

Genetic divergence studies in castor (*Ricinus communis* L.)

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Abstract : Thirty six genotypes of castor were evaluated for genetic diversity by using Mahalanobis D^2 statistics and grouped into ten clusters. The single plant yield contributed maximum to the genetic divergence. The hybridization between the genotypes from the clusters VII (TRC 207, TRC 223 and Bhagya) and IX (TMV 3 and Aruna) should give rise to highly heterotic hybrids and wide spectrum of variability in subsequent segregating generations. (*Key Words :* Castor, Genetic divergence).

Castor is mainly grown in marginal lands and to some extent as a mixed and border crop in Tamil Nadu. This crop is one among the oil seeds which is having a high potential for non-edible oil but lesser work has been done for its full exploitation. Researchers looking for new genotypes and varietal improvement on this crop are substantially low. Hence to have an understanding about the availability of different genotypes and their divergence pattern, a study was undertaken, among 36 genotypes by using Mahalanobis D^2 statistics.

Materials and Methods

The materials for the investigation comprised of 15 Indian and 21 exotic castor genotypes raised in randomised block design replicated thrice during 1992-93, at Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai. Each genotype was raised in two rows of 4.8m length adopting a spacing of 90cm between plants in the row. The biometrical observations were recorded in five plants selected at random from the middle of the rows per replication for eight traits. Genetic divergence was estimated by Mahalanobis D^2 Statistics and the genotypes were grouped on the basis of minimum generalised distances using Tocher's method as described by Rao (1952).

Results and Discussion

The analysis of variance revealed highly significant difference among genotypes for eight characters. This indicated that the existence of significant amount of variability among the genotypes for the characters studied. On the basis of D^2 analysis, the 36 genotypes were grouped into 10 clusters (Table 1). The cluster I had as many as nine genotypes followed by cluster IV with eight genotypes and cluster II with four genotypes. The

clusters III and VII had three genotypes each and cluster X had only one genotype as constituents.

Thus the variation in the composition of individual cluster with regard to the number of genotypes indicated the presence of large amount of diversity in the population. The clustering pattern revealed that the genotypes originating from different geographical region got themselves grouped together into different clusters. Such grouping of genotypes from different geographic locations would be attributed to the exchange of breeding materials from one place to another and unidirectional selection practiced by plant breeders in different locations (Singh and Bains, 1968). The scattering of genotypes from the same geographic region to different clusters might be due to the heterogeneity, genetic architecture of the populations, past history of selection, developmental traits and degree of general combining ability (Murthy and Arunachalam, 1966). The results have clearly indicated that there is no parallelism between the geographic diversity and genetic diversity in castor. This is in confirmation with findings already reported by Bhatt and Reddy (1987) in castor and John Joel (1987) in sesame.

The minimum intra cluster distance (D value) was observed in cluster V (4.01) and the maximum in cluster IV (10.89). Similarly the least intercluster distance was observed between V and VI (5.32) while the highest between VII and IX (26.28) as given in Table 2. The hybridization between genotypes from these clusters (VII and IX) should result in maximum hybrid vigour and highest number of useful segregants. The inter cluster distances were higher than that of the intra cluster distances which indicated substantial diversity among the parents in the present study.

In addition to the general features of variation and divergence, this study also provides

Table 1. Composition of clusters

Cluster number	Number of Genotypes	Name of the Genotypes	Source
I	9	TRC 6	Africa
		TRC 18	U.S.A
		TRC 31	Egypt
		TRC 40	South Africa
		TRC 44	South Africa
		TRC 46	Italy
		TRC 54	Italy
		TRC 78	U.S.S.R
		TRC 97	Nigeria
II	4	TRC 85	India
		TRC 102	India
		TVC 11	Africa
		TVC 23	U.S.A
III	3	TRC 135	U.S.A
		RC 8	India
		VP 1	India
IV	8	TRC 181	U.S.A
		TRC 183	U.S.A
		TRC 201	U.S.A
		TRC 203	U.S.A
		TRC 205	India
		TRC 206	India
		TVC 28	U.S.A
		TVC 31	U.S.A
V	2	TVC 27	U.S.A
		TMV 4	India
VI	2	TVC 15	Africa
		48-1	India
VII	3	TRC 207	India
		TRC 223	India
		Bhagya	India
VIII	2	TVC 30	U.S.A
		Sowbhgya	India
IX	2	TMV 3	India
		Aruna	India
X	1	TMV 2	India

Table 3. Relative contribution of eight characters to genetic diversity in castor

Sl. No.	Character	Number of times appearing in first rank	Percentage of contribution
1.	Days to 50 per cent flowering	5	0.79
2.	Plant height	59	9.37
3.	No. of nodes upto primary raceme	1	0.16
4.	Length of primary raceme	9	1.43
5.	No. of capsules in primary raceme	8	1.27
6.	No. of racemes per plant	33	5.24
7.	100 seed weight	57	9.05
8.	Single plant yield	458	72.69
Total		630	100.00

Table 2: Inter and Intra cluster D² and D (within parenthesis) Values

Cluster Number	I	II	III	IV	V	VI	VII	VIII	IX	X
I	53.76 (7.33)	87.36 (9.35)	247.70 (15.74)	114.25 (10.69)	62.54 (7.91)	68.35 (8.27)	149.60 (12.23)	59.70 (7.73)	360.86 (19.00)	196.62 (14.02)
II		107.74 (10.38)	154.98 (12.45)	177.46 (13.32)	53.01 (7.28)	53.68 (7.33)	253.40 (15.92)	100.15 (10.01)	233.25 (15.27)	204.67 (14.31)
III			19.37 (4.40)	440.46 (20.99)	107.90 (10.39)	132.34 (11.50)	596.35 (24.42)	238.47 (15.44)	77.55 (8.81)	435.90 (20.88)
IV				118.62 (10.89)	165.43 (12.86)	143.17 (11.97)	114.44 (10.70)	147.11 (12.13)	516.32 (22.72)	143.50 (11.98)
V					16.11 (4.01)	28.28 (5.32)	234.05 (15.30)	49.80 (7.06)	187.40 (13.69)	212.09 (14.56)
VI						23.46 (4.84)	218.18 (14.77)	86.78 (9.32)	189.78 (13.78)	134.59 (11.60)
VII							110.90 (10.53)	164.58 (12.83)	690.48 (26.28)	197.32 (14.05)
VIII								45.14 (6.72)	356.65 (18.89)	273.39 (16.54)
IX									70.57 (8.40)	390.03 (19.75)
X										0.00 (0.00)

information on the characters that contributed maximum to the total divergence among genotypes (Table 3). The analysis for estimating the contribution of various characters towards the expression of the genetic divergence indicated that the single plant yield (72.69%), plant height and 100 seed weight along with seed yield accounted for more than 90 per cent of total divergence in the material. The importance of single plant yield, number of seeds, seed weight and plant height for genetic diversity in sesame was indicated by John Joel (1987) and Anitha and Stephen Dorairaj (1990). Days to 50 per cent flowering and number of nodes upto primary raceme contributed minimum to the genetic divergence among the genotypes studied. Low variability of these traits in such wide variety of genotypes may suggest high degree of consistency and heritability of these traits.

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