

Study of genetic parameters in moth bean [*Vigna aconitifolia* (Jacq.)]

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A research was initiated to examine the genetic diversity of seed yield in moth bean crops during the kharif-2022 season, specifically at the agricultural farm of RNB Global University in Bikaner. Using a randomized block design with 3 replications, the study utilized 30 different genotypes of moth beans as its experimental material. The results of the analysis of variance pointed to the substantial genetic variation present within the genotypes for all the measured attributes, including the duration to reach 50% flowering, days to maturity, plant height, the number of branches per plant, the number of seeds per pod, and seed yield per plant. High genotypic and phenotypic coefficient variance

values were evident for days to 50% flowering, plant height, the number of branches per plant, and seed yield per plant. Furthermore, heritability estimates were notably high for days to 50% flowering, days to maturity, plant height, the number of branches per plant, the number of seeds per pod, and seed yield per plant. Days to 50% flowering, days to maturity, plant height, the number of branches per plant, the number of seeds per pod, and seed yield per plant displayed a combination of high heritability and significant genetic advance, underscoring their genetic value.

Key Words: Moth bean; Genetic variability; Heritability; Genetic advance; GCV; PCV

INTRODUCTION

Moth bean, scientifically known as *Vigna aconitifolia*, falls under the *Vigna* genus and is a part of the Leguminaceae family, situated in the Papilionaceae subfamily. It possesses a unique chromosome number of $2n=2x=22$. Typically, this plant exhibits a bushy to semi-erect growth pattern, characterized by abundant leaves and a compact stem. Its deep roots contribute to its impressive drought tolerance. Historical records, including accounts by de Candolle [1], Vavilov [2], and Jain et al. [3], trace the origins of moth bean back to India, particularly the central plateau region, considered its primary center of origin. Globally, India leads in the cultivation of moth beans, with substantial plantings also observed in territories like Pakistan, Sri Lanka, Malaysia, Myanmar, South China, and the USA. Moth bean cultivation in India is predominantly centered in the state of Rajasthan, with the kharif season being the primary timeframe for this agricultural practice. Rajasthan plays a significant role, accounting for 75% of the nation's total cultivation area and 55% of its production, making it the top contributor in terms of both cultivation area (13.87 lakh hectares) and production (4.34 lakh tonnes). Additionally, the state achieves an impressive productivity rate of 310 kilograms per hectare. Other states, including Punjab, Uttar Pradesh, Haryana, and Madhya Pradesh, also engage in moth bean cultivation, particularly on marginal lands. Moth bean serves as a vital pulse crop, well-suited for the hot, arid regions of India, demonstrating its adaptability to extreme ecological niches, particularly its ability to withstand harsh drought and scorching climatic conditions.

Moth bean seeds are a valuable protein source, boasting a protein content of approximately 22-24%. What makes them particularly noteworthy is their affordability compared to other pulse crops, which positions them as a dietary staple for low-income individuals and tribal communities residing in the provincial areas where they are cultivated. Moth beans exhibit a productivity of 4 quintals per hectare, mainly because they thrive in poor and marginal soils, often without requiring extensive inputs. This resilient legume is well-suited to hot and arid climates, showcasing exceptional drought resistance thanks to its robust deep root system. It can endure high temperatures without hindering its flowering and fruit development. Moreover, it serves as a valuable source of hay, on par with the quality of alfalfa. In culinary contexts, moth beans play versatile roles, being used to prepare Dal (Mogar), sprouts, and green pods for vegetable consumption. Notably, they play a central role in the creation of the famous spicy snack, Bikaneri Bhujia. Additionally, the extensive canopy of moth bean plants serves as a natural moisture preserver and helps protect soil against erosion. Beyond human consumption, moth beans act as a provider of green fodder for animals, further enhancing their

agricultural significance. Moth bean has long been considered a neglected crop, primarily from an evolutionary perspective, and consequently, it remains a secondary choice for many farmers. This neglect is further underscored by the scarcity of research efforts and the shortage of a systematic literature base concerning this legume. To harness the full potential of moth bean, there is a pressing requirement for extensive research focusing on its adaptability to diverse environmental conditions, the development of innovative cultivation practices, responses to inputs, and the creation of high-yielding varieties. In any breeding program, the ultimate goal is to achieve high yield, a complex trait influenced by a polygenic system and environmental fluctuations.

The assessment of genetic variability in seed yield and other traits is a critical step in the selection of favored plant types. This evaluation helps in determining the relative performance of different genotypes in terms of various characteristics, serving as the foundation for the selection of suitable parent plants to enhance yield. The selection of genotypes can be informed by a range of genetic parameters, aiding breeders in making informed decisions. In any crop, the presence of variability within the plant population is the initial requirement for genetic improvement. The extent of this variation is measured using parameters such as Genetic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), which offer insights into the diversity observed in various traits. Meanwhile, heritability provides valuable data on the potential for enhancing a trait through breeding endeavors. It provides indications of the genetic basis and complexity involved in enhancing a particular trait within a breeding program. The formulation of a plant breeding strategy heavily relies on genetic information concerning the inheritance and behavior of key quantitative traits linked to yield or other economically significant characteristics relevant to plant breeding endeavors.

MATERIALS AND METHODS

Kharif season of 2022, the research project was executed at the agricultural facility of RNB Global University located in Bikaner. The experiment followed a randomized block design with three replications and involved the examination of 30 different moth bean genotypes. Individual plants were placed 15 cm away from one another and the rows were spaced 30 cm apart. Each experimental plot included two rows, each of which was four meters long. The assessment of variability within the experimental treatments involved the consideration of eight distinct characteristics: Days to 50% flowering, days to maturity, plant height, number of branches per plant, pod length, seed index, number of seeds per pod, and seed yield per plant. Figure 1, on the other hand, illustrates weekly averages for total rainfall, relative humidity, temperature, and BSSH. The crop was grown in recommended

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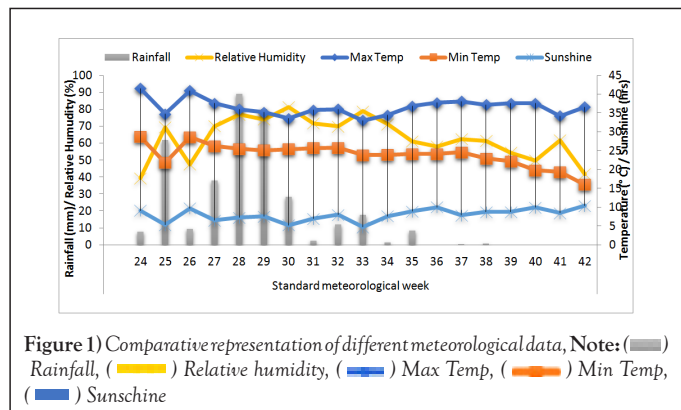
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package of practices and better crop growth was accomplished. The mean values of five plants were statistically analyzed for all characters with the exception of days to 50% flowering and days to maturity. These two data were recorded as the plot basis. The collected information was combined and statistically examined. The mean values of these observations were subjected to statistical analysis in order to compute the analysis of variance [4], PCV and GCV [5,6], heritability in a broad sense for all the characters [7,8] and genetic advance for each character [8].



RESULTS AND DISCUSSION

In the experimental study, a collection of 30 moth bean genotypes was laid out using a Randomized Block Design with three replications. The purpose of this study was to analyze the variance in the means of various traits among the individuals of a plant population. Variability, in this context, signifies the presence of differences among individual plants within a population of

moth beans. This variability can arise from variations in the genetic makeup of the plants or differences in the environmental conditions they are grown in. Understanding the nature and extent of this variation within the initial collection of moth bean genotypes is crucial for effectively identifying and selecting superior genotypes for breeding purposes. Therefore, it is vital for the original population to possess a substantial amount of inheritable diversity. The results of the analysis of variance showed that there was considerable variation among the genotypes for each of the eight traits. This crop might be improved by taking advantage of the high variance for these yield and yield-related variables found. For all the traits, the phenotypic variability range was wide. A wide range of variability for various traits has been observed earlier by Sahoo et al., [9], Sahoo et al., [10], Ramakrishnan et al., [11], Garg et al., [12], Kakani et al., [13].

To examine the variation in genotypes for each of the eight characteristics, an analysis of variance was conducted and the results are shown in Table 1. The results revealed that the mean squares due to genotypes were highly significant for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of seeds per pod and seed yield per plant which indicated the considerable amount of variability among genotypes for various traits were presented. The mean, range, coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean are presented in Table 2. The mean value of the genotypes showed a wide range for all the characters. The estimates of Genotypic Coefficient of Variation (GCV) were high (>20%) for days to 50% flowering, plant height, number of branches per plant and seed yield per plant. While the variability in days to maturity and the number of seeds per pod was moderate, ranging from 10% to 20%. Phenotypic Coefficient of Variance (PCV) was high (>20%) for days to 50% flowering, plant height, number of branches per plant and seed yield per plant. Whereas, it was moderate (10-20%) for days to maturity, pod length, seed index and number of seeds per pod.

TABLE 1
Analysis of variance (mean sum of square) for different characters in moth bean

Source of variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Pod length (cm)	Seed index (g)	Number of seeds per pod	Seed yield per plant (g)
Genotypes	29	338.83 ^{**}	673.81 ^{**}	622.28 ^{**}	3.77 [*]	0.38	0.31	1.86 [*]	69.90 ^{**}
Replications	2	78.49 [*]	129.69 ^{**}	33.3	9.18	1.41	91.24 ^{**}	1.52	0.47
Error	58	8.52	9.98	0.13	0.02	0.1	0.31	0.01	0.01

Note: *, ** Significant at 5% and 1% level of significance, respectively.

TABLE 2
Estimation of different variability parameters of moth bean genotypes

S. No	Characters	Mean	Range	G.C.V. %	P.C.V. %	Heritability (%) (bs)	Genetic advance	GA as % of mean
1	Days to 50% flowering	48.97	14.00-85.00	21.43	22.24	0.93	20.82	42.53
2	Days to maturity	84.77	49.00-119	17.55	17.94	0.96	29.98	35.36
3	Plant height (cm)	33.67	13.02-70.45	42.77	42.78	0.99	29.66	88.07
4	Number of branches per plant	4.13	1.35-6.95	27.03	27.33	0.98	2.27	55.08
5	Pod length (cm)	3.73	2.31-5.55	8.2	11.78	0.48	0.43	11.76
6	Seed index (g)	3.42	1.60-6.89	9.26	18.35	0.89	1.15	21.36
7	Number of seeds per pod	5.46	3.29-7.05	14.4	14.51	0.98	1.61	29.41
8	Grain yield per plant (g)	9.09	2.20-20.64	53.09	53.09	0.99	9.94	109.36

The degree of genotypic variation in a population cannot be accurately determined by the phenotypic variance. To better evaluate the amount of genetic variability present for each characteristic in the experimental material, the genetic parameters genotypic and phenotypic coefficient of variation, heritability, and genetic progress were calculated in the current study. Heritability estimates were high (>90%) for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of seeds per pod and seed yield per plant, Whereas, it was moderate (50>90%) for seed index, while it was low (<50%) for pod length. Expected genetic advance as per cent over mean was high (>20%) for days to 50% flowering, days to maturity, plant height, number of branches per plant, seed index, number of seeds per pod and seed yield per plant, Whereas, genetic advance as per cent of mean was medium (10-20%) for pod length. Comparing the coefficients of variance revealed that for all the characteristics, the phenotypic coefficient of variance was larger than the genotypic coefficient of variance, indicating that the environment has an impact on how characters are expressed. Among all the characters, both high GCV and PCV were observed for days to 50% flowering, plant height, number of branches per plant and seed yield per plant in comparison to other characters indicating the presence of high amount of genetic variability for these characters. The response to selection is exactly proportional to the variety contained in the genetic material employed, hence selection for these traits would be successful. For the quantity of seeds per pod and days to maturity, medium GCV and PCV were observed. These results are in accordance with the earlier finding of Sahoo et al., [9], Sahoo et al., [10], Tabsum et al., [14], Singh et al., [15] and Patel et al., [16] reported for various characters.

The genetic coefficient of variance does not offer a clear indication of the proportion of heritable components within the variation. Estimating the heritability of a quantitative trait is of paramount importance because the phenotypic expression of a genotype can be influenced by environmental factors at different stages of development. Heritability serves as a critical metric for assessing the potential success of genotype-based selection in light of a trait's phenotypic variation. It quantifies the extent to which individual phenotypes are determined by their underlying genotypes. Heritability estimates are invaluable to breeders as they provide guidance on the ease of selection for traits. Traits with high heritability facilitate straightforward selection because there is a close correspondence between genotypes and phenotypes, with the environment having a relatively minor impact on the phenotype. However, for traits with low heritability, selection may be less effective due to the significant influence of the environment on the genotypic effect. The response to selection hinges on the balance between heritable and non-heritable variations within the observed variability. Hence, it is beneficial to dissect the observed variation into its heritable and non-heritable components. It's important to note that heritability estimates alone do not provide information about the specific genes governing the expression of a particular trait, nor do they indicate the extent of genetic improvement resulting from the selection of superior individuals. Johanson et al., [8] had pointed out that the heritability estimates along with genetic advance were more useful than heritability estimates alone in predicting the response to selection.

In the present investigation genetic advance was estimated for all the characters. Expected genetic advance as per cent over mean was high (>20%) for days to 50% flowering, days to maturity, plant height, number of branches per plant, seed index, number of seeds per pod and seed yield per plant. It was moderate (10-20%) for pod length. Heritability and genetic advance are two complementary concepts. Thus, heritability values may be used to estimate the genetic advance through selection for predicting the utility and value of selection. In the present investigation, high heritability along with high genetic advance was observed for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of seeds per pod and seed yield per plant which indicated that these characters might be governed by additive genetic variance and hence simple selection procedure would be effective in the improvement of moth bean genotypes. It was moderate for pod length and seed index. A comparative analysis of various parameters for this experiment is presented in Figure 2. However, none of the character showed low heritability and genetic advance. Similar estimation of heritability for various characters have been reported by Sahoo et al., [9], Kohakade et al., [17], Kumar et al., [18], Hemavathy et al., [19], Yogeesh et al., [20], Tabsum et al., [14], Sihag et al., [21], Solanki et al., [22], Garg et al., [12,23].

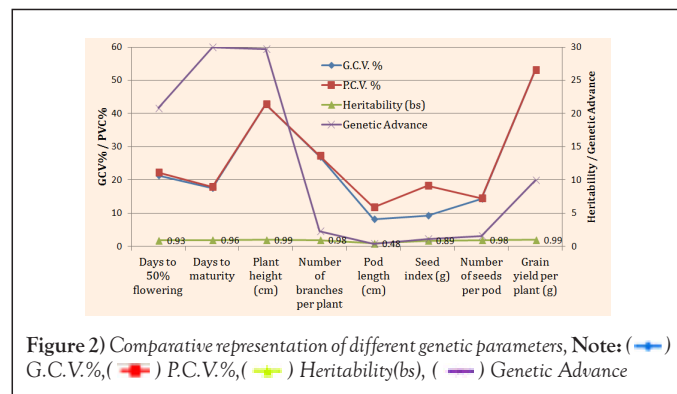


Figure 2) Comparative representation of different genetic parameters, Note: (—) G.C.V.%, (—) P.C.V.%, (—) Heritability (hs), (—) Genetic Advance

CONCLUSION

The experimental study involving 30 moth bean genotypes revealed significant variability among individuals for eight key traits, emphasizing the importance of understanding and harnessing this diversity. The study identified traits such as days to 50% flowering, plant height, number of branches per plant, number of seeds per pod, and seed yield per plant as particularly variable, offering valuable insights for crop improvement. Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variance (PCV) assessments underscored the high variability in critical traits, providing breeders with valuable information for selecting superior genotypes. With wide phenotypic variability ranges observed across all traits, these findings suggest the potential for targeted breeding strategies to enhance yield and related variables in moth beans. Overall, this study lays a foundation for informed and effective breeding practices aimed at advancing moth bean cultivars for improved agricultural productivity.

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