

## GENETIC DIVERGENCE IN MOTH BEAN

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Mahalanobis  $D^2$  statistic was used as a quantitative measure of genetic divergence in the present investigation conducted on one hundred lines of moth bean (*Vigna aconitifolia* L.) single plant progenies and varieties emanated from Gujarat (12), Haryana (16), Karnataka (3), Maharashtra (10), Punjab (4), Rajasthan (43) and Uttar Pradesh (12). The crop was grown as rainfed on soils having 0.09% N, 30.4 kg/ha P and 370 kg/ha K. Crop was fertilized with 20 kg N, 40 kg P and 10 kg K. FYM was applied @ 10 t/ha. The crop received 264 mm rainfall (no irrigations) during crop growth period. The experiment was laid down in a randomised block design with three replications. Each genotype had six rows, 2 m long at 30 cm apart with plant to plant distance of 10 cm. Observations on thirteen characters (Table 2) were recorded on fifty randomly selected plants out of the four middle rows. Total straw obtained (just before leaf fall) from each of the fifty plants was weighed and averaged. Harvest index was calculated in each of the fifty plants (Singh and Stoskopf 1971) as percentage of biological yield represented by economic yield and averaged. Plant habit was recorded by scoring technique, viz., 3 for erect, 2 for intermediate and 1 for spreading growth habit. The choice of characters was arrived at after Arunachalam (1981). The data were subjected to analysis of variance and then multivariate analysis of  $D^2$  statistic according to Mahalanobis (1936). The genotypes were grouped into different clusters following the Tochers method (Rao, 1952).

Table 1. Cluster composition and origin of one hundred genotypes of moth bean

Cluster number	Number of genotypes	Place of origin
I	13	Haryana, Maharashtra, Punjab and Rajasthan
II	5	Gujarat, Haryana, Rajasthan and U.P.
III	13	Gujarat, Haryana, Karnataka and Rajasthan.
IV	8	Gujarat, Maharashtra, Rajasthan and U.P.
V	28	Haryana, Karnataka, Maharashtra and Rajasthan.
VI	19	Gujarat, Haryana, Punjab, Rajasthan and U.P.
VII	13	Gujarat, Haryana, Karnataka, Maharashtra, Rajasthan and U.P.
VIII	1	Rajasthan

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The analysis of variance showed significant differences among the genotypes for all the thirteen characters. Significant V-statistic ( $\chi^2=10107.51$  with 1287 d.f.) indicated that differences between the means in respect of pooled effects of all the characters between genotypes were significant. The hundred lines were grouped into eight clusters (Table 1). Cluster VIII which included only one line (originating from Barmer, Rajasthan) was widely divergent from all other clusters. The inter cluster distance ( $D=37.73$ ) was maximum between clusters V and VIII followed by that between clusters I and VIII (34.93). The least inter cluster distance was between clusters I and V (11.20) followed by I and III (11.92). The results revealed that different genotypes from different sources and states were distributed to different clusters, indicating that genetic diversity and geographic diversity are not related. At least one line of Rajasthan was present in all the clusters. Lines having their origin in Nagore-Merta regions (including adjoining areas) of Rajasthan were present in four different clusters. Lines evolved in common habitat exhibited ample genetic diversity and fell into different clusters. Similar findings were earlier reported by Henry and Krishna (1986) and Jindal (1988) in moth bean.

Out of hundred moth bean genotypes there were only 5 lines in cluster II, but intra-cluster average  $D^2$  values of this cluster were the highest (11.05). Intra-cluster divergence ranged from 0.0 for cluster VIII to 11.05 for cluster II.

Intra-cluster group means for thirteen characters in moth bean (Table 2) revealed that cluster IV had highest mean values for plant height, days to 50% flowering and maturity, cluster V for harvest index, cluster VII for pod length and seeds per pod, and cluster VIII for erect plant type, number of effective branches, pods per plant, seed weight, grain yield per plant, straw yield per plant and grain yield per day per plant. Table 2 revealed that low yielding clusters variably had low straw yields and vice versa.

Straw yield per plant was the most important character contributing (25.8%) towards genetic divergence followed by seed weight (10.3%) and grain yield/day/plant (9.8%) in present studies.

Varieties included in clusters with maximum intercluster distance are obviously genetically more divergent. Varieties in the clusters V and VIII are the most divergent. It would be therefore to incorporate such varieties in the breeding programme.



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