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## Genetic diversity assessment among advanced breeding lines of castor (*Ricinus communis* L.)

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### Abstract

Castor (*Ricinus communis* L.) a non edible oilseed crop belongs to the family *Euphorbiaceae*. Castor is cultivated mainly for industrial trade as non edible oil, since it has no food value. Based on the  $D^2$  statistic 51 castor genotypes were grouped into three clusters. Cluster I was the largest with maximum number of genotypes (49). Cluster II and cluster III were solitary cluster with single genotype. Plant height up to primary spike ranked first for 340 times with a maximum contribution of 26.67% to the total divergence followed by number of capsules on primary spike. The inter-cluster distances varied from 31.64 (between clusters I and II) to 40.31 (between clusters I and III). All the other inter-cluster  $D^2$  values were lying between these values. These values suggest that the genotypes from distant clusters exhibit wide diversity. Hence genotypes from divergent clusters should be selected for breeding programme for generating wide spectrum of variability and for selecting superior lines. Cluster I had maximum intracluster distance followed by cluster II. Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses. The intracluster  $D^2$  values of any cluster were less than the intercluster  $D^2$  values of any two closely related clusters. Genotypes grouped into the same cluster presumably diverge little from one another. Theoretically, crossing of genotypes belonging to the same cluster is not expected to yield superior hybrids or segregants.

**Keywords:**  $D^2$  statistics, Castor, genetic divergence

### Introduction

Castor (*Ricinus communis* L.) a non edible oilseed crop belongs to the family *Euphorbiaceae* is one of the ancient oilseed crops of the world. Castor is a cross pollinated diploid species with chromosome number  $2n = 20$ . Castor is cultivated mainly for industrial trade as non edible oil, since it has no food value. The seed oil is unique in terms of its dominance of a single fatty acid- ricinoelic acid (Maiti *et al.*, 1988)<sup>[4]</sup>. The oil is used as a high quality lubricant because of its property to remain liquid at low temperatures ( $-32^{\circ}\text{C}$ ), and viscous at high temperatures. Castor oil and its derivatives are being used in textiles, soaps, cosmetics, nylon fibers, bullet-proof glass and bone prostheses and as antifreeze for fuels and lubricants utilized in aircrafts and space rockets (Ogunniyi, 2006)<sup>[5]</sup>.

A broad spectrum of variability in segregating generations can be generated by crossing genetically diverse parents. For this, precise information about the extent of parental genetic divergence is crucial. Genetic diversity between populations or genotypes indicates the difference in gene frequencies and any measure of genetic divergence must reflect these differences. Phenotypic diversity is usually considered as an indication of underlying genetic differences. Genetically diverse parents giving more productive hybrids than those which are more closely related is a proven fact. The maximum contribution to total divergence is an important consideration for the purpose of further selection and choice of parents for hybridization. For quantifying the diversity in 51 advanced breeding lines were evaluated for twelve quantitative characters and their fitness was assessed using the concept of Mahalanobis generalized distance ( $D^2$ ).

### Materials and methods

The material for diversity study comprised of 51 genotypes procured from Directorate of Oilseeds Research, Hyderabad. The genotypes used are pre breeding lines developed at Directorate of Oilseeds Research, Hyderabad. The list of material is given in Table 1. The experiment was laid out under rainfed condition at Main Agricultural Research Station, Raichur during *kharif* 2012. The randomized block design was followed with two replications and each treatment was in two rows of 7.2 m length with inter row spacing of 90 cm and intra row spacing of 60 cm. All the recommended practices were followed to raise good crop. From each entry in each replication, five randomly selected plants were tagged for recording observations on all the quantitative characters except days to 50 per cent flowering and days to maturity.

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Mean of five plants for each entry for each character was calculated and used for statistical analysis. The analysis of variance for each character was carried out as per the method suggested by Panes and Sukhatme (1967) [6]. Mahalanobis (1936) [3]  $D^2$  statistic was used for assessing the genetic divergence among genotypes.

### Results and discussion

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the prevalence of substantial variability and the appropriateness of choice of material (Table 2). Based on the  $D^2$  statistic 51 castor genotypes were grouped into three clusters. Cluster I was the largest with maximum number of genotypes (49). Cluster II and cluster III were solitary cluster with single genotype. (Table 3 and Fig. 1).

The knowledge on the characters that contribute most towards influencing divergence is an important aspect for a breeder while selecting genotypes for hybridization. Character wise rank totals (Table 4) have shown that any single character had not had greater contribution to total divergence. Nevertheless, relatively maximum contribution was by Plant height up to primary spike ranked first with contribution of 26.67% to the total divergence followed by number of capsules on primary spike (20.24%), hundred seed weight (15.65%), effective spike length (14.43%), effective number of spikes per plant (9.41%), oil content (4.63%), primary spike length (3.53%) days to 50% flowering (2.67%), yield per plant (2.12), Node number up to primary spike (0.31%), secondary spike length (0.24%) and Days to maturity (0.08%).

The inter-cluster distances varied from 31.64 (between clusters I and II) to 40.31 (between clusters I and III). All the other inter-cluster  $D^2$  values were lying between these values (Table 5). For days to 50% flowering, cluster means ranged between 47 and 75 days. Genotypes of cluster-I showed characteristic of early flowering habit with mean number of days to flowering being 47 days while genotypes of cluster III

had late flowering habit with 75 days. For days to maturity, cluster mean ranged between 107 and 137 days. Genotype under cluster-I was of early maturity type with number of days to mature being 107 days (Table 6). While that under cluster-III were of late maturity type (137 days). Cluster mean for plant height up to primary spike ranged from 81.58 cm (Cluster I) to 253 cm (Cluster II), for primary spike length genotype of cluster mean ranged from 27.60 cm (cluster III) to 52.50 cm (cluster II).

For effective spike length cluster mean ranged from 24.50 cm to 46.40 cm. Genotype of cluster III was having shortest effective spike length (24.50cm), while cluster II with longest effective spike length (46.40 cm). Cluster mean for secondary spike length ranged from 19.70 cm (cluster III) to 29.65 (cluster I). Cluster mean for node number up to primary spike length ranged from 13.75 (cluster I) to 28.8 (cluster II). Cluster mean for number of capsules on primary spikes ranged from 34.80 (cluster II and cluster III) to 65.88 (cluster I). For effective spikes per plant cluster mean ranges from 4.30 (cluster III) to 7.68 (cluster I). Cluster mean for yield per plant ranged from 78.83 gm (cluster II) to 141.49 gm (cluster III). For hundred seed weight cluster mean ranges from 29.06 gm (cluster I) to 82.61 gm (cluster III). Cluster mean for oil content ranged from 45.05% (cluster II) to 46.80% (cluster III). Similar results were reported by Costa and Pereira (2006) [2], Patel *et al.* (2010) [7] and Chavan *et al.* (2010) [1].

The intracluster  $D^2$  values of any cluster were less than the intercluster  $D^2$  values of any two closely related clusters. Genotypes grouped into the same cluster presumably diverge little from one another. Theoretically, crossing of genotypes belonging to the same cluster is not expected to yield superior hybrids or segregants. Several empirical studies in many crop plants support this theoretical expectation. However, in the present study only three clusters were formed and two out of three were solitary clusters this may be due the highly divergence of two genotypes from rest of the genotypes.

**Table 1:** Salient features of 51 advanced inbred lines in castor

SL. No	Genotype	Stem colour	Bloom	Plant type	leaf shape	Branching	Capsule type	Sex	others
1	K11-1039-1	red	triple	medium tall	flat leaf	divergent	non spiny	monoecious	
2	K11-1181-1	red	double	medium tall	flat leaf	divergent	spiny	monoecious	
3	J1-384	red	double	medium tall	flat leaf	divergent	spiny	monoecious	
4	ANDe1-8	mahogany	single	medium tall	flat leaf	divergent	spiny	monoecious	
5	JC-4	red	single	tall	flat leaf	divergent	spiny	monoecious	
6	JC-22	red	single	tall	flat leaf	divergent	spiny	monoecious	early flowering
7	JC-24	red	double	tall	flat leaf	divergent	spiny	monoecious	
8	JC-26	red	single	medium tall	flat leaf	divergent	semi spiny	monoecious	
9	MCI-12	red	double	medium tall	flat leaf	divergent	spiny	monoecious	
10	MCI-13	green	double	medium tall	flat leaf	divergent	spiny	monoecious	
11	SKI-337	red	triple	medium tall	flat leaf	divergent	spiny	monoecious	
12	SKI-343	green	triple	medium tall	flat leaf	divergent	spiny	monoecious	early flowering
13	SKI-346	mahogany	double	medium tall	flat leaf	divergent	non spiny	monoecious	
14	J1-96	red	triple	medium tall	flat leaf	divergent	spiny	monoecious	
15	DCS-59	green	double	tall	flat leaf	divergent	semi spiny	monoecious	
16	DCS-103	red	double	medium tall	flat leaf	divergent	spiny	monoecious	early flowering
17	RG-1155	green	double	tall	flat leaf	divergent	spiny	monoecious	
18	RG-2114	red	triple	tall	flat leaf	divergent	spiny	monoecious	
19	PVT-06-17	red	double	medium tall	flat leaf	divergent	spiny	monoecious	
20	PCS-43	green	double	medium tall	flat leaf	divergent	spiny	monoecious	
21	DCS-107	green	double	medium tall	flat leaf	divergent	spiny	monoecious	
22	RG-1582-1	red	double	medium tall	flat leaf	divergent	nonspiny	monoecious	
23	MCI-16	red	triple	dwarf	flat leaf	divergent	nonspiny	monoecious	
24	RG-964	green	double	medium tall	flat leaf	divergent	spiny	monoecious	
25	JC-3	red	double	medium tall	flat leaf	divergent	spiny	monoecious	
26	RG-1608	mahogany	triple	medium tall	flat leaf	divergent	spiny	monoecious	

27	KIRAN	red	double	dwarf	flat leaf	divergent	nonspiny	monoecious	early flowering
28	RG-2797	red	zero	tall	flat leaf	divergent	spiny	monoecious	
29	RG-3352	red	triple	medium tall	flat leaf	divergent	nonspiny	monoecious	
30	RG-2661	green	triple	tall	flat leaf	divergent	spiny	monoecious	late flowering
31	CO-1	green	zero	tall	flat leaf	divergent	spiny	monoecious	late flowering
32	NIES-6	red	double	dwarf	flat leaf	divergent	nonspiny	pistillate	very early flowering
33	DPC-9	green	single	medium tall	flat leaf	divergent	spiny	pistillate	early flowering
34	M-619	green	triple	dwarf	cup leaf	convergent	spiny	pistillate	
35	M-574	green	triple	dwarf	cup leaf	convergent	spiny	pistillate	
36	SKP-84	red	triple	dwarf	cup leaf	convergent	spiny	pistillate	
37	DCS-78	green	double	medium tall	flat leaf	divergent	spiny	monoecious	
38	DCS-94	green	triple	medium tall	flat leaf	divergent	spiny	monoecious	
39	DCS-5	red	double	medium tall	flat leaf	divergent	spiny	monoecious	
40	DCS-106	green	triple	medium tall	flat leaf	divergent	nonspiny	monoecious	
41	DCS-17	green	triple	medium tall	flat leaf	divergent	nonspiny	monoecious	
42	K11-1135-1	red	double	medium tall	flat leaf	divergent	spiny	monoecious	
43	K11-1166-1	green	triple	medium tall	flat leaf	divergent	nonspiny	monoecious	
44	K11-1174-1	green	triple	medium tall	flat leaf	divergent	nonspiny	monoecious	
45	K11-1009-1	green	double	medium tall	flat leaf	divergent	spiny	monoecious	
46	K11-1063-1	red	triple	medium tall	flat leaf	divergent	spiny	monoecious	
47	DCS-9	red	double	medium tall	flat leaf	divergent	spiny	monoecious	
48	48-1	red	double	medium tall	flat leaf	divergent	nonspiny	monoecious	
49	TMV-5	red	triple	medium tall	flat leaf	divergent	spiny	monoecious	
50	DCS-96	red	triple	medium tall	flat leaf	divergent	spiny	monoecious	
51	DCS-97	red	double	medium tall	flat leaf	divergent	spiny	monoecious	

**Table 2:** Analysis of variance for twelve different quantitative traits in castor

Source of Variations	Mean sum of squares												
	DF	DF	DM	NN	PH	PSL	ESL	SSL	NCPS	ESPP	YPP	HSW	OC
Replication	1	0.01	41.18	1.51	27.95	37.20	35.41	5.27	40.56	0.71	378.36	3.57	0.04
Genotypes	50	259.50**	268.90**	31.28**	4962.20**	261.36**	253.67**	80.49**	1076.62**	4.81**	1234.29**	178.59**	4.94**
Error	50	5.28	11.30	0.80	40.27	9.42	9.03	4.15	11.02	0.18	97.68	1.52	0.19

\* Significant at 5% probability level, \*\* Significant at 1% probability level

DF= Days to 50 per cent flowering, DM= Days to maturity, NN= Node no. up to primary spike, PH= plant height up to primary spike (cm), PSL= Primary spike length (cm), ESL= Effective spike length (cm), SSL= Secondary spike length

(cm), NCPS= No. of capsules on primary spike, ESPP= Effective spikes per plant, YPP= Yield per plant (g), HSW= Hundred seed weight (g) and OC= Oil content (%).

**Table 3:** Cluster wise grouping of 51 inbred lines in castor

Cluster	No. of genotypes	Genotypes
I	49	K11-1039-1, K11-118-1, JI-384, ANDe1-8, JC-4, JC-22, JC-24, JC-26, MCI-12, MCI-13, SKI-337, SKI-343, SKI-346, JI-96, DCS-59, DCS-103, RG-1155, RG-2114, PVT-06, PCS-43, DCS-107, RG-1582, MCI-16, RG-964, JC-3, RG-1608, Kiran, RG-279, RG-3352, NES-6, DPC-9, M-619, M-574, SKP-84, DCS-78, DCS-94, DCS-5, DCS-106, DCS-17, K11-1135-1, K11-1166-1, K11-1174-1, K11-1009-1, K11-1063-1, DCS-9, 48-1, TMV-5, DCS-96 and DCS-97
II	1	RG-2661
III	1	CO-1

**Table 4:** Percentage contribution of each character towards genetic divergence in castor

Characters	No. of times Percent Ranked first	Contribution (%)
Days to 50 Per cent flowering	34	2.67
Days to Maturity	1	0.08
Number of nodes up to the primary spike	4	0.31
Plant height up to primary spike (cm)	340	26.67
Primary spike length (cm)	45	3.53
Effective spike length (cm)	184	14.43
Secondary spike length (cm)	3	0.24
Number of capsules on primary spike	258	20.24
Effective number of spikes per plant	120	9.41
Yield per plant (g)	27	2.12
100 seed weight (g)	200	15.69
Oil content (%)	59	4.63

**Table 5:** Average intra and inter cluster distances in castor inbred lines

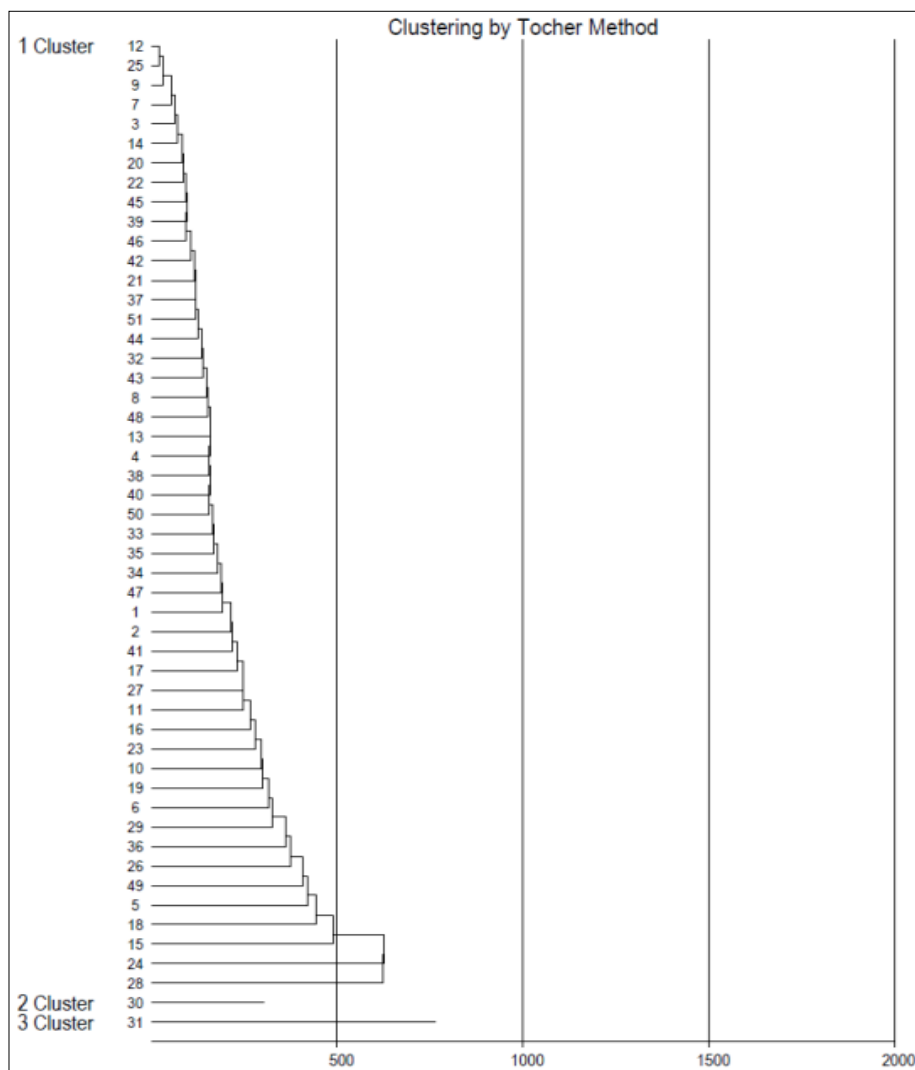
Cluster	CI	CII	CIII
CI	17.16	31.64	40.31
CII		0	35.50
CIII			0

**Table 6:** Cluster means for twelve different characters in castor inbred lines

Cluster	No. of genotypes per cluster	DFE	DM	PH	PSL	ESL	SSL	NN	NCPS	ESPP	YPP	HSW	OC
I	49	47	107	81.58	42.48	37.27	29.65	13.75	65.88	7.68	112.92	29.06	46.04
II	1	72	132	253.00	52.50	46.40	29.60	28.80	34.80	5.30	78.83	33.45	45.05
III	1	75	137	151.50	27.60	24.50	19.70	24.00	34.80	4.30	141.49	82.61	46.80

DFE= Days to 50 per cent flowering, DM= Days to maturity, NN= Node no. up to primary spike, PH= plant height up to primary spike (cm), PSL= Primary spike length (cm), ESL= Effective spike length (cm), SSL= Secondary spike length

(cm), NCPS= No. of capsules on primary spike, ESPP= Effective spikes per plant, YPP= Yield per plant (g), HSW= Hundred seed weight (g) and OC= Oil content (%).

**Fig 1:** Dendrogram showing clustering pattern of 51 inbred lines of castor

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