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Genetic diversity and variability studies in moth bean [*Vigna aconitifolia* (Jacq.)]

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Abstract

A field experiment entitled "Genetic diversity and variability studies in moth bean [*Vigna aconitifolia* (Jacq.)] was conducted at Agricultural Botany Research Farm, College of Agriculture, Pune during *Kharif* 2018. Thirty genotypes were obtained from Dry Land Agricultural Research Station, Solapur. The experiment carried out in randomized block design with three replications. Analysis of variance showed significant difference among genotypes for all characters. Phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the characters showing higher influence of environment on characters. High heritability coupled with high genetic advance as per cent of mean was for the characters *viz.*, clusters per branch, seed yield per plant, primary branches per plant, seeds per pod and secondary branches per plant and suggested that these characters are under the influence of additive gene action. Genetic diversity studies was carried out by using Mahalanobis D² statistics which grouped 30 genotypes in 5 clusters. Cluster I having maximum genotypes followed by cluster II with 4 genotypes.

Keywords: moth bean, genetic variability, genetic diversity, heritability, genetic advance

Introduction

Moth bean, a short day crop, is one of the most drought resistant pulses in India. Grown at an altitude up to 1300 mm above sea level, it has a wide pH range (3.5-10) and can tolerate slight salinity. While dry sandy soil is most suitable for production, moth bean can tolerate a variety of soil types. The low lying soil cover the crop creates help prevent soil erosion by preventing moisture loss. Its spreading type makes it ideal crop for soil conservation which help in checking soil erosion. Growing of moth bean also enriches soil by fixing atmospheric nitrogen in soil, thus helps in improving soil fertility. Moth bean plant is normally bushy to semi erect with large number of leaves and short stem; it is deep rooted, drought tolerant plant. The average temperature requirement for growth and development of the crop is 25-30°C, but has been shown to tolerate up to 45°C during the day. Bright sunshine and normal humidity are considered good for growth and high yield. According to De Candolle (1884)^[2], Vavilov (1926)^[16], Zuckovski (1962)^[19] and Jain and Mehta (1980)^[4], moth bean is originated in India. Plateau of central India is considered as its primary centre of origin. India has major area under moth bean cultivation in the world. Moth bean seeds contain about 59% carbohydrates, 23.26% protein, 0.7% fat, 4% fiber, 4% ash and 9.3% moisture (Rathore and Rathore 2002)^[13]. It is a multipurpose crop. In our country seed is used either whole or split as a pulse. In spite of the fact that moth bean occupies a large area, a very limited work has been done to develop suitable improved varieties for different agro climatic regions due to lack of genetic information like variability, correlation, path analysis, genetic diversity, combining ability, heritability and cytological studies. There is great scope for its improvement and to increase the productivity by developing high yielding varieties having disease resistance, pest resistance, and draught resistance with improvement in nutritional value. Good amount of variability has been reported in moth bean for various characters such as plant height, days to maturity, plant canopy, pods per plant, number of seeds per pod. Their utilization in breeding programme resulted in identification and release of good number of varieties in moth bean. However, these released types cannot be continued longer due to genetic drift and susceptibility to disease and pest. This demands replacement of old varieties by many developed ones, as said in Boom and Burst cycle. Based on the above mentioned considerations, present investigation has been undertaken to study the variability and genetic diversity in moth bean.

Material and Methods

The present investigation was carried out at Agricultural Botany Research Farm, College of Agriculture, Pune during *Kharif* 2018. The experiment was laid down in a Randomized Block

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Design with three replications. The experimental material with 30 genotypes of Moth bean was collected from Dry Land Agricultural Research Station, Solapur (MS). The spacing between rows was 30 cm and plants were 15 cm. Plot consist of 1 row of 4.5 meters length each. Data were collected for 12 characters *viz.* days to 50 per cent flowering, days to maturity,

plant height, primary branches per plant, secondary branches per plant, pod length, peduncle length, clusters per branch, seeds per pod, 100 seed weight, seed yield per plant and protein content. The statistical analysis was carried with WINDPWSTAT program with 30 genotypes shown in Table.1.

Table 1: List of 30 genotypes of moth bean

| Sr. No. | Genotypes | Sr. No. | Genotypes | Sr. No. | Genotypes |
|---------|-----------|---------|-----------|---------|-----------|
| 1. | MBS-1 | 11. | MBS-15 | 21. | MBS-27 |
| 2. | MBS-2 | 12. | MBS-16 | 22. | MBS-28 |
| 3. | MBS-4 | 13. | MBS-17 | 23. | MBS-29 |
| 4. | MBS-6 | 14. | MBS-19 | 24. | MBS-30 |
| 5. | MBS-8 | 15. | MBS-20 | 25. | MBS-34 |
| 6. | MBS-9 | 16. | MBS-21 | 26. | MBS-35 |
| 7. | MBS-10 | 17. | MBS-22 | 27. | MBS-36 |
| 8. | MBS-11 | 18. | MBS-23 | 28. | MBS-37 |
| 9. | MBS-13 | 19. | MBS-24 | 29. | MBS-38 |
| 10. | MBS-14 | 20. | MBS-26 | 30. | MBS-39 |

Results and Discussion

The genotypic coefficient of variation and phenotypic coefficient of variation were high for the following characters *viz.* seed yield per plant, clusters per branch, primary branches per plant, secondary branches per plant, Peduncle length and protein content. Similar result were reported by Tikka *et al.* (1973) [15]; Jindal and Vir (1983) [5]; Bhavsar and Bihari (1989) [1]; Yogeesh *et al.* (2016) [18]; Garg *et al.* (2017) [3]. The estimate of PCV and GCV were moderate for 100 seed weight, days to 50 per cent flowering and pod length. Similar

result were observed by Kumar (1996) [8], Khairnar *et al.* (2003) [6]; Garg *et al.* (2017) [3]. Plant height and days to maturity had very low GCV and PCV estimates, suggesting narrow range of variation for these characters. These results were according with Veeraswamy *et al.* (1973) [17]; Garg *et al.* (2017) [3]. The difference between GCV and PCV were minimum for all the characters except seed yield per plant suggesting less influence of environment in the expression of these characters and one may rely upon the phenotypic values for direct selection

Table 2: Analysis of variance for different characters in moth bean

| Sr. No. | Characters | Mean sum of square | | |
|---------|-------------------------------------|--------------------|----------------|------------|
| | | Replication (2) | Treatment (29) | Error (58) |
| 1. | Days to 50 per cent flowering (No.) | 2.9778 | 73.8731** | 2.4260 |
| 2. | Days to maturity (No.) | 0.4111 | 158.3846** | 2.6224 |
| 3. | Plant height (cm) | 0.3540 | 9.4310** | 0.4830 |
| 4. | Primary branches per plant (No.) | 0.0109 | 1.4197** | 0.0176 |
| 5. | Secondary branches per plant (No.) | 0.0238 | 4.3294** | 0.0040 |
| 6. | Pod length (cm) | 0.0037 | 0.3342** | 0.0020 |
| 7. | Peduncle length (cm) | 0.0004 | 1.3941** | 0.0005 |
| 8. | Clusters per branch (No.) | 0.0108 | 1.9470** | 0.0020 |
| 9. | Seeds per pod | 0.0194 | 2.4275** | 0.0170 |
| 10. | 100 seed weight (g) | 0.0028 | 0.3067** | 0.0003 |
| 11. | Seed yield per plant (g) | 0.0918 | 2.2659** | 0.0765 |
| 12. | Protein content (%) | 0.6584 | 43.8371** | 1.1932 |

Heritability and genetic advance

The heritability values are most important to plant breeders because it indicates that the selection of parents bearing particular measurements will produce offspring's of similar phenotypes. Thus, the improvement of valuable traits depends upon a fairly accurate evaluation of the heritability. (Table 3). In present study, high heritability coupled with high genetic advance as per cent of mean was for the characters *viz.*, clusters per branch, seed yield per plant, primary branches per plant, seeds per pod and secondary branches per plant, suggested that these characters are under the influence of additive gene action. Similarly, high heritability coupled with

moderate expected genetic advance as per cent of mean was for the characters *viz.*, peduncle length, protein content and 100 seed weight which is indicative of both additive and non-additive gene actions. High heritability coupled with low expected genetic advance as per cent of mean was for the characters *viz.*, pod length, days to 50 per cent flowering, plant height and days to maturity revealed the importance of non-additive components of variance. The results of present study are in accordance with the findings of Tikka *et al.* (1973) [15]; Reddy *et al.* (2003) [14]; Bhavsar and Bihari (1989) [1]; Kohakade *et al.* (2017) [7]; Rajora *et al.* (2012) [10]; Ramkrishnan *et al.* (2018) [11].

Table 3: Parameters of genetic variability in 30 genotypes in moth bean

| Sr. No. | Character | Mean | Range | GCV (%) | PCV (%) | h ² % (B.S) | Genetic Advance. | Gen. Adv. as % of Mean |
|---------|-------------------------------------|--------|--------------|---------|---------|------------------------|------------------|------------------------|
| 1 | Days to 50 per cent flowering (No.) | 53.95 | 45.33-66.67 | 9.03 | 9.49 | 90.80 | 9.57 | 17.73 |
| 2 | Days to maturity (No.) | 105.95 | 91.33-117.00 | 6.80 | 6.97 | 95.10 | 14.47 | 13.66 |
| 3 | Plant height (cm) | 19.54 | 14.22-22.84 | 8.83 | 9.52 | 86.00 | 3.30 | 16.88 |
| 4 | Primary branches per plant (No.) | 3.17 | 2.10-4.57 | 21.50 | 21.90 | 96.40 | 1.38 | 43.48 |
| 5 | Secondary branches per plant (No.) | 6.12 | 3.86-8.41 | 19.60 | 19.63 | 99.70 | 2.47 | 40.33 |
| 6 | Pod length (cm) | 3.73 | 2.41-4.44 | 8.92 | 9.00 | 98.20 | 0.67 | 18.20 |
| 7 | Peduncle length (cm) | 3.67 | 2.87-5.38 | 18.56 | 18.58 | 99.90 | 1.40 | 38.21 |
| 8 | Clusters per branch (No.) | 3.51 | 2.13-5.40 | 22.90 | 22.94 | 99.60 | 1.65 | 47.09 |
| 9 | Seeds per pod (No.) | 4.51 | 2.93-6.54 | 19.90 | 20.03 | 98.70 | 1.83 | 40.72 |
| 10 | 100 seed weight (g) | 2.23 | 1.61-2.69 | 14.33 | 14.35 | 99.70 | 0.65 | 29.40 |
| 11 | Seed yield per plant (g) | 3.65 | 2.26-5.63 | 23.38 | 24.58 | 90.50 | 1.67 | 45.83 |
| 12 | Protein content (%) | 24.10 | 16.61-30.59 | 15.63 | 16.28 | 92.30 | 7.46 | 30.94 |

Genetic Divergence

Cluster formation was done by following Tocher's method as described by Rao (1952) [12]. The 30 genotypes were grouped into five clusters. Cluster I with 22 genotypes followed by clusters II with 4 genotypes, cluster III with 2 genotypes. While, remaining all other clusters viz., IV and V were solitary. (Table 4). Genetic divergence in 30 genotypes of moth bean was measured by Mahalanobis (1936) [9] D² statistics. The calculated D² values varied from 464.83 to

5146.62 (Table 5). This high range for D² values indicate high amount of genetic diversity present in the genotypes. The lowest value was between the cluster III while, the highest was between cluster I and III.

The basic concept behind the formation of clusters is to get intra and inter cluster distance. This acts as index for selection of parents with diverse origin. The intra and inter cluster values are means derived from D² values of cluster elements.

Table 4: Distribution of 30 genotypes of moth bean into different clusters

| Clusters | No. of genotypes included | Genotypes |
|----------|---------------------------|--|
| I | 22 | MBS-28, MBS-29, MBS-24, MBS-26, MBS-21, MBS- 35, MBS-13, MBS-10, MBS-11, MBS-8, MBS-16, MBS-4, MBS-6, MBS-22, MBS-36, MBS-14, MBS-19, MBS-17, MBS- 20, MBS-9, MBS-37, MBS-2. |
| II | 4 | MBS-1, MBS-39, MBS-15, MBS-30 |
| III | 2 | MBS- 23, MBS-27 |
| IV | 1 | MBS-38 |
| V | 1 | MBS-34 |

Table 5: Average intra and inter cluster D² and D (in parenthesis) values in moth bean

| Cluster No. | I | II | III | IV | V |
|-------------|-------------------|--------------------|--------------------|---------------------|--------------------|
| I | 918.69 (30.31) | 1469.18 (38.33) | 5146.62 (71.74) | 2147.39 (46.34) | 3733.21 (61.10) |
| II | | 757.90 (27.53) | 4396.21 (66.10) | 3001.94 (54.79) | 2968.07 (54.48) |
| III | | | 464.83 (21.56) | 4017.024 (63.38) | 2692.57 (51.89) |
| IV | | | | 0.00 (0.00) | 1367.52 (36.98) |
| V | | | | | 0.00 (0.00) |

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