimeter) was taken as average length of 10 randomly selected pods per plot. Pods per plant was taken by dividing the total number of pods per plot by the number of plants per plot at harvest. Seeds per pod was taken by threshing 10 randomly selected pods per plot and average of the total seeds estimated. 1000 seed weight was taken after threshing by counting and weighing 1000 seeds per plot, and expressed in gram. Pod weight (kg/plot) was taken by weighing all harvested pods per plot, while seed weight (kg/plot) was taken by weighing all the seeds after threshing all the dry harvested pods per plot.

2.3. Statistical Analyses

Mean, standard error, range, phenotypic (PCV) and genotypic coefficient of variation (GCV) were estimated. PCV and GCV were computed following [9] as.

$$PCV = \sqrt{\sigma^2_{ph}/\bar{x}} \times 100$$

$$GCV = \sqrt{\sigma^2_g/\bar{x}} \times 100$$

Where σ^2_{ph} is phenotypic variance, σ^2_g is genotypic variance, and \bar{x} is mean.

Combined analysis of variance (ANOVA) across environments was conducted using this statistical model.

$$Y_{ijkl} = \mu_i + E_{ij} + R(E)_{ijk} + G_{il} + GE_{ijl} + e_{ijkl}$$

Where μ_i is mean effect; E_j is the effect of the environment j ; $R(E)_{ijk}$ is effect of replication k within environment j ; G is effect the genotype l ; GE_{ijl} is the effect of the interaction between environment j and genotypes l and e_{ijkl} is the experimental error effect associated with genotype l and replication k within environment j .

Values of genetic variances, environmental variance, genotype by environment interaction variance and phenotypic variance were obtained from mean squares from ANOVA according to Hallauer and Miranda [3].

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 σ^2_g = Component of variance estimate due to genotype.

σ^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 following Hallauer and Miranda [3] as.

$$\Delta G = k \cdot \sigma_{ph} \cdot h^2.$$

Where k is selection differential expressed in standard form (=1.216 at 25 % selection intensity); σ_{ph} = 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.

Phenotypic and genotypic correlation coefficient analysis were also conducted among traits.

3. RESULTS AND DISCUSSION

3.1. Mean, Range and Estimates of Variability for the Traits Measured

Means of traits is shown in Table 1. Mean days to 50% flowering and podding was 48 and 52 days, respectively, indicating that pod develops three days after fertilization in mung bean. Pods produced per plant was high with mean value of 37 pods/plant, and mean seed weight of 1.17 kg/plot. Range was wide for all the traits measured. The wide range obtained for all the traits in this study indicates that the genotypes constitute a pool of germplasms with high variability. Hence, selection for desirable characters will bring about significant progress in the improvement of mung bean. The range and overall mean for pod length, pods per plant and seeds per pod obtained in this study were similar to those obtained by Yoseph, et al. [8] and Gayacharan, et al. [10] for mung bean, but higher than those reported by Garg, et al. [11]. Mung bean grows luxuriantly especially in the rainy season produces between 4 -9 pods per peduncle and this contributes to high pod number per plant, and pod and seed weight per plot.

PCV was slightly higher than GCV except for pods per plant, pod and seed weight, where the gap was wide. The magnitude of difference between PCV and GCV reveals environmental influence on any character. Wide gap between PCV and GCV for pods per plant, pod and seed weight per plot indicates great environmental influence on these traits, while slight gap for other traits suggests high genetic influence on them. PCV and GCV above 20 % was regarded to be high, between 10-20 % as moderate and less than 10 % as low [12]. The moderate to high PCV and GCV recorded for some parameters is similar to what was obtained by Yoseph, et al. [8]; Gayacharan, et al. [10] and Garg, et al. [11]. The high PCV estimates for pods per plant, the low PCV and GCV estimates for days to 50% flowering, and the moderate PCV and GCV for pod length and seeds per pod were similar to what was obtained by Garg, et al. [11].

Table 1. Mean±SE, range and estimates of variability for seed yield and its components in the mung bean genotypes evaluated at Ile-Ife, Ibadan and Kishi in 2022 and 2023.

Traits	Mean±SE	Range	PCV	GCV
Days to 50% flowering	48.08±0.79	43.3 - 56.2	5.92	5.19
Days to 50% podding	52.10±0.97	48 - 60.51	5.59	4.56
Pod length (cm)	8.25±0.21	4.9 - 9.09	12.97	12.16
Pods/Plant	37.76±4.38	19.54 - 57.97	20.66	4.82
Seeds/Pod	12.49±0.39	7.7 - 13.92	11.74	10.45
1000 seed weight (g)	39.28±0.86	34.97 - 45.41	5.56	4.06
Pod weight/Plot (kg/Plot)	1.73±0.26	0.71 - 3.63	26.8	4.37
Seed weight/Plot (kg/Plot)	1.17±0.15	0.53 - 2.26	25.41	11.18

Note: SE: Standard error; PCV: Phenotypic coefficient of variation.
GCV: Genotypic coefficient of variation; cm- centimeter; g- gram; kg- kilogram.

3.2. Mean Squares from Combined ANOVA for the Parameters Measured

Mean squares from combined ANOVA is shown in Table 2. The environmental mean square was significantly different for all the parameters assessed, suggesting wide variation in the study locations. Belay, et al. [13] also observed significant environmental variation for some yield parameters except for pods per plant. Highly significant genotypic mean squares was observed for most of the parameters measured, except for pods per plant, pod and seed weight, indicating the existence of substantial level of genetic variability among the genotypes. Significant mean squares of genotypes for yield traits in mung bean was also observed by Yoseph, et al. [8]; Garg, et al. [11]; Mwangi, et al. [14] and Azam, et al. [15]. However, Garg, et al. [11] observed significant mean square of genotypes for number of pods per plant and seed yield as against what was obtained in this study.

Mean squares of environment by genotype interaction was significant for days to 50% podding, seeds per pod and 1000 seed weight. Coefficient of determination (R^2) was high for all the parameters. The significant mean squares of environment by genotype interaction for days to 50% podding, seeds per pod and 1000 seed weight, suggests that genotypes will respond differently to different environments with respect to these traits.

Table 2. Mean squares from the combined ANOVA for seed yield and its components in the mung bean genotypes evaluated at Ile-Ife, Ibadan and Kishi in 2022 and 2023.

Sources of variation	df	Days to 50% flowering	Days to 50% podding	Pod length (cm)	Pods/ Plant	Seeds/ Pod	1000 seed weight (g)	Pod weight/Plot (kg/Plot)	Seed weight/Plot (kg/Plot)
Env.	5	498.54**	271.5**	27.96**	5195.34**	1.41**	172.44**	84.25**	34.94**
Rep (Env)	12	22.87**	30.50*	0.46	1396.53**	0.02	32.38*	4.97**	1.49**
Geno.	20	147.88**	121.34**	20.13**	377.84	0.84**	68.39**	1.01	0.60
Env. x Geno.	100	12.14	23.03**	0.71	529.8	0.08**	27.72**	1.17	0.44
Error	240	9.19	15.57	0.56	486.86	0.05	17.71	1.34	0.60
CV%		6.3	7.57	9.1	58.4	11.72	10.71	66.94	66.3
R ²		0.77	0.64	0.88	0.56	0.81	0.63	0.73	0.73

Note: Env- Environment; Rep- Replication; Geno.- genotypes; cm- centimeter; g- gram; kg- kilogram; R²: Coefficient of determination.
 *, **, Significant at 5% and 1% level of probability, respectively.

3.3. Variance Estimates of the Traits Measured

Estimates of genotypic variance component were significant and larger than environmental variance estimates for most of the traits except for pods per plant, and pod and seed weight per plot (Table 3). Genotype by environment (GxE) variance was positive in most cases except for pod and seed weight/plot. The GxE variances were lower than the estimates of genotypic variance for days to 50 % flowering and podding, pod length and seeds per pod, but higher for other traits. The moderate estimates of genotypic variance for almost all the traits, with the broad range revealed substantial genetic variability in the mung bean genotypes for these traits. The low estimates of genotypic variance for pod and seed weight/plot is not surprising in the view of the higher environmental and GxE variance for these traits, indicating the important role the environment plays on yield.

Large phenotypic variance was recorded for some of the traits. High heritability values were also gotten for most of the parameters except for pods per plant (5.5 %) and pod weight per plot (2.65 %). Heritability estimate was however moderate for seed weight/plot (19.36 %) (Table 3).

High heritability for seeds per pod and 100 seed weight was also reported by Yoseph, et al. [8]. Heritability estimates reveal the extent of genetic control on a trait. It determines the level of inheritance of traits in a crop population. Dabholkar [16] considered heritability values less than 10% as low, between 10-30% as moderate and those above 30% as high. Abbas, et al. [17] reported high heritability values for pods per plant and seed yield on mung bean genotypes. This report however, did not support the findings in this study where number of pods/plants had very low heritability estimate, while heritability was only moderate for seed weight/plot. The high heritability value for days to 50% flowering corroborates the report of Gayacharan, et al. [10]. Moderate to high heritability values recorded for most traits in the present study indicates the prevalence of additive gene action with low environmental effects on the traits. This suggests that the traits are under genetic control and some improvement could be made in these traits through selection in the breeding programme.

Table 3. Variance components, broad-sense heritability and genetic gains of seed yield and its components in the mung bean genotypes evaluated at Ile-Ife, Ibadan and Kishi in 2022 and 2023.

Traits	σ^2_e	$\sigma^2_g \pm SE$	σ^2_{ge}	σ^2_{ph}	$H^2 \pm SE$	ΔG	$\Delta G\%$
Days to 50% flowering	1.88	6.22 \pm 2.48	0.98	8.1	76.79 \pm 0.31	4.5	9.36
Days to 50% podding	2.83	5.64 \pm 2.04	2.49	8.48	66.51 \pm 0.24	3.99	7.66
Pod length (cm)	0.14	1.01 \pm 0.33	0.05	1.14	87.89 \pm 0.30	1.93	23.49
Pods/Plant	57.52	3.32 \pm 7.55	14.31	60.84	5.5 \pm 0.12	0.88	2.32
Seeds/Pod	0.45	1.70 \pm 0.01	0.01	2.15	72.93 \pm 0.01	2.39	19.16
1000 seed weight (g)	2.23	2.55 \pm 1.16	3.34	4.77	53.38 \pm 0.24	2.40	6.12
Pod weight/Plot (kg/Plot)	0.21	0.01 \pm 0.02	-0.06	0.21	2.65 \pm 0.09	0.03	1.46
Seed weight/Plot (kg/Plot)	0.07	0.02 \pm 0.01	-0.05	0.09	19.36 \pm 0.12	0.12	10.14

Note: σ^2_e - Environmental variance; σ^2_g - genotypic variance; σ^2_{ge} - variance of genotype by environment interaction; σ^2_{ph} -phenotypic variance; H^2 - broad - sense heritability, ΔG - genetic gain, $\Delta G\%$ -genetic gain expressed as percentage of the means; SE =Standard error; cm- centimeter; g- gram; kg- kilogram.

Percentage genetic gains from selection for the traits measured ranged from 1.46 % for pod weight/plot to 23.49 % for pod length. Expected gain helps to predict progress in selection. It is regarded high when greater than 20%, low when less than 10% and moderate when it falls in between 10-20% [18]. Moderate genetic gains in addition with high broad-sense heritability observed for pod length and seeds per pod in this study was also observed by Garg, et al. [11] and Dhunde, et al. [19]. The very low values for heritability and genetic gains for pods per plant and pod weight/plot indicates the extent of environmental influence on these traits, and also suggests that selecting for these traits will not be efficient. The high heritability with low genetic gains for days to 50% flowering and podding, pods/plant, 1000 seed weight, and pod weight/plot may be influence of non-additive gene action, suggesting that improvement may be slow in selection for these traits. To ensure sufficient improvement in a selection programme, high heritability with significant amount of genetic advance is necessary [20].

3.4. Correlation Among Traits of the Mung Bean Genotypes

Correlation coefficient of parameters measured are shown in Table 4. Strong positive phenotypic correlation exists between days to 50% flowering and podding ($r_p = 0.85^{**}$). Days to 50% flowering had negative and strong phenotypic correlation with pods per plant ($r_p = -0.25^*$) and 1000 seed weight ($r_p = -0.27^*$). Days to 50% podding also had negative and significant phenotypic correlation with pod length ($r_p = -0.25^*$) and 1000 seed weight ($r_p = -0.25^*$). Pod length had significant positive correlation with seeds per pod, 1000 seed weight, pod and seed weight per plot. Pods per plant had significant positive phenotypic correlation with pod weight/plot ($r_p = 0.28^*$) as expected. Number of seeds per pod had strong positive phenotypic correlation with 1000 seed weight ($r_p = 0.45^*$), pod weight/plot ($r_p = 0.34^*$) and seed weight/plot ($r_p = 0.49^{**}$). Highly significant positive correlation exists between pod and seed weight/plot ($r_p = 0.75^{**}$).

Genotypic correlation followed the same trend with days to 50% flowering having strong positive correlation ($r_g = 0.97^{**}$) with number of days to 50% podding (Table 4). Pod length also had significant negative genotypic correlation with days to 50% podding ($r_g = -0.40^{**}$). Number of pods/plants had highly significant negative genotypic correlations with days to 50% flowering ($r_g = -1.0^{**}$) and podding ($r_g = -1.0^{**}$). Number of seeds/pods also had strong positive genotypic correlation with pod length ($r_g = 0.98^{**}$), but negative correlation with number of pods per plant ($r_g = -0.56^{**}$). 1000 seed weight was also negatively correlated with days to 50% podding ($r_g = -0.47^{**}$) and pods per plant ($r_g = -0.51^*$), but positive correlations with pod length ($r_g = 0.82^{**}$) and seeds per pod ($r_g = 0.66^{**}$). Pod weight/plot had highly significant positive correlations with pod length ($r_g = 0.79^{**}$) and number of seeds/pod ($r_g = 0.98^{**}$), but negative correlation with number of days to 50% podding ($r_g = -0.71^{**}$). Seed weight/plot also had significant negative correlation with number of days to 50% podding ($r_g = -0.44^{**}$). However, its genotypic correlations with pod length, number of seeds/pod and pod weight/plot were positive and significant ($r_g = 0.94^{**}$, 1.0^{**} and 1.0^{**} , respectively).

Table 4. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients between seed yield and yield components in the mung bean genotypes evaluated at Ile-Ife, Ibadan and Kishi in 2022 and 2023.

Traits	Days to 50% flowering	Days to 50% podding	Pod length (cm)	Pods/Plant	Seeds/Pod	1000 seed weight (g)	Pod weight/Plot (kg/Plot)	Seed weight/Plot (kg/Plot)
Days to 50% flowering		0.85**	-0.08	-0.25*	-0.04	-0.27*	0.04	0.04
Days to 50% podding	0.97**		-0.25**	-0.16	-0.24	-0.25*	-0.05	-0.11
Pod length (cm)	-0.09	-0.40**		-0.02	0.94**	0.59**	0.31*	0.51**
Pods/Plant	-1.00**	-1.00**	-0.43		0.07	0.04	0.28*	0.15
Seeds/Pod	-0.04	0.38	0.98**	-0.56**		0.45**	0.34**	0.49**
1000 seed weight (g)	-0.32	-0.47**	0.82**	-0.51*	0.66**		-0.22	0.12
Pod weight/Plot (kg/Plot)	0.05	-0.71**	0.79**	0.23	0.98**	-0.17		0.75**
Seed weight/Plot (kg/Plot)	0.06	-0.44**	0.94**	-0.03	1.00**	0.34	1.00**	

Note: cm- centimeter; g- gram; kg- kilogram; *, **: Significant at 5% and 1% level of probability, respectively.

Correlation measures the extent of relationship between traits. Correlation between two traits may be as a result of pleiotropy or tight linkage in the genes controlling them [21]. The strong positive phenotypic and genotypic correlations existing between days to 50% flowering and podding, and between pod and seed weight/plot indicates that either of the parameters in the pairs could be selected to get similar results. The significant positive association among pod and seed traits suggests the contribution of these traits to yield in mung bean. Pod length and seeds/plot had highly significant positive phenotypic and genotypic correlation with pod and seed weight/plot in the present study. This showed that these traits contribute significantly to yield. Pod length was reported to be

one of the major yield components in mung bean [11]. Yield/plant, pod weight, 100 seed weight and pod length have been reported to show positive relationship and positive direct effect on mung bean's seed yield [15]. The more the number of pods/plots, the more the weight of pods, and the more the seed yield.

Pods per plant showed a strong positive correlation with seeds/pod, but significant negative correlation with days to 50% flowering. 1000 seed weight was positively correlated with pod length. This was also reported by Garg, et al. [11]. The significant positive genotypic correlation between pod length and seeds per pod, as well as seed weight/plot, indicates that genes that increases pod length, also increases number of seeds/pods, as well as seed weight. It therefore implies that, the longer the pods, the more the number of seeds, and this will consequently result in high seed weight/plot.

The high heritability recorded in pod length and seeds per pod may also cause their strong genotypic correlation. Falconer [22] declared that the phenotypic correlation will be chiefly determined by environmental correlation, in two characters with low heritability, but the genotypic correlation will be more important in two characters with high heritability. The significant genotypic correlation of pod length and seeds per pod with seed weight/plot, their significant genetic variances and the moderate GCV for these two traits, suggests their efficiency as selection criteria in the yield improvement programme for mung bean.

4. CONCLUSION

The high heritability and wide range of some parameters in this study revealed that substantial variability exists in the mung bean germplasm for possible improvement. The low expected gains for some traits however showed that progress may be slow in selection for them. Hence, breeding strategy such as hybridization may be employed for rapid progress. It may be concluded from this study that seeds per pod and pod length are very important yield parameters that should be considered as selection criteria in the cause of seed yield improvement of mung bean.

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