



## GENETIC DIVERGENCE ANALYSIS FOR YIELD AND QUALITY TRAITS IN CASTOR (*Ricinus communis* L.)

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### ABSTRACT

In order to assess the genetic divergence among the 60 germplasm accessions in castor, Mahalanobis  $D^2$  statistics was applied. The 60 germplasm were grouped into 11 clusters where, cluster I was largest containing 41 genotypes followed by cluster II with 7 genotypes, cluster III with 4 genotypes and cluster IV, V, VI, VII, VIII, IX, X, and XI with each having single genotype. Based on inter cluster distance, the highest inter cluster distance was observed between cluster X and cluster XI followed by cluster IX and cluster X, cluster VIII and cluster X and cluster VI and cluster XI. Days to flowering (12.40 %) were main contributors to the total divergence, which was followed, by Number of branches per plant (10.90 %) and Seed yield per plant (10.04 %). The genotypes included in the diverse clusters can be used as promising parents for hybridization programme for obtaining high heterotic response and thus better segregants in castor.

**KEY WORDS:** Castor, Clusters, Genetic diversity

### INTRODUCTION

Genetic diversity is of major interest to plant breeder. As more diverse the parents with an overall limit of fitness, the greater is the chance of higher amount of heterotic expression in  $F_1$ 's and greater is the possibility of generating broad-spectrum variability in segregating generations. Genetic diversity between populations/genotypes indicates the differences in gene frequencies. Multivariate analysis using Mahalanobis  $D^2$  statistics (1936) is valuable tools to study genetic divergence at inter varietal and sub species level in classifying the crop plants. This has been successfully utilized in castor to classify the genotypes and determine their interrelationship by many workers Sevugaperumal *et al.* (2001) and Lakshamma *et al.* (2002). The present study was carried out to ascertain the nature and magnitude of genetic divergence among 60 castor genotypes.

### MATERIALS & METHODS

Genetic material for the present investigation comprised of 60 castor genotypes. The experiment was carried out in a Randomized Block Design (RBD) with three replications at Castor-Mustard Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, during August-2016 to March-2017. Sowing of seeds was carried out through dibbling method. Each genotype was grown in single row of 10 dibbles. The distance between two successive rows was 120 cm, while between two

dibbles within a row was 60 cm. All the agronomic practices were followed uniformly. The observations were recorded on 5 randomly selected plants and tagged from each genotype in each replication for 10 characters. These data were subjected to divergence analysis (Mahalanobis, 1936) and Tocher's method as described by Rao (1952) for determining group constellation. Average intra and inter cluster distances were estimated as per the procedure outlined by Singh and Chaudhary (1977).

### RESULTS & DISCUSSION

Tocher's method (Rao, 1952) was employed for the formation of clusters. Sixty germplasm were grouped in eleven clusters are presented in Table 1. Cluster I was the largest and comprised of 41 genotypes, which were collected from different location among the India, followed by cluster II (7 genotypes), cluster III (4 genotypes) and clusters IV, V, VI, VII, VIII, IX, X and XI each having single genotype were collected from different location among the India. This revealed that the genetic diversity had no any relevance with Originating centers of the studied genotypes. This could be due to intermingling of gene pool among genotypes by crossing and germplasm exchange programmes. Moreover, the genetic drift and selection in different environments could also cause greater diversity than geographical distance. The results are in accordance with those of Bhatt and Reddy (1987) and Jaimini (2002).

**TABLE 1:** Cluster group of 60 genotypes on the basis of D<sup>2</sup> statistics in castor

No. of Cluster	Number of genotypes	Name of genotypes
I	41	VH-11, JH-118, SH-42, PUNJAB - 1, SPS-37-3, 48-1, SKI-270, EC-80852, SKI-314, VH-74-1-6, SH-9, JGG, JMP, TC-1, VH-55-2-1, SPS-56-9, T-3, VH-39, HC-8, 144, SH- 67, 39962, JI-15, VH-60-2-1 EC-103746, 12560-TB, HC-3, JI-61, SKI-346, EB-16, 6209-A, BAKER-147, SH-2, SH-18, SKI-241, EC-97707, BHAGYA, 822, AMBAJI BHARAI-24-SELECTION, RC-1377-B2
II	7	SPS-56-10, SKI-64, SKI-267, SKI-291, SKI-333, SKI-341, SH-4
III	4	RAPAR, 26004, JAN-21, 1092
IV	1	RVS-2-B-1
V	1	21844
VI	1	954
VII	1	K-6
VIII	1	SPS-76-7
IX	1	6-219-22
X	1	GCH - 7
XI	1	IC-25335 BIG

**TABLE 2:** Average intra cluster distance in D<sup>2</sup> statistics in castor

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	43.0	101.83	100.13	87.01	87.77	100.11	72.78	95.18	146.32	109.0	150.71
II		44.14	181.09	113.33	109.03	101.39	215.40	158.72	205.22	111.87	324.37
III			73.57	148.91	108.77	77.73	162.02	65.54	106.89	188.11	146.3
IV				0.00	141.14	116.24	113.3	93.98	88.45	179.64	87.77
V					0.00	220.30	110.48	135.10	98.54	193.31	215.40
VI						0.00	110.33	112.38	180.91	76.10	294.98
VII							0.00	153.97	226.60	111.0	232.75
VIII								0.00	150.99	300.33	114.99
IX									0.00	394.39	78.8
X										0.00	417.62
XI											0.00

**TABLE: 3** Per cent Contribution of different characters to total genetic divergence

Sr. No.>`	Characters	Number of times characters ranked first	% contribution
1	Days to flowering	104	12.4
2	Days to Maturity	78	9.3
3	Plant height	80	9.6
4	Number of branches per plant	91	10.9
5	Number of capsules per plant	75	9.0
6	Total raceme length	78	9.3
7	Effective raceme length	80	9.6
8	Oil %	82	9.8
9	Number of nodes per plant	81	9.7
10	Seed yield per plant	87	10.4
Total		836	100.0

The average intra and inter cluster distance (Table 2) revealed that the genetic diversity among the genotypes in intra-cluster distance was found to be the maximum for cluster I (43.00), followed by cluster II (44.14) and cluster III (73.57). The minimum intra-cluster distance was, however, depicted by clusters IV, V, VI, VII, VIII, IX, X, and XI all cluster had 0.0 values. Cluster I in which 41 genotypes are included having considerable intracluster

distance can be hybridized for obtaining superior inbreds over existing populations through recombination breeding. The maximum inter cluster distance was observed between, cluster X and cluster XI (417.62), followed by cluster IX and cluster X (394.39), cluster VIII and cluster X (300.33) and cluster VI and cluster XI (294.98). The lowest inter cluster distance was found between cluster VI and cluster X (76.10). The results revealed that the

genotypes included in clusters X, XI, IX, VIII and VI showed the great deal of genetic diversity and the hybridization between the genotypes from between cluster X and cluster XI followed by cluster IX and cluster X, cluster VIII and cluster X and cluster VI and cluster XI, can provide potential genotypes in the subsequent generations after hybridization. The genotypes from different clusters can also be utilized for development of hybrids, which can give higher yield under diversified agro-climatic conditions. The contribution of individual characters towards the divergence (Table 3) indicated that

days to flowering (12.4 %) was main contributors to the total divergence, which was followed by number of branches per plant (10.90 %) and seed yield per plant (10.40 %). Other characters like days to oil % (9.80 %), number of nodes per plant (9.70 %), effective raceme length (9.60 %), plant height (9.60 %), total raceme length (9.30 %), days to maturity (9.30 %) and number of capsules per plant (9.00 %) had moderate contribution towards total divergence. The results were akin to the reports of Sevugaperumal *et al.* (2001) and Jaimini (2002).

**TABLE 4:** Cluster mean for different character in castor

Cluster	Days to flowerin g	Days to maturity	Plant height	Number of branches per plant	Number of capsules per plant	Total raceme length	Effective raceme length	Oil %	Number of nodes per plant	Seed yield per plant
I	70.3	150.4	65.0	9.3	54.3	43.4	35.8	41.3	16.0	198.6
II	69.3	145.9	73.7	10.8	111.1	58.7	56.3	40.5	17.2	277.3
III	86.3	169.3	84.2	10.6	54.8	54.4	42.8	41.8	17.4	281.6
IV	78.3	153.7	38.8	6.0	53.9	29.5	21.7	39.2	17.9	61.59
V	83.0	150.0	114.7	5.4	110.2	68.9	51.5	43.5	19.8	311.4
VI	62.7	139.0	55.9	16.2	51.6	41.3	38.1	40.7	14.4	73.19
VII	62.0	133.7	102.5	6.8	59.8	40.7	28.2	44.8	16.3	275.1
VIII	70.3	173.3	78.5	6.3	64.8	53.1	37.5	30.3	17.6	130.2
IX	95.0	170.3	75.8	6.7	72.7	33.2	29.4	42.9	19.6	206.5
X	65.0	138.3	70.4	14.9	76.6	58.9	53.2	50.4	17.2	344.6
XI	86.7	171.3	55.9	4.7	12.2	18.5	12.1	37.1	16.2	107.5

There was a wide range of variation in the cluster mean values for most of the characters under study (Table 4). Cluster mean showed that the cluster X had genotype with the maximum values for the earliness, oil per cent and seed yield per plant. Cluster VII had genotypes with the maximum values for earliness. Cluster VI had superior genotype for number of effective branches per plant. Genotypes in cluster II had highest total and effective raceme length and number of capsules. Crosses among the diverse parents are likely to yield desirable combinations. Therefore, a crossing programme should be initiated between the genotypes belonging to different clusters. The greater the distance between two clusters, the wider the genetic diversity among the parents to be included in hybridization programme. Parents combining high yield potential with wide genetic diversity are likely to yield superior segregants with in short period. The genotypes with high mean values from any cluster can either straight away be used for adoption or can be used in hybridization for yield improvement.

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