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Pattern of Genotypic Diversity in Indigenous Castor (*Ricinus communis* L.) Genotypes

J. Jawahar Lal* and C. Lavanya

ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad-30, India

**Corresponding author*

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A B S T R A C T

Castor genotypes (30) were evaluated for ten yield and yield attributing characters to study the genetic diversity existing among them by using Mahalanobis D^2 statistics. Analysis of variance revealed significant difference among genotypes for all the ten character studied. Based on the D^2 values the genotypes were grouped into six different clusters. Maximum inter cluster distance was observed between III and VI (6170.49) while, lowest divergence was noticed between clusters I and II (742.33) indicating close relationship and similarity for most of the traits of the genotypes in this cluster. Among the nine clusters studied, yield at 180 days contributed highest towards genetic divergence (48.74%). Principal component (PC) analysis revealed that first three PC axes explained 72.48% of the total multivariate variation while the first five PC axes explaining 88.94%. These results have an important implication for castor germplasm characterization, improvement, agro morphological evaluation and conservation.

Introduction

Castor is a member of the Euphorbiaceae family that is found across all the tropical and semi-tropical regions of the world (Weiss, 2000). Castor is one of the ancient and important non-edible oilseeds that has immense industrial and medicinal value. Castor is an ideal candidate for production of high value, industrial and oil feed-stocks because of the very high oil content (48-56%) of the seed. Castor oil is used in more than 700 industrial products and its demand is increasing by 3-5 percent per annum (Anjani 2012). India is the largest exporter of castor oil in the world market. Castor plant has unique ability to produce oils with extremely high levels of ricinolic acid (80-90%) (Brigham, 1993; Hegde and SudhakaraBabu, 2002). Historically, commercial production of castor has been limited by concerns about the toxins found in castor seed, unstable global market for the oil and lack of efficient technologies to produce and process the crop (Brigham, 1993). The ultimate goal of any plant breeding programme is to improve plant traits for agronomic and economic superiority. Genetic improvement of castor has the potential to overcome many production constraints. Genetic diversity in crop plants is essential to sustain level of high productivity (Rabbani *et al*., 2010). It is an

established fact that, genetically diverse parents result in desirable gene combinations and produce high heterosis. Earlier, geographical diversity has been considered as a remarkable index of genetic diversity (Joshi and Dhawan, 1966). The choice of suitable parents is of paramount importance for a planned and successful hybridization programme. Hence, efforts have to be made to identify the best parents with wide genetic divergence from germplasm pool for the characters of economic importance, so as to utilize them in hybridization programme.

Materials and Methods

The present study was conducted at the research field of Indian Institute of Oilseeds Research, Narkhoda farm, Hyderabad. The experimental material for the present study, comprised of thirty genotypes of castor procured from castor AICRP centre, Junagadh Agricultural University, Junagadh and S.D. Agricultural university, S.K.Nagar. The experiment was laid out in a randomized complete block design replicated thrice. Each genotype in each replication was sown by dibbling the seeds in two rows of plot 6 m length, with a spacing of 90 cm between the rows and 60 cm between the plants. The recommended packages of practices were adopted to raise a healthy crop. Ten randomly selected plants from each plot per replication were scored for recording observations on 10 metric traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of nodes to primary spike, total length of primary spike, effective length of primary spike, total spikes per plant, 100 seed weight, oil content and seed yield at 120, 150 and 180 days. The mean of ten plants for all the characters, except days to 50% flowering and days to maturity was utilized for carrying out statistical analysis. For days to 50% flowering and days to maturity was recorded on plot basis. Multivariate analysis was done as per Mahalanobis D^2 statistics described by Rao (1952) and the grouping of genotypes into different clusters was done according to Tochers method. The data were subjected to principal component analysis (PCA). PCs with Eigen values >0.5 were selected, as proposed by Jeffers (1967).

Results and Discussion

The analysis of variance revealed highly significant differences among the 30 genotypes for all the characters indicating considerable genetic variation in the material studied (Table 1). A wide range of variation for agronomic parameters in castor was reported by Anjani (2000) and Anjani (2012). It was possible to group the examined castor genotypes into six different clusters (Table 2). Cluster I with seven accessions, Cluster II and VI each with four accessions respectively. Cluster IV was constituted by twelve accessions. Cluster V contains two genotypes. The pattern of group constellations proved that significant amount of variability existed. This is an indication for the absence of relationship between genetic diversity and geographic diversity. Similar results have been reported by Bhatt and Reddy (1987), Ramesh *et al.*, (2012) and Chavan *et al.*, (2012).

Based on values of inter cluster distance (Table 3), it was found that the highest divergence occurred between cluster III and VI (6170.49) followed by cluster I and VI (4602.67), indicating the wider genetic diversity between genotypes of these groups. The cluster III involved accession of DCS-107 variety which high yielding, cluster II involves accessions of pistilate lines M-574, DPC-9 which are cross derivatives of other geographically diverse accessions as per the catalogue of castor germplasm indicating genetic diversity being contributed by geographical diversity or cross combinations

involving geographically diverse genotypes. This was in contradiction to studies like Chakrabarty and Banu (1999), and Singh and Srivastava (1978) in castor. Hence, selection of parents from these clusters for hybridization programme would help in achieving novel recombinants. On the other hand, the lowest divergence was noticed between clusters I and II (742.33) indicating close relationship and similarity for most of the traits of the genotypes in this cluster. The inter cluster distance was higher than the intra cluster distance Ramesh *et al.,* (2012) which indicates the existence of substantial diversity among the genotypes.

The characters contributing maximum to the divergence need greater emphasis for deciding on the clusters for purpose of further selection and choice of the parents for hybridization. The highest contribution (Fig. 1) in this regard was made by seed yield at 180 days (49%) by ranking 212 times first ranking followed by seed yield at 120days (20%). These results are in conformity with the findings of Sudhakar *et al.,* (2006) and *Ramesh et al.,* (2012). Based on the inter cluster distances, the genotypes JI-226, JI-227, JI-244 and SKI-301from cluster I, M-574 and DPC-9 from cluster II, M-571, VP-1 and JI-340 from cluster IV, Geetha and JI-322 from cluster V were selected for hybridization programme as they are expected to produce high heterotic crosses.

Multivariate analysis of the accessions revealed that the first five PCs (PC1 to PC5) gave Eigen-values > 0.5 and cumulatively accounted for 88.94% of the total variation (Table4). The cumulative proportion of the variation reached 72.48% in the first three PC axes, and 88.944% in the first five axes. The high degree of variation in the first five PC axes indicates a high degree of variation for these characters.

There are no guidelines to determine the significance or importance of a coefficient, that is, Eigen-vector. However higher coefficients for a certain trait indicate the relatedness of that trait to respective PC axes (Seymus Furat and Bulent Uzun, 2010). Characters with high coefficients in the PC1 to PC4 should be considered as more important since these axes explain more than half of the total variation (Fig. 2).

Table.1 Analysis of variance for eleven characters in 30 genotypes of castor

S. No.	Character	Mean sum of squares		
		Replications (df = 2)	Treatments (df = 29)	Error (df=58)
1.	Days to 50% flowering	0.02	27.13**	**0.36**
2.	Days to maturity	0.02	105.33**	**0.53**
3.	Plant height (cm)	1.19	600.95**	**25.29**
4.	Number of nodes to primary Spike	1.93	15.37**	**0.54**
5.	Total primary spike length	2.69	100.42**	**21.27**
6.	Effective primary spike length	25.22	132.53**	**23.16**
7.	Total spikes/ plant	6.80	19.44**	**5.43**
8.	100 seed weight	1.7923	43.76**	**1.22**
9.	Yield 120 DAS	21.84	2203.08**	**15.31**
10.	Yield 150 DAS	26.21	1562.69**	**17.45**
11.	Yield 180 DAS	1.90	3707.05**	**17.09**
12.	**Oil content %**	**0.02**	**16.80****	**0.76**

* Significant at P = 0.05 level
** Significant at P = 0.01 level

Table.2 Distribution of thirty genotypes of castor into different clusters

Cluster number	Number of genotypes	Genotypes
I	7	JI-244, DCS-94, JI-226, JI-227, 48-1, JI-338, SKI-301
II	4	SKI-215, M-574, DPC-9, Haritha
III	1	DCS-107
IV	12	SKI-291, DCS-84, Kranthi, DCS-9, M-571, DCS-81, JI-340, JI-319, SKI-294, JI-315, DCS-89, VP-1
V	2	SKI-232, SKI-283
VI	4	Geetha, SKI-304, DCS-86, JI-322

Table.3 Intra (diagonal) and intercluster average of D^2 and D values of thirty genotypes of castor

Cluster Number	I	II	III	IV	V	VI
I	263.14	742.33	4073.00	1109.33	2963.40	**4602.67**
II		336.95	2367.92	1174.36	1632.34	**4413.12**
III			0	4595.83	3451.37	**6170.49**
IV				690.52	1683.64	**2595.09**
V					682.22	**3274.53**
VI						**1078.52**

Table.4 Percentage and cumulative variances and Eigen-vectors on the first five principal components for each character in 30 castor accessions

Parameters	PC1	PC2	PC3	PC4	PC5
Eigene values (root)	5.31	1.88	1.51	1.25	0.73
% Var. Exp.	44.23	15.64	12.61	10.38	6.09
Cum. Var. Exp.	44.23	59.87	72.48	82.86	88.94
Variables	Eigen vectors				
Days to 50% Flowering	0.37	0.18	0.04	0.06	0.41
Days to Maturity	0.40	0.20	0.03	0.07	-0.06
Plant Height	0.27	-0.09	-0.45	-0.18	-0.45
No.of Nodes to Primary Spike	0.21	-0.17	-0.17	-0.64	0.11
Total Length Primary Spike	0.17	-0.06	0.35	-0.64	0.11
Effective Length Primary Spike	-0.37	-0.17	-0.21	-0.20	-0.18
Total Spikes/ Plant	0.41	0.12	0.03	0.11	0.17
100 Seed Weight	0.32	0.16	-0.25	0.09	-0.46
Yield 120 Days	0.24	-0.25	-0.43	0.15	0.32
Yield 150 Days	-0.20	0.58	-0.16	-0.17	0.15
Yield 180 Days	-0.12	0.65	-0.16	-0.19	-0.06
Oil Content %	-0.21	-0.05	-0.55	-0.03	0.45

Fig.1 Relative contribution of characters to genetic diversity in castor

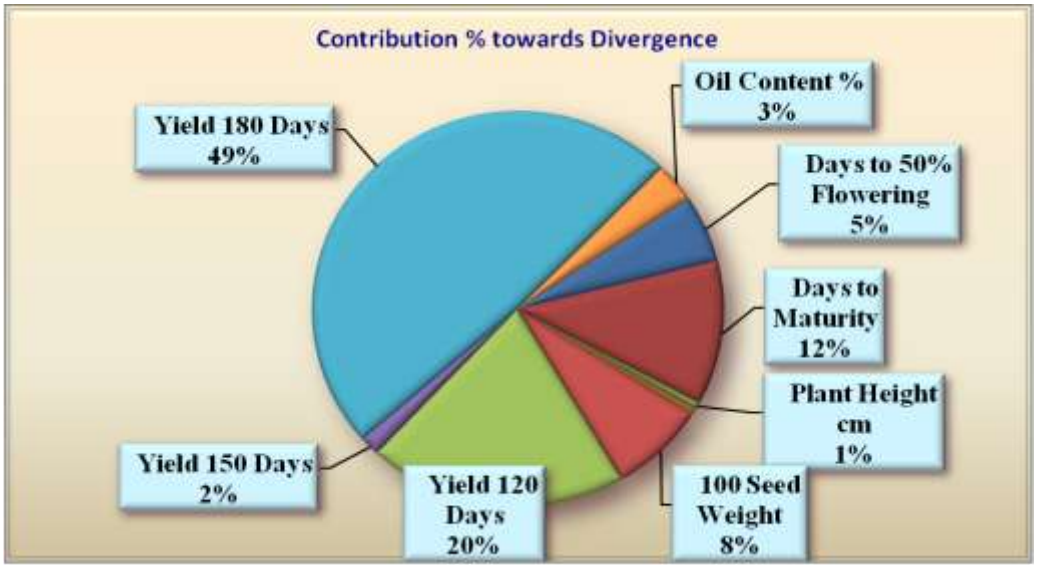
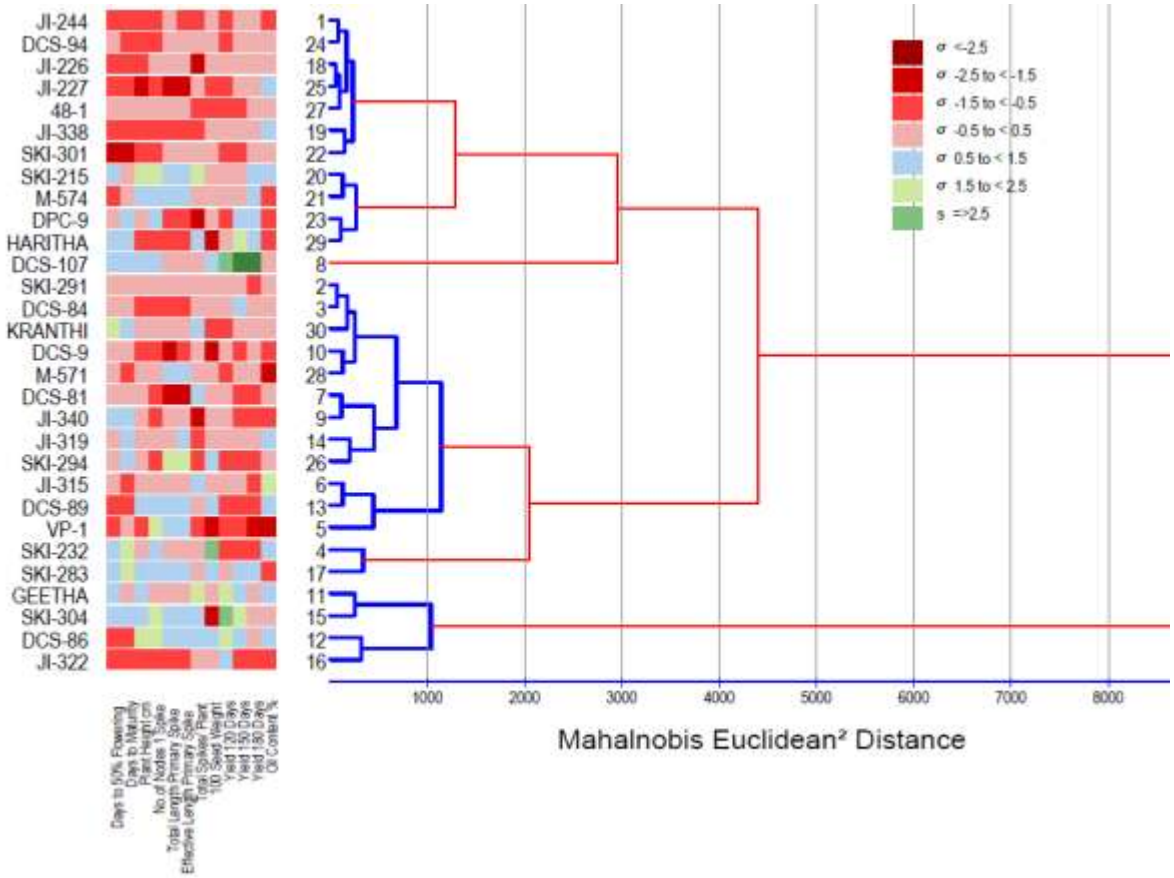


Fig.2 Mahalanobis Euclidean Distance



Principal component analysis was done using 10traits which contributed high level of variability to total variation. The Eigen values of 10 principal components and principal component matrix of three principal components has been shown in Table 4. The contribution of first three principal components was 72.48 per cent as compared to PCs of total genotypes. It was found that principal component 1 (PC1) contributed 44.23 per cent, PC2 15.64 and PC3 12.61per cent of total variation. The traits having was positive contributed to PC1, were total spikes/plant (0.41), days to maturity (0.40), days to 50% flowering (0.37), 100 seedweight (0.32), plant height (0.27), yield at 120 days (0.24), no. of nodes to primary spike (0.21), total length of primary spike (0.17), whereas effective length of primary spike, yield at 150, 180 days and oil content had negative contribution to PC1. The results revealed that the genotypes with high PC1 values were high yielding along with early time of flowering and maturity. Maximum genetic variance to PC2 was contributed by yield at 180 days (0.65), yield at 150 days (0.58), days to maturity (0.20), days to 50% flowering (0.18), 100 seed weight (0.16), total spikes/plant (0.12), whereas plant height, no. of nodes to primary spike, total length of primary spike, effective length of primary spike and oil content traits were negative to PC2. In case of PC3, only four characters namely, total length of primary spike (0.35), days to 50% flowering(0.04), total spikes/plant (0.03) and days to maturity (0.03) had significantly contributed to variation, while the remaining traits had negative contribution to PC3. It is evident from the result that days to50% flowering, days to maturity, total length of primary spike, 100 seed weight contributed maximum to total genetic variability in 30 castor genotypes. Similar results were reported by Bhand and Patel (1999), Shaheen (2002), Sunil *et al.*, (2005) and Amar *et al.*, (2010).

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