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MORPHOLOGICAL DIVERSITY AND GENETIC VARIABILITY IN MOTH BEAN

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Abstract: Moth bean is a native minor pulse crop found major in hot and dry habitats of Northern-Western parts of India. Genotypes representing different geographical regions were collected to study genetic Variability and divergence study using Mahalanobis D^2 statistic grouped 121 genotypes into eight clusters. Cluster I was the largest with 90 genotypes followed by cluster III with 25 genotypes. Cluster III recorded maximum intra-cluster distance with wide divergence followed by cluster I. The maximum inter-cluster distance was between cluster III and VI followed by cluster IV and VIII showing grater divergence. Analysis of variance showed the presence of significant variability among the genotypes studied and for all the traits excluding 100 seed weight. The estimates of PCV and GCV were high for plant height, primary branches per plant, secondary branches per plant, 100 seed weight, pods per plant and seed yield per plant. High heritability and Genetic Advance was observed for days to 50 per cent flowering, plant height, secondary branches per plant, pod length, pods per plant and seed yield characters studied offering scope for improvement of these traits through simple selection. Diverse Genotypes selected based on present study and will be used in Moth bean Improvement Programme.

Keywords: Cluster, Genetic Divergence, Mahalanobis D^2 statistic.

Introduction

Moth bean belongs to genus *Vigna*, sub-family Papilionaceae and family Leguminaceae (Marechal *et al*., 1978). In severe soil moisture deficit situations encountered with exceeding evaporative demands, moth bean is rated as the most economic and useful annual legume. This is probably due to genetic buffering embedded in this arid legume to quickly adjust and adopt to fast fluctuating situations. These adjusting abilities have rendered this crop as the indispensable component of cropping systems in arid regions of India. Major moth bean growing states are Rajasthan, Maharashtra, Gujarat, Jammu and Kashmir, Punjab, Haryana and Uttar Pradesh (Arora, 1985). It is popular as Turkish gram (Yaqoob et al 2015), Dew

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gram, Aconite bean and Kidney gram in world with several vernacular names in different parts of country *viz*., Moth, Mat, Matki (Hindi), Kheri (Bengali), Kumkuma (Telugu), Tulkapulpyrai (Tamil) and Madike (Kannada) in different linguistic zones of India. Moth bean is grown in India over an area of 13.53 lakh hectares with an annual production of 2.91 lakh tonnes and productivity of 215 kg per hectare. In Karnataka production of moth bean is least amongst other growing states in India and mainly grown in Northern districts of Karnataka. Besides low productivity, moth bean is also known for plant types of primitive nature, conferring its evolution for survival but not for grain productivity. Thus alteration in plant types should be productive and physiologically efficient in terms of early maturing and semi erect to erect growth types may be profuse over traditional ones.

Collection, maintenance and evaluation of germplasm for studying genetic variability of economically important traits is one of the basic steps for initiating breeding programme for genetic improvement of any crop. Collected land races and existing germplasm lines should be evaluated for estimation of genetic diversity and assessment of variability is essential before proceeding to the further steps in any crop improvement programme. The elite lines are to be chosen from germplasm either for direct release or to be used as diverse parents in crop breeding programme. Hence, assessment of genetic diversity and estimation of genetic variability parameters becomes the initial step in Moth bean improvement programme. In the present study 121 accessions of moth bean collected from different parts of north Karnataka, Maharashtra and Rajasthan were evaluated in the experimental plots of Gandhi KrishiVignana Kendra, Bangalore to know the presences of morphological diversity and genetic variability parameters.

Materials and Method

Experimental Design: The experimental material comprised of 121 moth bean genotypes collected from different sources under Adhoc project on moth bean funded by Kirkhouse Trust, United Kingdom at Gandhi KrishiVignana Kendra, Bangalore. A total of 121 genotypes of moth bean were sown in a single row of three meter length with spacing of 30 cm between rows and 10 cm between plants. The experiment was laid out in Simple Lattice Design with two replications. The crop was raised as per the recommended package of practices and better crop growth was achieved. The field was kept weed free by hand weeding and protective irrigation was given whenever the crop suffered moisture stress and during critical stages of crop growth. At the time of maturity five plants selected at random from each genotype were tagged in each replication and observations on quantitative traits

were recorded and the average of these five plants for each quantitative character was made to compute mean for further analysis. Total soluble protein was estimated in dry seeds by Bradford (1976) dye-binding method using Bovine Serum Albumin (BSA) as standard.

Statistical Analysis: The mean values on these observations were subjected for statistical analysis to compute analysis of variance (Cochran and Cox, 1957), Phenotypic co-efficient of variation [PCV] and Genotypic co-efficient of variation GCV (Burton and De Vane 1953); Sivasubramanian and Menon (1979), Heritability in broad sense for all the characters (Lush 1946 and Robinson (1949)] and genetic advance for each character (Johnson et al., 195).The correlated unstandardized means of 12 characters studied were transformed to standardized uncorrelated set of variables using Dwyer's square root method (Rao, 1952). The statistical distance (Mahalanobis-D^2) *i.e*., the square of the distance between pairs of genotypes was obtained as the sum of squares of differences between pairs of corresponding uncorrelated values of any two genotypes and these were used for final grouping of the genotypes. Tocher's method (Singh and Chaudary, 1977) was followed to group the entries into different clusters considering the estimated D^2 values. The data was analyzed using computerized statistical packages like Window STAT and Spar-2 at the Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Bangalore.

Result and Discussion

Genetic Variability: Analysis of variance (Table 1) revealed that the genotypes exhibited significant difference for all the traits studied except 100 seed weight indicating the presence of genetic variability and the choice of the material for the investigation is appropriate. One of the ways to appreciate the extent of variability is to examine the range, which reflects the extent of phenotypic variability in respect of the trait under consideration, encompassing genotypic, environmental and interaction components. In the present study, the moth bean genotypes exhibited wide range values for all characters *viz.,* days 50 per cent flowering, plant height, primary branches per plant, secondary branches per plant, pod length, pods per plant**,** seeds per pod**,** 100- seed weight, root nodules per plant, nodules dry weight, seed protein content and seed yield per plant High range values indicate good scope for selection for any trait of interest for the breeder to exercise his selection.

The difference between GCV and PCV values was more for plant height, primary branches per plant and 100- seed weight indicating that selection based on phenotypic observations may not be very effective for these traits (Table 2). In general, the PCV and GCV were quite high for plant height, primary branches per plant, secondary branches per plant, 100-seed

weight, pods per plant and seed yield per plant indicating that there is greater scope for selection for improvement of these characters. These findings are in confirmation with Byregowda et.al., (1997), Khainar et al. (2003), Lakshmi Narayana Reddy et al. (2003b), Nasser Ahmed and Lavanya (2005) RangaRao et al. (2005), Ritu et al., (2005) and MallikarjunaRao et al. (2006) in mungbean. Contrary to the above the traits namely days to 50 per cent flowering and pod length showed moderate values of PCV and GCV while for the remaining characters viz., seed per pod, root nodules per plant, nodules dry weight and seed protein content, PCV and GCV values were low. Similar results have been reported by MallikarjunaRao et al. (2006) in mungbean.

Broad sense heritability and Genetic Advance: High heritability coupled with high genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene actions in their expression (Panse, 1957). But lower values of genetic advance indicate the prevalence of narrow range of variability, high G x E interaction or non-additive gene action. For moderate values of genetic advance, both additive and non-additive gene actions might be responsible for the expression of traits. High heritability coupled with high genetic advance as per cent of mean was observed for days to 50 per cent flowering, plant height, secondary branches per plant, pods per plant and seed yield suggesting that these characters are under the control of additive genes and phenotypic selection for these characters may be effective. These results are in agreement with the results obtained in mungbean by Byregowda et al. (1997) and Mallikarjuna Rao et al. (2006). High heritability and moderate genetic advance were observed for the characters root nodules per plant and nodules dry weight. This moderate value may be due to moderate values for phenotypic standard deviation as the heritability is high for these characters. However, there is no literature available for the traits either in moth bean or any other related pulses in support of the result obtained. Moderate heritability associated with high genetic advance were observed 100-seed weight and primary branches per plant indicating the prevalence of additive gene action and high value for phenotypic standard deviation, as the heritability was moderate. Moderate heritability coupled with low genetic advance was observed for seeds per pod. Whereas, seed protein content showed low heritability and low genetic advance indicating considerable influence of environment apart from non-additive gene action. Therefore, simple selection may not be effective in improvement of these traits.

Genetic Diversity: The 121 germplasm accessions were grouped into 8 clusters (Table- 3). Of the 8 clusters, cluster I was the largest one comprising of 90 genotypes followed by cluster

III with 25 genotypes, However, clusters II, IV,V, VI VII and VIII were solitary with each one genotype. Clustering pattern indicated that the accessions originating from different geographical regions were grouped together. As statement by Murthy and Arunachalam (1966), this none parallelism may be due to genetic drift and intense natural and human selection for diverse adaptive gene complexes under different environments causing greater diversity among genotypes rather than their geographic distances.Proportional contribution of seed yield and its associated characters to divergence was worked out and presented in the Table 4.Seed yield per plant recorded maximum contribution (39.49%) followed by days to 50 per cent flowering (31.57 %) and nodules per plant (10.66%). Whereas nodules dry weight per plant (0.74%), pod length (0.81%) and seeds per pod (0.91%) contributed minimum to the total genetic divergence. Inter and intra cluster distances are presented in the Table 5. Maximum inter cluster distance (8.64) was observed between cluster III and VI followed by IV and VIII (7.74), II and III (7.69) and III with V (7.62). Minimum inter cluster distance was observed between cluster II and IV (1.77) followed by II and V (2.22) and between IV and VI (3.28). Intra cluster distance ranged from 0.00 to 4.81, and the maximum intra cluster distance was observed for cluster III (4.81) followed by cluster I (4.43). There were six solitary clusters (II, IV, V, VI, VII and VIII) with no intra cluster values as they had only one accession each. The genotypes falling in a particular cluster will have close genetic background with smaller intracluster distance between the genotypes within a cluster. The genotypes between the clusters have more D^2 value with more genetic distance. Further, genotypes present in the more distanced clusters will serve as good sources of divergent genes which is very much required for breeding to exploit heterosis as reported by Gill *et al.*(1995) or and to get good transgressive segregants in the segregating population. The intracluster D^2 values of any cluster were less than the intercluster D^2 values of any two closely related clusters. Genotypes grouped into the same cluster presumably diverge little from one another as the aggregate of characters measured.

Cluster means were computed for all the 12 characters studied on pooled basis and presented in Table 6. Cluster III exhibited higher mean for plant height followed by Cluster I, whereas the cluster IV with one genotype showed lowest mean. Genotype in cluster IV recorded lowest mean indicating earliness in flower, whereas cluster III exhibited high mean value for flowering. Genotype with more number of primary branches was grouped into cluster III whereas genotype with less number of branches was grouped into cluster VIII. Genotypes with maximum number of secondary branches per plant were grouped into cluster III and

genotype grouped under cluster V recorded the lowest means was for this trait. Highest mean was recorded for pod length in cluster VIII. Highest mean values were noticed for seeds per pod under cluster III and lowest number of seeds per pod was recorded from genotype under cluster VI. Cluster I exhibited the highest mean for pods per plant however; genotypes with less number of pods per plant were grouped under cluster II. The trait 100 Seed weight recorded highest mean values for cluster VIII and it was lowest for cluster VI. Cluster IV having higher mean values for Seed Protein content followed by cluster III and cluster II. For seed yield per plant cluster VII exhibited the highest mean values and lowest was observed for cluster V. Here, it is worthy to note that in calculating cluster means, the superiority of a particular genotype in respect of a given character get diluted by other genotypes that are related and grouped in the same cluster which are inferior or intermediary for that character in question. Hence apart from selecting lines from clusters which have high intercluster distance for hybridization, selecting parents based on the extent of divergence in respect to a character of interest. This is to mean that, if breeder's intention is to improve the seed yield per plant, we can select parents, which are highly divergent with respect to these characters.

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Table 1. Mean sum of squares for seed yield and its attributing characters in moth bean

Sources of Variation		Df	Days to 50% flowering	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Pod length (cm)	Seeds per pod
Replications		1	1.33	11.52	21.42	0.33	1.078	0.103
Genotypes	(Unadjusted)	120	57.79**	328.48**	3.74**	1.675**	0.639**	0.917**
	(Adjusted)		59.23**	302.28**	3.52**	1.679**	0.648**	0.908**
Blocks within Reps (Adjusted)		20	2.57	16.73	3.88	0.176	0.106	0.194
Error	(Intra block)	100	178	18.58	0.376	0.67	0.070	0.185

Sources of Variation		Df	100 - seed weight (g)	Pods per plant	Seed yield (g/plant)	Nodules per plant	Nodules dry weight (mg/plant)	Seed protein content (%)
Replications		1	0.013	283.65	2.159	187.47	65.66	68.37
Genotypes	(Unadjusted)	120	0.173	2065.22**	62.47**	5.74**	132.65**	11.12**
	(Adjusted)		0.160	2081.00**	62.49**	8.21**	127.28**	10.88**
Blocks within Reps (Adjusted)		20	0.123	28.92	0.346	5.4	7.73	3.86
Error	(Intra block)	100	0.157	12.18	0.345	1.68	0.76	2.10

** Significant at 1% level

Table 2. Mean, range and variability parameters for different quantitative characters in moth bean

Sl.No	Characters	Mean ±SEm	Range	PCV (%)	GCV (%)	h^2 (%) Bs	GAM (%)
1	Days to 50% flowering	41.09±1.37	33-52	13.51	13.07	93.65	26.06
2	Plant height(cm)	16.97±5.07	6-61.10	71.52	64.93	82.41	121.42
3	Primary branches per plant	2.94±0.85	1.0-9.0	41.81	29.99	51.44	44.30
4	Secondary branches per plant	2.73±0.48	1.0-5.4	28.79	22.73	62.34	36.96
5	Pod length(cm)	4.49±0.416	3.4 -10.10	09.62	2.49	06.69	01.32
6	Seeds per pod	5.36±0.367	4.3- 7.0	09.17	06.45	49.51	09.34
7	100 - Seed weight(g)	03.70±0.24	1.8-4.9	35.88	23.44	42.68	31.54
8	Pods per plant	71.6±19.40	26.75-203.5	55.25	54.95	98.90	29.01
9	Root nodules per plant	27.03±0.94	21.99-32.29	07.31	06.43	77.45	11.65
10	Nodules dry weight (mg/plant)	85.18±1.96	74.89-98.00	09.37	09.08	93.94	18.13
11	Seed protein content (%)	23.66±1.72	18.54-26.62	08.47	04.29	25.60	04.46
12	Seed yield (g/plant)	10.14±1.96	1.8-41.8	45.06	44.74	98.57	112.32

Table3. Clustering Pattern of moth bean accessionsbased on morphological traits

Cluster no.	No. of. Genotypes	Genotypes
I	90	Bijapur-1, Bijapur-2, Bijapur-3, Bijapur-4, Bijapur-5, Bijapur-6, Bijapur-7, Bijapur-8, Bijapur-9, Bijapur-10, Bijapur-11, Bijapur-12, Bijapur-13, Bijapur-14, Bijapur-15, Bijapur-22, Bijapur-23,Bijapur-24, Bijapur-27, Bijapur-28, Bijapur-29, Muddebihal-1,Muddebihal-3,Muddebihal-4, Muddebihal-5, Muddebihal-6,Muddebihal-7,Muddebihal-8,Muddebihal-9, Muddebihal-10, Muddebihal-11,Muddebihal-12 Muddebihal-13,Honnali-1, Honnali-7, Honnali-8, Honnali-9, Honnali-10, Honnali-11, Soudatti-1, Soudatti-2, Soudatti-3, Soudatti-4,Soudatti-5, Soudatti-6, Soudatti-7, Basavanabagewadi-1, Basavanabagewadi-2, Basavanabagewadi-3, Basavanabagewadi-4, Basavanabagewadi-5, Bhemaryanagudi-2, Bagalkot-1, Bagalkot-2, Bagalkot-3, Bagalkot-4, Bagalkot-5, Bagalkot-6, Maharashtra -1, Maharashtra -2, Maharashtra -3, Gulbarga- Hosagar-4, Gulbarga-Vanadurga-5, Gulbarga-Shahapur-6, Gulbarga-7, Gulbarga-Golasar-9, Gulbarga- Moratagi-10, Gulbarga-11, GMO-3, GMO-14, GMO-25, GMO-01-04, GMO-01-09, RMO-42, RMO-140, RMO-435, RMB-25, RMB-100, CZM-1, CZM-2, CZM-3, MH-43, MH-61, P1, P2, P3, P4, P5
II	1	Gulbarga-1
III	25	Bijapur-17, Bijapur-18, Bijapur-19, Davanagere-1, Maharashtra -4, Maharashtra -5, Davanagere-2, RMO-423, Honnali-2, Honnali-4, Davanagere-3, RMO-257, RMO-225, Gulbarga-sindhi-8, Muddebihal-2, RMO-40, Bijapur-16, Honnali-3, Honnali-6, Honnali-5, Local-2, Bijapur-20, Bijapur-21, Shikaripura-1, Shikaripura-3
IV	1	Gulbarga-Kannoli-3
V	1	Gulbarga-Halisagar-2
VI	1	Shikaripura-4
VII	1	Bijapur-25
VIII	1	Bijapur-26

Table 4. Proportional contribution of seed yield and its attributing characters to divergence among moth bean accessions

Sl.No	Characters	No. of times appearing in first rank	Per cent contribution
1	Days to 50% flowering	2292	31.57
2	Plant height (cm)	192	2.64
3	Primary branches per plant	204	2.81
4	Secondary branches per plant	149	2.05
5	Pod length (cm)	59	0.81
6	Seeds per pod	71	0.98
7	100 Seed weight (g)	217	2.99
8	Pods per plant	202	2.78
9	Nodules per plant	773	10.66
10	Nodules dry weight per plant (mg/plant)	54	0.74
11	Seed protein content (%)	180	2.48
12	Seed yield (g/plant)	2867	39.49
	Total	**7260**	**100**

Table 5. Average intra (diagonal) and inter cluster distances of moth beanaccessionsbased on morphological data.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	4.43	5.66	6.48	6.36	5.6	5.62	6.6	6.45
II		0	7.69	1.77	2.22	2.54	6.08	6.34
III			4.81	8.64	7.62	7.49	6.36	6.52
IV				0	3.37	3.28	7.18	7.74
V					0	3.34	6.1	5.64
VI						0	4.91	6.18
VII							0	4.65
VIII								0

Table 6. Cluster wise mean performance of moth bean accessions for seed yield and its attributing characters

Cluster	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}
I	38.22	12.06	2.62	2.48	4.38	5.56	74.38	3.79	27.47	84.92	23.48	9.97
II	35	9.93	2.4	2.81	4.43	5.85	48.5	3.7	23.5	97.18	24.24	7.44
III	48.98	36.44	4.24	3.65	4.82	6.06	66.2	3.44	26.1	83.32	24.31	10.27
IV	33.5	8.11	3.13	2.48	3.98	5.9	50.5	3.8	22.5	97.21	26.73	8.54
V	35	10.13	1.98	1.71	5.6	5.5	49.5	3.4	23.5	95.85	22.57	3.57
VI	36	9.4	2.08	2.56	4.25	5.1	59	3.8	24	96.74	23.67	23.39
VII	46	10.4	2	3	4.35	5.5	53.5	2.85	27.5	97.33	23.57	23.7
VIII	46	10.5	1	2.5	6.9	5.5	67	3.9	28	97.06	22.49	6.25

X_1: Days to 50% flowering

X_2: Plant height(cm)

X_3: Primary branches per plant

X_4: Secondary branches per plant

X_5: Pod length (cm)

X_6: Seeds per pod

X_7: Pods per plant

X_8: 100 -seed weight (g)

X_9: Nodules per plant

X_{10}: Nodules dry weight (mg/plant)

X_{11}: Seed protein content (%)

X_{12}: Seed yield (g/plan)