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Assessment of Variability, Heritability, Genetic Advance and Correlation in Elite Germplasm of Moth Bean [*Vigna aconitifolia* (Jacq.)]

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ABSTRACT

Background: Moth bean [*Vigna aconitifolia* (Jacq.)] is an important leguminous crop known for its drought resistance and nutritional value.

Methods: This study evaluates genetic variability, Heritabilit correlation among 20 elite moth bean genotypes. Conducted at ITM University, Gwalior, the experiment followed a randomized block design (RBD) with three replications. Eleven quantitative traits, including seed yield, harvest index and protein content, were analyzed.

Result: Indicating involvement of environmental effects, phenotypic coefficients of variation (PCV) were consistently higher than genotypic coefficients of variation (GCV). The highest GCV was observed for harvest index (27.99%), seed yield per plant (26.16%) and number of pods per plant (21.76%), suggesting high genetic variability. Heritability in broad sense was very high for number of seeds per pod (98.82%), harvest index (98.80%), number of pods per plant (98.40%) and seed yield (96.84%). Genetic advance as per cent of mean was highest for harvest index (57.32%), seed yield per plant (53.03%) and number of pods per plant (44.04%), indicating the potential for substantial improvement through selection. Correlation analysis revealed strong positive associations between seed yield and harvest index (r=0.958) and number of pods per plant (r = 0.854) at genotypic level, suggesting these as key contributors to yield enhancement. These findings provide valuable insights for genetic improvement and breeding strategies aimed at enhancing moth bean productivity.

Key words: Correlation, Genetic advance, Heritability, Moth bean, Variability.

INTRODUCTION

The moth bean [*Vigna aconitifolia* (Jacq) Marechal] family is Leguminosae/Fabaceae, subfamily: Papilionaceae. It is a self-pollinated diploid (2n= 22) crop (Kohakade *et al.,* 2017). The crop is annual with spreading prostrate habit forming a mat like a cover on the soil, hence it is termed as a mat or moth bean. The canopy of moth bean covers the field surface area which conserves moisture and protects the soil from erosion. The pods, sprouts and seeds of moth bean are usually used for consumption by people in India as it is rich in protein. Among *kharif* pulses, it has the greatest resistance to drought. Moth Bean is an excellent source of high-quality protein (23.6%) in the diet of low-income groups in underdeveloped countries. According to the Food and Agriculture Organization (FAO), the total area and production of moth bean in the world in 2020 was 0.43 million hectares. According to the Ministry of Agriculture and Farmers Welfare, Government of India, the total area under production of moth bean in India in 2020-2021 was 0.41 million hectares. According to the Food and Agriculture Organization (FAO), the world production of moth bean in 2020 was approximately 413,406 metric tons. India is the world's largest producer of moth bean, accounting for roughly 90% of global production. Other significant producers of moth bean include Pakistan, Nepal and Bangladesh. According to the Ministry of Agriculture and Farmers Welfare, Government of India, the country produced around 361,200 metric tons of moth bean in 2020-2021. The major states producing moth bean in India are Madhya Pradesh, Maharashtra, Rajasthan, Gujarat and Uttar Pradesh. Madhya Pradesh is the leading producer of moth bean in India, accounting for around 60% of the total production. Since the crop under study is considered underutilized and less explored, the current study was undertaken keeping in view its potential variability in India for its utilization in breeding programs with the objectives: Assessment of variability in 20 genotypes of Moth Bean, estimation of heritability (bs) and genetic advance and

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correlation study of ten component characters with the yield.

MATERIALS AND METHODS

The experimental material for the study consisted of 20 genotypes of moth bean obtained from the National Bureau of Plant Genetic Resources, Pusa, New Delhi. The experiment was laid out in RBD with three replications at Crop Research Centre-I, School of Agriculture, ITM University, Gwalior. By adopting recommended spacing between rows and plants respectively. Defined agronomic practices were followed to raise good and healthy crop stand. No irrigation was given to *kharif* experiments as rains were sufficient before and after sowing of the experiments during the season. *Kharif* experiments were sown on July 31, 2022.

Observations were recorded on five randomly selected plants for 11 characters *viz*. days to 50% flowering, days to maturity, plant spread at harvest (cm), no. of branches per plant, no. of pods per plant, pod length (cm), no. of seeds/ pod, 100 seed weight (g), protein content (%), harvest Index (%), seed yield/plant (g).

The statistical software used for analysis was R studio and the statistical methods to calculate the genetic components of variances used for the current study was given by Burton (1952) and Panse and Sukhatme (1985). Genotypic coefficient of variation (GCV) was assessed by the formula suggested by Burton (1952). Phenotypic coefficient of variation (PCV), was estimated by the formula suggested by Burton (1952). Heritability percentage in broad sense was calculated as per Burton (1952); Genetic advance was calculated by the formula given by Johnson *et al.* (1955a). The genotypic and phenotypic correlation coefficients were calculated in order to gain a better understanding of the relationship between the traits by adopting the method described by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

Parameters of genetic variability and Anova

The analysis of variance, which can be found in Table 1 found highly significant differences between the genotypes for ten characters, with the exception of protein content. After recording the highest magnitude of treatment mean sum of squares, the character number of pods per plant (365.82) followed by days to maturity (214.81) and then harvest index (145.037). The 100-seed weight and pod length characters, on the other hand, exhibited a low magnitude of treatment mean sum of squares.

Range of variability, estimates of genotypic and phenotypic coefficient of variation, heritability in broad sense, genetic advance and genetic advance expressed as per cent of mean are presented in Table 2. The important findings are presented as below:

Coefficient of variation

The estimates for genotypic coefficients of variation (GCV) were lower than phenotypic coefficient of variation (PCV) for all the eleven characters under study. Highest PCV was recorded for harvest index % (28.16), followed by seed yield (26.58), number of pods per plant (21.72), number of seeds per pod (20.45) and number of branches per plant (20.17). The harvest index (27.99) recorded the highest GCV estimate followed by seed yield per plant (26.16), number of pods per plant (21.55), number of seeds per pod (20.33) and number of branches per plant (19.25). The lowest GCV and PCV were recorded for protein content % (4.72) and days to 50% flowering (8.28), respectively. The highest difference between GCV and PCV was recorded for protein content % (10.56), followed by plant spread at harvest (cm) (0.94) whereas, the lowest difference was found for number of seeds per pod (0.12).

In general, since GCV is an integral part of PCV this trend is very obvious. This indicates the effect of environmental factors on these characters. These results are in confirmation

Table 1: ANOVA table.

Characters	Mean sum of squares		
	Replication (2)	Treatment (19)	Error (38)
Days to 50 per cent flowering	0.026	41.59**	2.03
Days to maturity	2.574	214.81**	3.14
Plant spread at harvest (cm)	1.301	46.036**	1.87
Number of branches per plant	0.054	1.282**	0.04
Number of pods per plant	0.92	365.82**	1.96
Pod length (cm)	0.077	0.625**	0.024
Number of seeds per pod	0.009	2.6**	0.010
100-seed weight (g)	0.009	0.457**	0.006
Protein content (%)	5.338	12.472	9.466
Harvest index (%)	0.331	145.037**	0.582
Seed yield per plant (g)	0.117	4.632**	0.050

with the finding of Yaqoob *et al.* (2007) and Garg *et al.* (2017) who found that PCV was higher than the GCV values for all characters.

The estimates of GCV and PCV were high for harvest index followed by seed yield, number of pods per plant, number of seeds per pod, number of branches per plant and 100 seed yield indicating the good scope for their improvement through selection. Tikka *et al.* (1973) and Jindal and Vir (1983) reported that PCV was greater than GCV for seed yield per plant, number of primary branches per plant and plant height. Bhavsar and Birari (1989) observed higher values of GCV and PCV for seed yield per plant and number of primary branches per plant. Yogeesh *et al.* (2016) revealed high PCV and GCV for primary branches per plant, secondary branches per plant and seed yield per plant. Vir and Singh (2015) depicted high genetic variability for major yield contributing characters like plant height, pod length, peduncle length and clusters per branch. Garg *et al.* (2017) reported high GCV and PCV estimates for number of pods per plant, biological yield per plant and seed yield per plant in mung bean.

The estimate of GCV and PCV was moderate for plant spread at harvest. Similar result was reported by Kumar (1996) and Khairnar *et al.* (2003) they observed moderate GCV and PCV for 100 seed weight, days to 50 per cent flowering and pod length. However, these results show contrast to Veeraswamy *et al.* (1973) who reported low magnitude of GCV and PCV for pod length. Garg *et al.* (2017) reported moderate PCV and GCV for plant height, number of branches per plant, pod length, number of seeds per pod and 100 seed weight.

Heritability (broad sense)

According to Robinson *et al.* (1949), heritability estimates in the present investigation shall be classified as medium to high. The number of seeds per pod (98.82) recorded very high heritability followed by harvest index% (98.80), number of pods per plant (98.40), seed yield (96.84), 100-seed weight(g) (96.11), days to maturity (95.74) and number pod branches per plant (91.12). These were followed by pod length (cm) (89.22), plant spread at harvest (cm) (88.73), days to 50% flowering (86.68), the characters showing high heritability. The protein content% (9.57) showed minimum heritability.

Similar results were reported by Vir and Singh (2015) for peduncle length, Tikka *et al.* (1980) for days to maturity, days to flowering; Natarajan *et al.* (1988) for 100 seed weight; Sahoo *et al.* (2019) recorded that the characters seed yield per plant, 100 seed weight, number of seeds per pod, days to 50 per cent flowering portraying high heritability.

Genetic advance

The highest estimate of genetic advance was recorded for number of pods per plant (22.50) followed by days to maturity (16.93), harvest index (14.21), plant spread at harvest (7.44) and days to 50% flowering (6.96). The lowest genetic advance was estimated for protein content (0.63), followed by 100 seed weight (0.78), pod length (0.87), number of branches per plant (1.26) and number of seeds per pod (1.90).

The results of present study are in accordance with the findings of Tikka *et al.* (1973) who reported a high heritability along with high genetic advance as per cent of mean for number of primary branches per plant and seed yield per plant. Yogeesh *et al.* (2016) reported a high heritability along with high genetic advance as per cent of mean for secondary branches per plant. Reddy *et al.* (2003) reported a high heritability along with moderate genetic advance as per cent of mean for 100 seed weight. Bhavsar and Bihari (1989) reported a high heritability along with low genetic advance as per cent of mean for pod length. High heritability coupled with low expected genetic advance as per cent of mean was for days to maturity, days to 50 per cent flowering and plant height contrary result were obtained by Kohakade *et al.* (2017) and Yogeesh *et al.* (2016) for plant height. Rajora *et al.* (2012) reported that days to 50% flowering, peduncle length and plant height had high heritability coupled with high genetic advance in moth bean. Garg *et al.* (2017) evaluated 30 genotypes of mung bean

Table 2: Parameters of genetic variability.

Characters	General mean	GCV	PCV	Heritability in broad sense	Genetic advance	G.A. as a per cent mean
Days to 50% flowering	47.09	7.71	8.28	86.68	6.96	14.78
Days to maturity	97.65	8.60	8.79	95.74	16.93	17.33
Plant spread at harvest (cm)	25.21	15.21	16.15	88.73	7.44	29.53
Number of branches per plant	3.34	19.25	20.17	91.12	1.26	37.86
Number of pods per plant	51.09	21.76	21.72	98.40	22.50	44.04
Pod length (cm)	3.50	12.76	13.51	89.22	0.87	24.83
Number of seeds per pod	4.57	20.33	20.45	98.82	1.90	41.63
100 seed weight (g)	2.20	17.60	17.95	96.11	0.78	35.54
Protein content %	21.16	4.72	15.28	9.57	0.63	3.01
Harvest Index %	24.78	27.99	28.16	98.80	14.20	57.32
Seed yield (g)	4.72	26.16	26.58	96.84	2.50	53.03

and reported high heritability coupled with high genetic advance for plant height, number of branches per plant, pod length and seeds per pod. Ramakrishnan *et al.* (2018) recorded high heritability and genetic advance for days to harvest, plant height, number of branches, pod length, number of seeds per pod, pod yield per plant and seed yield per plant.

Correlation

The correlation of characters at genotypic level and phenotypic level are presented in the Fig 1 and Fig 2 respectively.

The yield components, harvest index (0.958), number of pods per plant (0.854), protein content (0.404), demonstrated a strong and statistically significant positive association with seed yield per plant at genotypic level. However, two characters, 100 seed weight (-0.019) and days to 50% flowering (-0.044) were found have non-significant and negative association with the seed yield per plant when analyzed at the genotypic level. Other characters, number of seeds per pod (0.222), pod length (0.186) and plant spread at harvest (0.019) showed non-significant positive correlation with seed yield per plant at genotypic level (Fig 1).

At phenotypic level, harvest index (0.938), number of pods per plant (0.837), showed highly significant positive association with seed yield per plant. 100-seed weight (-0.014) and days to 50% flowering (-0.047) were observed non-significant and negatively associated with seed yield per plant at phenotypic level. Number of seeds per pod (0.232) and pod length (0.177) and protein content (0.099) showed non-significant and positive association with seed yield per plant at phenotypic level. The magnitude of correlation between plant spread at harvest (0.007) and seed yield per plant were negligible at phenotypic level (Fig 2).

Seed yield exhibited negative correlation with days to 50% flowering, day to maturity, 100 seed weight and number of branches per plant, while seed yield per plant exhibited positive correlation with plant spread at harvest, number of pods per plant, pod length, protein content and harvest index. Kumar *et al.* (2017) also came to the same conclusions and recorded that the days to maturity, pod length, peduncle length, number of seeds per pod, pod length, number of clusters per branch and protein content were all significant and positively correlated with each other in the association between component characters. The findings that Kakani *et al.* (2002) discovered were comparable to these results. Bhavsar and Birari (1989) found that there was a positive correlation between yield per plant and all of the characteristics of moth bean, with the exception of 100 seed weight. The correlation coefficients were extremely significant for the number of days until maturity, number of primary branches, height of the plant, number of clusters produced by each branch, number of pods produced by each cluster, number of seeds produced by each pod and the total number of pods produced by the plant. According to the findings of Singh *et al.* (2009), the seed yield per plant of mung bean exhibited a positive association with the number of days until it

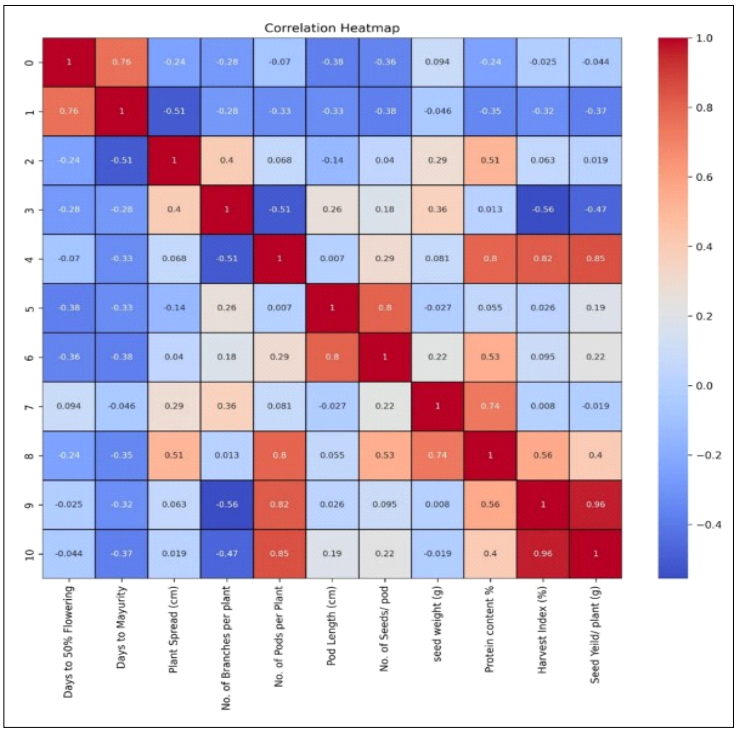


Fig 1: Genotypic correlation.

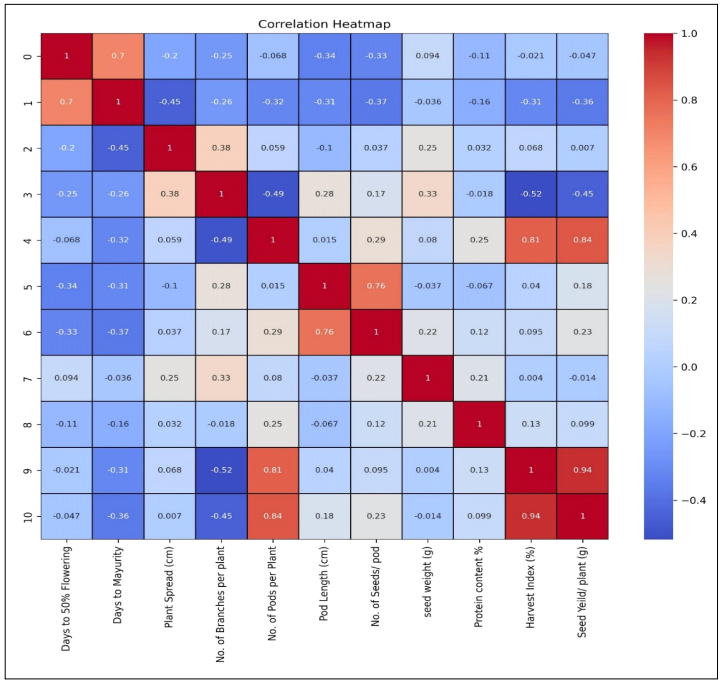


Fig 2: Phenotypic correlation.

reached 50% flowering at both the genotypic and phenotypic correlation levels. According to Tabsum *et al.* (2010), there is a significant positive genotypic and phenotypic correlation of seed yield with pods per plant, total plant weight and harvest index, but there is a significant negative correlation with pods per cluster. According to the findings of Kumar *et al.* (2016), the only trait that had a positive correlation with seed yield per hectare was number of pods per plant. All of the other characteristics had a negative correlation with seed yield per hectare. Dhoot *et al.* (2017) found that seed yield had a significant and positive correlation with pods per plants and harvest index in F_2 population of Meha Pusa × Vishal in mung bean. They also found that seed yield had significant and positive correlations with plant height, primary branches per plant, cluster per plant, pods per plants and straw yield per plant and harvest index in F_2 population of Meha Pusa × Vishal.

According to the findings of Sahoo *et al.* (2018), the seed yield per plant was found to have a significant and positive association with the number of primary branches per plant, the weight of 100 seeds and the height of the plant. A statistically significant and inverse relationship between seed yield per plant and days to maturity was discovered. When looking at the interrelationships, we found that plant height had a significant and positive association with 100 seed weight; days to 50 per cent flowering had a positive association with days to maturity; pod length had a positive association with the number of seeds per pod; and so on and so forth in moth bean.

Association between remaining 10 yield components

The following figure presents, at both the genotypic and the phenotypic level, the interrelationships between the component characters. At both genotypic level and phenotypic level the number of days until 50% flowering showed a highly significant and positive correlation with the number of days to maturity. Plant spread recorded highly significant positive correlation with number of branches per plant and protein content at genotypic level and at phenotypic level it showed non-significant association with protein content. Number of branches per plant showed significant positive correlation with 100 seed weight and pod length, at both genotypic and phenotypic levels. Number of pods per plant was significantly and positively correlated with pod length, harvest index, number of seeds per pod and seed yield at both genotypic and phenotypic levels. Pod length showed highly significant and positive correlation with number of seeds per pod at both genotypic and phenotypic level.

There was a highly significant and positive correlation between the number of seeds per pod and the total amount of protein at the genotypic level. At the genotypic level, there was a highly significant positive correlation between the 100 seed weight and protein content. At the genotypic level, a highly significant positive correlation between protein content and harvest index and seed yield was discovered. Both the genotypic and phenotypic levels of analysis demonstrated a highly significant and positive correlation between harvest index and number of seed yield.

CONCLUSION

The present study revealed substantial genetic variability among 20 moth bean genotypes, especially for number of pods per plant (GCV- 21.76%, PCV- 21.72%), harvest index (GCV- 27.99%, PCV- 28.16%) and seed yield per plant (GCV: 26.16%, PCV: 26.58%). High heritability was recorded for number of seeds per pod (98.82%), harvest index (98.80%), number of pods per plant (98.40%) and seed yield per plant (96.84%), suggesting strong genetic control and minimal environmental influence on these traits.

High genetic advance as per cent of mean was observed in harvest index (57.32%), seed yield per plant (53.03%) and number of pods per plant (44.04%), indicating the predominance of additive gene effects and effectiveness of direct selection for yield improvement.

Correlation analysis revealed that seed yield per plant had a strong positive genotypic correlation with harvest index (0.958), number of pods per plant (0.854) and moderate positive correlation with protein content (0.404). Traits like number of seeds per pod and pod length also showed positive but smaller correlations, indicating their potential secondary contributions.

The low heritability and genetic advance for protein content (Heritability- 9.57%, GA as % mean- 3.01%) suggest that improvement in this trait may require hybridization or biotechnological approaches rather than direct selection alone.

Overall, these findings emphasize the potential for significant yield gains by focusing on traits like number of pods per plant and harvest index.

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Disclaimers

The views and conclusions expressed in this original research article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Informed consent

The current research under publication was performed upon plant system (20 moth bean genotypes) hence no animals were used/harmed.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish or preparation of the manuscript.

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