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INTRA-SPECIFIC DIVERGENCE IN MOTH BEAN FOR GRAIN YIELD AND ITS COMPONENTS

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ABSTRACT

Genetic divergence, as measured by Mahalanobis D^2 statistics was studied in 22 diverse genotypes of moth bean [*Vigna aconitifolia* (Jacq) Marechal]. The genotypes were grouped into seven clusters. Geographic diversity did not seem to have a direct association with genetic diversity. Use of IPCMO 1015, IPCMO 569, IPCMO 939, IPCMO 911 and Jadia in crossing programme is advocated.

Information on the genetic diversity is important for selecting desirable parents. Using Mahalanobis (1986) D^2 - statistics, many workers (Katiyar and Singh, 1979; Singh et al., 1982 in chickpea; Bainiwal and Jatasra, 1980 in pigeonpea ; Chandel and Joshi, 1983 in green-seeded pea) have estimated the degree of divergence. But no information in moth bean [*Vigna aconitifolia* (Jacq.) Marechal] is available. The present study, therefore, was undertaken to analyse the genetic divergence of 22 genotypes and to find out the relationship between geographic and genetic diversity, if any.

MATERIAL AND METHODS

The experimental material consisting of twenty two genotypes was grown in randomized complete block design with three replications in kharif 1980, under rainfed conditions. Each genotype was sown in a single-row plot of 2.25 meter length spaced 30 cm apart. Five plants were selected at random from each plot for recording the observations on (i) days to flowering (ii) duration of flowering (iii) primary branches (iv) plant height (cm) (v) inflorescences (vi) bunches (vii) pods (viii) pod length (cm) (ix) seeds/pod and (x) seed yield (g). The mean values were subjected to analysis of variance and then multivariate analysis of D^2 – statistics to Mahalanobis (1936). The grouping of genotypes in different clusters was done as per Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the populations for all the ten characters. Significant V-statistic ($\chi^2 = 379.1$ with 210 df) indicated that differences between the means in respect of pooled effect of all the characters between populations were significant.

After computing D^2 - values for the 231 possible combinations of populations and assuming that intra-cluster distance is less than inter-cluster distance, the 22 genotypes were grouped into seven clusters (Table 1).

Table 1. Composition of clusters based on D^2-statistics in moth bean

Cluster	No. of genotypes	Genotypes
I	10	IPCMO 259, IPCMO 845, IPCMO 893, IPCMO 943, IPCMO 925, IPCMO 1016. IPCMO 1035, T 25, Jadia, Local
II	3	IPCMO 569, IPCMO 848, IPCMO 939
III	4	IPCMO 344, IPCMO 102, T 18, T 23
IV	2	IPCMO 911, IPCMO 942
V	1	T-16
VI	1	T 2
VII	1	IPCMO 1015
Total	22	

Cluster I had the maximum number of genotypes (10) followed by clusters III (4), II (3) and IV (2). Three clusters, viz., V, VI and VII had one genotype each. The results revealed that different genotypes from different sources were distributed to different clusters, indicating that genetic diversity and geographic diversity are not related. Similar findings have also been reported by other workers in different crops (Murty and Arunachalam, 1966; Das and Borthakur, 1973; and Singh et al., 1982).

Intra-and inter-cluster D^2 values between all possible pairs of clusters are presented in Table 2. The intra-cluster distances ranged from 0 (clusters V, VI and VII) to 3.617 (cluster III), while inter-cluster distances ranged from 4.437 (cluster I-III) to 7.678 (cluster II-V). Intermediate value (6.003) was recorded between clusters I and VII. In hybridization programme, to have desirable segregants, role of diverse parents is well known to plant breeders. Therefore, while selecting parents inter-cluster distance must be considered. More the inter-cluster distance, more is the genetic diversity among the genotypes. But while considering inter-cluster distance, yield potential should also be considered.

Table 2. Intra- and inter-cluster distances (D^2) among 7 clusters in moth bean

Cluster	I	II	III	IV	V	VI	VII
I	3.439	4.508	4.437	4.975	5.824	4.695	6.003
II		2.873	5.772	5.601	7.678	6.747	5.982
III			3.617	4.792	4.461	4.737	5.616
IV				3.597	6.387	5.639	5,516
V					0.000	4.424	4.741
VI						0.000	5.238
VII							0.000

Table 3. Cluster means of 10 characters in moth bean

Cluster	Seed yield/ plant	Pods/ plant	Pod length	Seeds/ pod	Primary branches/ plant	Plant height	Inflore-scences/- plant	Bunches/ plant	Days to first flo-wering	Duration of flowering (days)
I	1.02	10.63	3.56	4.87	5.42	14.37	20 64	7.27	37.5	43.1
II	2.15	12.69	3.88**	5.50**	4.39*	15.25	16.79*	6 75*	37.2	44 0
III	1.12	13.25	3.35	5 42	7.03	15.15	24.58	9 28	37.3	39.7
IV	1.92	13.97	3.87	5.04	7.44**	18.44**	21.43	11 50	36.8	41.8
V	1.08	16.27	2.90*	4.73	5.60	14.53	31.13	14.80	39.0	37.7*
VI	0.89*	11.93	3.43	4.53*	7.07	11.40*	24.13	10.00	40.0**	41.3
VII	3.03**	25.20**	3.53	4.93	6.60	15.67	39.00**	20.6 **	36 7*	45 0**

* Minimum ** Maximum

Cluster means of all the characters showed that clusters were different from each other for one or more characters (Table 3). Cluster VII with only one genotype IPCMO 1015 had maximum mean values for five characters, namely, seed yield/plant, pods/plant, inflorescence/plant, bunches/plant and duration of flowering. Genotypes IPCMO 848, IPCMO 569 and IPCMO 939 present in cluster II had maximum pod length and seeds/pod which were also high yielding. It is interesting to note that the values for primary branches, inflorescence and bunches per plant were minimum for cluster II, but the genotypes were high yielding may be due to more pod length and more seeds/pod. Cluster IV, with only two genotypes IPCMO 911 and IPCMO 942, showed maximum number of primary branches and plant height. Highly adapted, locally grown variety Jadia with high seed yield (1.87 g), more bunches (13.5) and more pods (18.4) was in cluster I.

Thus from the present study it is concluded that geographical diversity is not related to genetic diversity. To have high heterosis, diverse genotypes with desirable attributes (IPCMO 1015, IPCMO 569, IPCMO 939, IPCMO 911 and Jadia) should be used in crossing programme.

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