

Genetic divergence in castor [*Ricinus communis* (L.)]

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ABSTRACT

Mahalanobis D² statistics analysis was employed to measure the genetic divergence of 34 genotypes of castor. Six different clusters were formed with a wide range of inter cluster distances (17.17 to 331.75) suggesting considerable diversity among the genotypes. Clustering pattern indicated that geographical distribution could not be taken as sole criterion of genetic diversity. The D² analysis revealed that harvest index, oil content, number of capsules/plant and seed yield/plant contributed maximum towards genetic divergence. It was suggested that the geotypes separated by higher statistical distance could be utilized in hybrid breeding programme as well as for obtaining wide spectrum of variation among the segregates.

Key words : Castor, genetic divergence, D² statistics

The choice of the parents is of paramount importance in any breeding programme. Genetic divergence analysis is attempted to identify parents for realizing high heterosis and superior recombination's in segregating generations (Arunachalam, 1981).

The D² statistics proposed by Mahalanobis (1936) is one of the potent techniques of estimating genetic divergence based on multivariate analysis and canonical analysis (Moll *et al.*, 1962 and Bhatt and Reddy, 1987). This technique measures the forces of differentiation at two levels, viz., intracluster and intercluster levels and thus helps in the selection of genetically divergent parents for exploitation in hybridization programme. In addition to aiding in the degree of diversification, it also determines the relative contribution of each component character to the total divergence. The genotypes grouped together are less divergent than the ones which are placed in different clusters. The clusters which are separated by the highest statistical distance show the maximum divergence.

MATERIALS AND METHODS

The experimental material consisting of 34 genotypes of castor were obtained from Research Scientist (Castor), S. D. Agricultural University Sardarkrushinagar. These genotypes were grown in a randomized block design with three replications at Main Castor-Mustard Research Station, S.D. Agricultural University, Sardarkrushinagar (Gujarat). Each genotype was grown in a single row of 12 dibbles, spaced at 90 cm with intra-row spacing of 60 cm. To raise the crop recommended package of practices for irrigated conditions were adopted. The observations were recorded on five randomly selected plants for each treatment and each replication for 12 characters viz. days to 50% flowering, days to 50% maturity, plant height, length of main spike, number of nodes up to primary spike, number of branches/plant, number of effective branches/plant, 100 seed weight, harvest index, oil content and seed yield/plant.

The Mahalanobis's D² statistics were used to measure the genetic divergence as suggested by Rao (1952). Transformation of original means of various characters (X's) to uncorrected varieties (Y's) was carried out by pivotal condensation as the common dispersion matrix on computer. This made D² value as a simple sum of

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squares of differences in transformed values for various characters. The generalized distance between any two populations is defined as

$$D^2 = b_1 d_1 + b_2 d_2 + \dots + b_p d_p$$

Where,

$X_1, X_2, X_3, \dots, X_p$ as a multiple measurements available on each individual, being the different in the mean of the two populations. In terms of variance, the D^2 value is obtained as follow:

$$D^2_p = W_{ij} (X_i^{-1} - X_i^{-2}) (X_j^{-1} - X_j^{-2})$$

Where,

W_{ij} = Inverse estimated variance and covariance.

Grouping of the genotypes was done by using Tocher's method (Rao, 1952). The criterion used for the clustering in this method is that, two genotypes belonging to the same cluster should on average show a smaller D^2 values, than those belonging to different clusters.

To start with two genotypes having smallest D^2 values between them were considered, to which a third genotype having a smallest average D^2 value from these genotype was added. Next the nearest fourth genotype was considered and the procedure was continued at a certain stage, when it was felt that inclusion of a genotype results in abrupt increase in the average D^2 of the genotypes (for the cluster), that genotype was not included in the cluster. In the similar way the other clusters were formed. This procedure was continued till all the genotypes were included in one cluster or the other. After the information of clusters, average intra-cluster distance (D) was calculated by using the formula:

$$D = \sqrt{\frac{\sum Di^2}{n}}$$

Where,

$\sum Di^2$ = Sum of distance between all possible combinations of the population included in the cluster,

n = Number of population in a cluster.

The inter-cluster distance was calculated by measuring the distance between cluster-I and II, between cluster-I and III, between II and III and so on. Likewise, one by one cluster was taken and their distances from other clusters were calculated. For

graphical presentation average intra and inter-cluster D values were used to obtain mutual relationship between the clusters.

RESULTS AND DISCUSSION

In the present study, Mahalanobis D^2 statistic was computed for all the possible pairs of genotypes in order to assess the genetic diversity present among 34 genotypes of castor studied. The 34 genotypes of castor were grouped in six clusters (Table 1).

Grouping of the genotypes was carried out by following the Tocher's method (Rao, 1952) with assumption that the genotypes within the cluster have smaller D^2 values among themselves than those from groups belonging to different clusters. The cluster V was the smallest having only two genotypes from Kutch and Surendranagar. Cluster I was the biggest cluster with 11 genotypes from Tamilnadu, Jamnagar, Vijapur, Kutch, Sardarkrushinagar (Gujarat and Uttaranchal) followed by cluster II with 8 genotypes from Hyderabad (Andhra Pradesh) and Kutch (Gujarat) and cluster III with six genotypes from Tamilnadu, Uttaranchal, Junagadh, Kutch, Sardarkrushinagar (Gujarat). The clustering pattern showed that the genotypes of different geographical areas were clubbed in one cluster and also the genotypes belonging to same geographical area were grouped in different clusters indicating that there was no formal relationship between geographical diversity and genetic diversity. Murty and Arunachalam (1981) have stated that genetic drift and selection in different environments could cause greater diversity than geographic distance. The absence of parallelism between geographic distribution and genetic diversity in the present study is in accordance to the findings of Sevagaperumal *et al.* (2001), Anjani *et al.* (2002) and Patel *et al.* (2004).

The D^2 statistic estimated for 34 accessions for 12 characters showed that the generalized distance ($\sqrt{D^2}$) within clusters ranged from 0.00 to 40.90 which was an indicator of diversity available in the material evaluated. On the bases of D^2 values, six clusters were formed from 34 genotypes. The inter and intra cluster distances (Mahalanobis Euclidean Distance-not to scale) amongst six clusters are diagrammatically presented in Fig.1.

Three clusters viz., cluster IV (with 4 accessions), cluster V (with 2 accessions) and cluster III (with 3 accessions) had least intra cluster distance (0.00) indicating that the genotypes included within these

Table 1 Composition of different clusters based on D^2 values of 34 genotypes of castor

Clusters	Number of genotypes	Name of genotypes	Origin/Source
I	11	TMV-2-6, JM-6, VH-38-2, VH-58-2-7, VH-71-2-3, EC-97708, EC-97709, SPS-47-8, SPS-57-8, SKI-147, T-3.	Tamilnadu, Jamnagar, Vijapur, Thailand, Kutch, Sardarkrushinagar, Uttaranchal.
II	8	HC-7, SPS-38-7, SPS-76-7, SPS-37-6, SPS-43-9, SPS-31-2, SPS-38-8, OTC-30-10.	Hyderabad, Kutch.
III	6	JI-23, ROSY, SPS-71-2, SKI-280, T-9, GC-2.	Junagadh, Tamilnadu, Kutch, Sardarkrushinagar, Uttaranchal.
IV	4	SKI-283, SKI-288, SKI-293, T-4.	Sardarkrushinagar, Uttaranchal.
V	2	OTC-30-5, SH-72.	Kutch, Sardarkrushinagar.
VI	3	GC-3, GCH-5, GCH-7.	Sardarkrushinagar.

Table 2 Average intra and inter-cluster distances, D ($D = \sqrt{D^2}$) values in castor

Cluster	I	II	III	IV	V	VI
I	25.68	48.83	63.21	43.79	36.94	234.22
II		34.58	75.85	83.96	82.61	305.17
III			40.90	89.59	96.50	331.75
IV				0.00	17.27	113.36
V					0.00	138.27
VI						0.00

Table 3 Cluster means for twelve characters in castor

Cluster	Days to 50% flowering	Days to 50% maturity	Plant height (cm)	Length of main spike (cm)	Nodes up to primary spike	Capsule/plant	Bran ches/plant	Effective bran ches/plant	100 Seed weight (g)	Harvest index (%)	Oil content (%)	Seed yield/plant (g)
I	66.67	131.36	71.30	45.42	88.66	44.18	3.53	2.74	30.67	15.68	40.54	76.46
II	66.42	130.75	90.67	52.13	18.82	64.50	3.19	2.26	33.46	18.23	49.13	97.17
III	66.17	130.05	75.83	49.83	17.16	45.61	3.49	3.13	35.11	24.38	45.23	118.44
IV	66.75	130.50	88.83	56.50	18.48	89.25	3.50	2.65	36.08	30.69	45.29	162.67
V	66.17	130.33	101.33	62.00	20.27	108.00	3.17	2.17	32.67	17.58	45.58	83.17
VI	64.56	128.89	75.67	54.78	17.93	58.11	5.74	4.66	38.00	33.11	47.99	191.11

Table 4 Per cent contribution of different characters to total genetic divergence in castor

Sr.No.	Character	Number of times character ranked first	Per cent Contribution (%)
1	Days to 50% flowering	0.01	0.00
2	Days to 50% maturity	2	0.36
3	Plant height	1	0.18
4	Length of main spike	6	1.07
5	Number of nodes up to primary spike	5	0.89
6	Number of capsule/plant	94	16.76
7	Number of branches/plant	34	6.06
8	Number of effective branches/plant	4	0.71
9	100 Seed weight	24	4.28
10	Harvest index	169	30.12
11	Oil content	160	28.52
12	Seed yield/plant	62	11.05

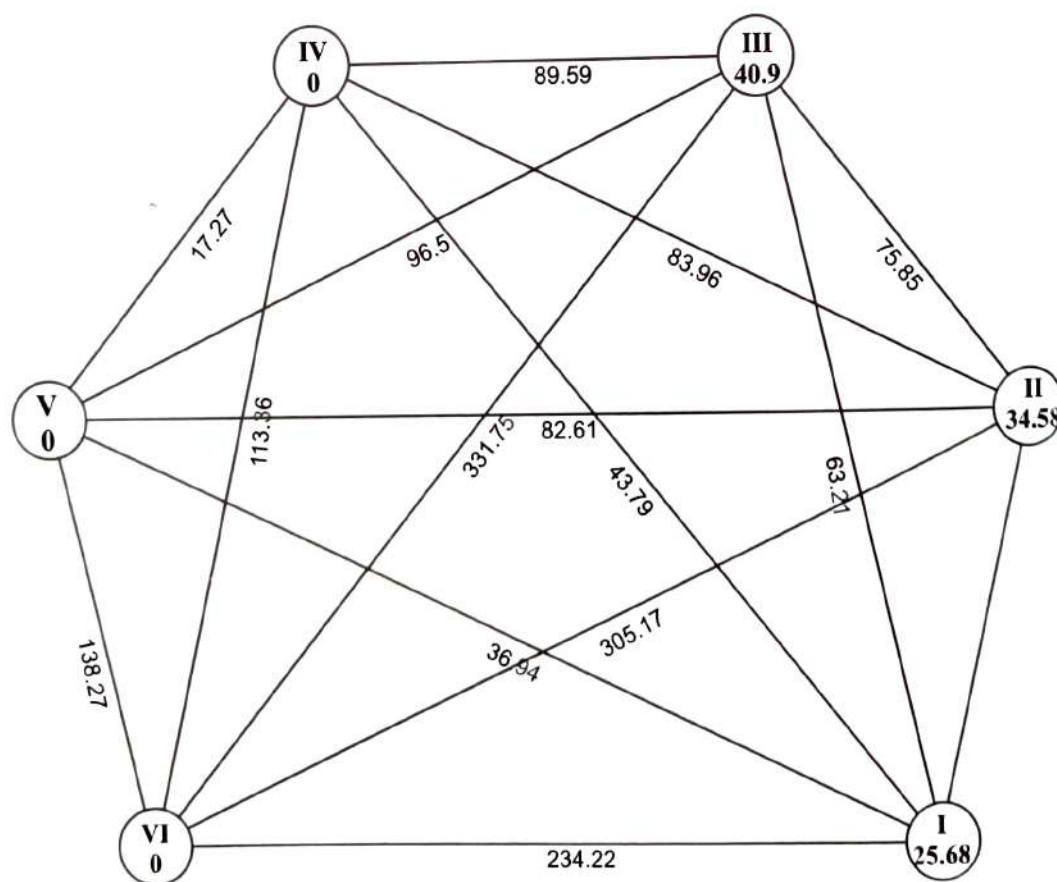


Fig. 1 Mahanobis Euclidean distance diagram

three clusters were not diverse from each other (Table 2). The intra cluster distance was highest for cluster III (with six genotypes) followed by cluster II (with eight genotypes) and cluster I (with eleven genotypes). The high intra cluster distance indicated the wider genetic diversity among the genotypes included within these clusters. In general the inter cluster distances were higher than the intra cluster distances. The highest inter cluster distance was recorded in cluster III and VI (331.75) followed by cluster II and VI (305.17) and cluster I and VI (234.22). The genotypes belonging to the clusters separated by high statistical distance could be used in heterosis breeding programme and also for obtaining wide spectrum variation among the segregates.

The clustering pattern could be utilized in deciding the cross combinations which may generate the highest possible variability for the traits. The cluster means for 12 characters are given in (Table 3). The genotypes with high values of any cluster can be used either for direct adoption or for hybridization or for further selection and improvement. In the present study cluster I was top ranking for dwarf plant height while cluster IV for higher length of the main spike, cluster V for higher number of capsules/plant and cluster II for higher oil content. It would be worthwhile to select the genotypes from these clusters for hybridization programme for genetic improvement. Since cluster VI included the three released variety/hybrids viz., GC-3, GCH-5 and GCH-7 this cluster had high cluster mean for most of the yield components viz., branches/plant, effective branches/plant, 100 seed weight, harvest index and seed yield/plant.

It is well established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad spectrum variability in segregating generations (Arunachalam, 1981). It has also been observed that the most productive hybrids may come from high yielding parents with a genetic diversity. Therefore, in the present investigation based upon high yielding genotypes and large inter cluster distances, it is advisable to attempt crossing of the accessions which may lead to broad spectrum of desirable genetic variability for yield improvement in castor.

The components of D^2 due to each character were ranked I being assigned to the highest value. The total

of these ranks over all possible $n(n-1)/2 = 561$ combinations would provide indirect information about the order of priority in terms of per cent contribution of the character to the total divergence. It was observed that harvest index (30.12%) followed by oil content (28.52%), number of capsules/plant (16.76%) and seed yield/plant (11.05%) were the main contributors towards the total divergence (Table 4). The remaining characters like number of branches/plant (6.06%) and 100 seed weight (4.28%) had moderate contribution where the rest of the characters had relatively lower contribution towards the total genetic divergence.

CONCLUSION

Genetic divergence was studied in 34 genotypes of castor performing Mahalanobis D^2 analysis. These genotypes were grouped in six clusters. The intra cluster distance was as minimum as 0.0 (cluster IV, V and VI) to 40.9 (cluster III). The inter cluster distance 331.75 (between III and VI). The clustering pattern suggested that the geographical diversity was not an indicator of genetic diversity. In terms of per cent divergence, it was revealed that harvest index (30.12%) followed by oil content (28.52%), number of capsules/plant (16.76%) and seed yield (11.05%) contributed substantially. It was suggested that the genotypes separated by higher statistical distance could be utilized in hybrid breeding programme as well as for obtaining wide spectrum of variation among the segregates.

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