

Genetic Divergence Studies for Yield Components and Root Traits in Castor (*Ricinus communis* L.)

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Magnitude of genetic divergence among 27 castor accessions was studied to identify diverse parents. Genotypes were characterized for physiological, morphological and root traits in an elevated root structure. Study identified seven clusters. Cluster means for traits showed considerable differences. Highest inter-cluster distance was found between clusters I and IV. Cluster I had highest variance for eight characters. Cluster II recorded the highest intra cluster distance. Seed yield recorded maximum divergence of 31.91% while root length, total root length, diameter, laterals and weight together contributed to 8.54% and showed significant correlation. The probability of obtaining better segregants and recombinants is expected when SKI-215, PCS-106 of cluster VII and II as females and Haritha, Kranthi, Kiran of cluster I can be used as male parents. Haritha, RG 48, Kranthi and SKI 215 which showed superior root and shoot characters, can be candidates in breeding for drought tolerance.

Key Words: Castor, Carbon isotope discrimination, D² analysis, Genetic divergence, Root length

Introduction

Castor (*Ricinus communis* L.) $2n = 20$, a member of the family Euphorbiaceae is cultivated throughout the world. The productivity of crop in India in 2011-12 is 1417 kg/ha *vis-a-vis* world average of 850 kg/ha. Under rainfed conditions crop productivity is low at 400-600 kg/ha. To bring about crop improvement through breeding programmes, it is necessary to quantify the available variability for effective use in planning the crossing programme (Ramesh *et al.*, 2012). Further, selection of diverse parents for hybridization programme will be effective by the identification of characters responsible for the total genetic diversity among the populations (Singh and Chaudhary, 1977). In case of roots, spatial distribution *i.e.*, the ability of root system to take up water and not root mass per se (Draye *et al.*, 2010), distribution of ca. 1 cm root/cm³ of soil (root length density) is an ideal root system suitable for most field conditions (Tardieu *et al.*, 1992). Steeper root angles and less branching are traits associated with drought tolerance in field (Hund *et al.*, 2009). Crosses between divergent parents usually produce greater heterosis than those between closely related ones (Moll and Stuber, 1971). Improvement in yield is normally attained through exploitation of the

genetically diverse parents as divergent parents throw heterotic crosses and also more variability could be expected in the segregating generations. In this context, Mahalanobis D² statistic provides an effective tool in quantifying the degree of divergence at genetic level and it also provides quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). D² is also a valuable tool to study genetic divergence at inter-varietal and sub-species level in classifying the crop plants (Rodge *et al.*, 2003). Earlier, Bhatt and Reddy (1987), Chakrabarty and Banu (1999) and Lakshamma *et al.* (2002) studied genetic diversity in castor genotypes through Mahalanobis D² statistic and identified the parents for future heterosis breeding. The present study was therefore carried out to measure the nature and magnitude of genetic divergence among the accessions to select superior material to be used in breeding programmes.

Materials and Methods

The experimental material consisted of 27 germplasm accessions obtained from RARS, Palem, Professor Jayashankar Telangana State Agricultural University (PJTSAU), and Directorate of Oilseeds Research

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(DOR), Hyderabad. The material includes twelve elite lines, three pistillate lines, four germplasm accessions, one male line and four checks (Table 1). The genotypes were selected based on their early flowering and tolerance or resistance to Fusarium wilt, Reniform nematode and leaf hopper. The accessions were planted in a specially designed temporary root structure of 25 m length, 4 m width and 1.5 m height in randomized block design with a permanent wall separating the replications (Lakshamma et al., 2010). Crop was raised for two consecutive years with same set of 27 genotypes with two replications with spacing of 90×45 cm during late *rabi* 2012 and 2013. Observations were recorded on four plants in each replication for 15 quantitative traits. Data was recorded before dismantling of root study structure in respect of SPAD chlorophyll meter readings (SCMR), Relative Water Content (RWC), fluorescence, plant height up to primary raceme, number of nodes up to primary raceme, effective length of primary spike, hundred seed weight and seed yield (kg/ha). Carbon Isotope Discrimination (CID) were quantified (‰) in Isotope Ratio Mass Spectrophotometer (IRMS) facility in UAS, Bengaluru.

CID is a tool that helps to understand photosynthesis and its coordination with water use in ecological and physiological studies in C_3 species (Farquhar et al., 1989). Structure was dismantled at 110 DAS when root growth was maximum and data was recorded on root system architectural traits (RSA) viz., root diameter, root length, number of laterals, total root length and root dry weight. Group distance was measured on multiple characters following Mahalanobis (1928). Clustering of genotypes was done according to Tocher's method.

Results and Discussion

This study revealed significant difference among the accessions for the characters studied. Based on the relative magnitude of D^2 values, 27 genotypes were grouped into seven clusters by Tocher's method (Fig. 1). Cluster II was the largest with 16 genotypes followed by cluster III (four), cluster I (three) while clusters IV, V, VI and VII possessed one genotype each (Table 2). Inclusion of maximum genotypes in one cluster revealed that the genotypes did not have wider diversity or limited gene exchange or narrow range of selection.

Table 1. Castor genotypes used in present study with source and available information

S.No.	Genotypes	Source	Remarks
1	DPC-9	DOR, Rajendranagar	Pistillate line
2	RG-48	DOR, Rajendranagar	Elite line (germplasm accession)
3	RG-43	DOR, Rajendranagar	Early flowering, resistant to reniform nematode and leaf hopper
4	RG-1354	DOR, Rajendranagar	Fusarium wilt resistant
5	RG-47	DOR, Rajendranagar	Fusarium wilt resistant and root rot
6	RG-67	DOR, Rajendranagar	Elite line (germplasm accession)
7	RG-1686	DOR, Rajendranagar	Male line (germplasm accession)
8	DCS-78	DOR, Rajendranagar	Male line
9	RG-20	DOR, Rajendranagar	Elite line (germplasm accession)
10	PCS-293	RARS, Palem, AP	High yielding
11	PCS-312	RARS, Palem, AP	High yielding
12	PCS-106	RARS, Palem, AP	High yielding, wilt resistant
13	PCS-236	RARS, Palem, AP	High yielding, wilt resistant
14	PCS-252	RARS, Palem, AP	High yielding
15	PCS-230	RARS, Palem, AP	High yielding
16	PCS-171	RARS, Palem, AP	High yielding, condensed internodes, cup shaped leaves
17	PCS-265	RARS, Palem, AP	High yielding, wilt resistant
18	PCS-228	RARS, Palem, AP	High yielding
19	PCS-224	RARS, Palem, AP	Early flowering
20	PCS-302	RARS, Palem, AP	Divergent branching
21	JP-65	Junagadh	Pistillate line
22	SKI-215	S.K. Nagar, Gujarat	Male line
23	M-574	DOR, Rajendranagar	Pistillate line, convergent branching, semi compact spike
24	RG1(Aruna)	DOR, Rajendranagar	Check variety
25	Kiran	RARS, Palem, AP	Check variety, Red stem, double bloom, monoecious
26	Kranthi	RARS, Palem, AP	Check variety, Red stem, double bloom, monoecious, shallow cup leaf
27	Haritha	RARS, Palem, AP	Check variety, Green stem, double bloom, monoecious, shallow cup leaf

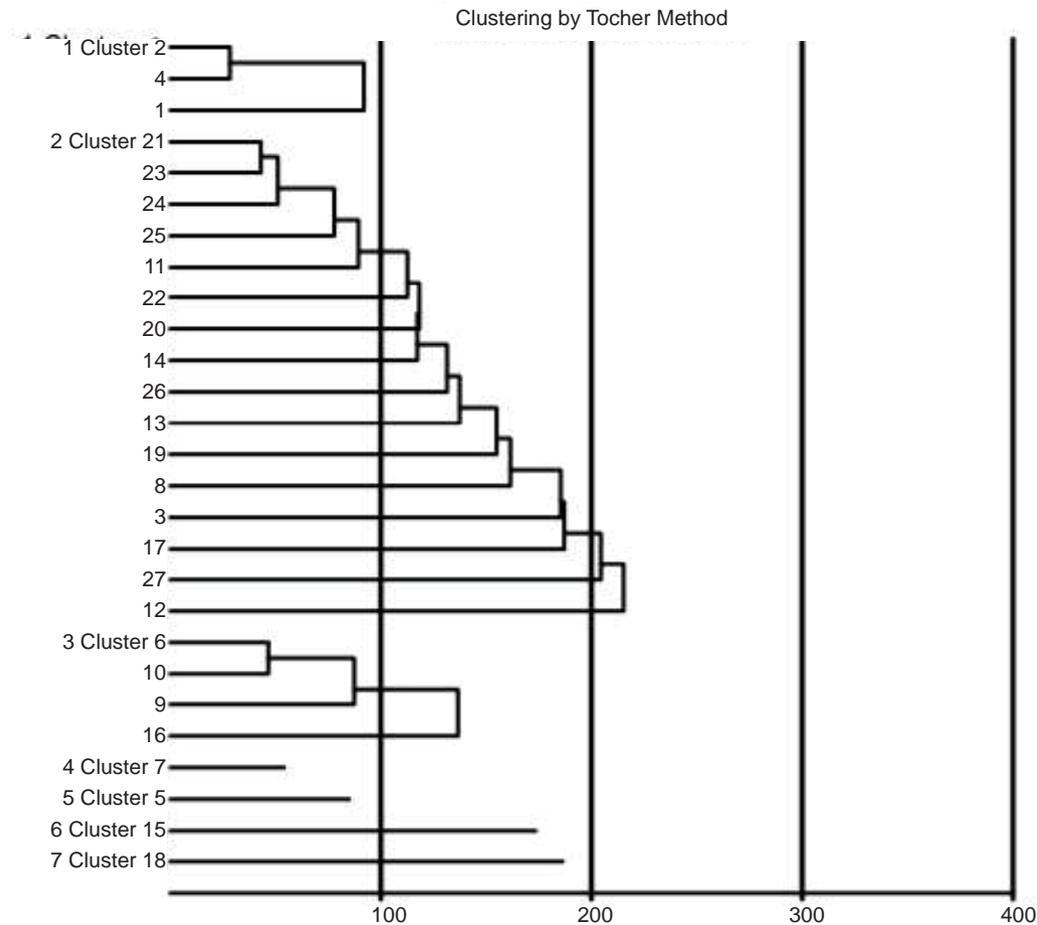


Fig. 1. Clustering pattern of 35 castor genotypes formed by Tocher's method

However, it was interesting to note that three pistillate lines *viz.*, DPC9, JP 65 and M 574 were placed in the same cluster II. Occurrence of genotypes in the same cluster indicated the same genetic background (Prasad and Kumar, 2013) or absence of geographic diversity

(Ganesh and Thangavelu, 1996). RG-43 which is early flowering, resistant to reniform nematode and leaf hopper was placed in separate cluster V. Elite lines occurred randomly in clusters. Any crossing programme taken up between genotypes of different clusters can have selective advantage when constant selection is practiced in the segregating populations (Ramesh *et al.*, 2012).

Table 2. Distribution of castor genotypes into different clusters

Cluster No.	No. of genotypes	Genotypes
I	3	Haritha, RG-48, Kranthi
II	16	DCS-78, RG-20, PCS-302, M-574, PCS-106, JP-65, PCS-265, PCS-236, RG-1686, Kiran, PCS-171, RG-47, DPC-9, PCS-230, PCS-224, RG-67
III	4	PCS-293, RG-1 (Aruna), PCS-312, RG-1686
IV	1	RG-1354
V	1	RG-43
VI	1	PCS-252
VII	1	SKI-215

The intra-cluster distance was highest in cluster II (13.27) followed by cluster III (11.94) and I (10.08) (Table 3). The cluster II was widely separated from cluster VI (34.84) which involved only one genotype PCS 252. Cluster VI recorded maximum variance for total root dry weight (39 g) and total dry matter (134 g). Crossing of genotypes of clusters II and VI can result in transgressive recombinants with superior root characters. Four clusters IV, V, VI and VII possessed one genotype each. Zero cluster distance has been attributed to the similarity in their source of cytoplasmic genetic male sterility or share the same genetic background or may belong to the same geographical area (Prasad

Table 3. Average intra and inter cluster distance (D²) values

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	10.08	38.84	27.76	47.18	42.34	18.44	19.62
Cluster II		13.27	20.39	17.07	16.24	34.84	27.15
Cluster III			11.94	25.28	22.72	19.78	21.25
Cluster IV				0	9.22	42.06	37.59
Cluster V					0	38.70	33.08
Cluster VI						0	20.46
Cluster VII							0

and Kumar, 2013) in pigeonpea. Genotypes belonging to same cluster showed smaller D² values than those belonging to different clusters (Parameshwarappa and Palakshappa, 2010).

The relative divergence of each cluster from other clusters (inter-cluster divergence) indicated high order of divergence between cluster I and IV (47.18) followed by I and V (42.34), IV and VI (42.06) and I and II (38.84). The least inter-cluster distance was found between cluster IV and V (9.22). Cluster I showed highest variance for eight characters such as root diameter (8.60 cm), RWC (83), SCMR (52), fluorescence (0.66), number of nodes (13), effective spike length (29 cm), 100 seed weight (28 g) and seed yield (1508 kg/ha). Haritha, RG 48 and Kranthi belonged to this group. These genotypes are at present used as male lines. Cluster II with 16 genotypes, recorded lower mean values for seven characters. Genotype DPC 9 of this cluster specifically showed S type pistillate nature and M-574 is presently used as a pistillate line in breeding programmes (DOR, 2013). Cluster III included four genotypes. Cluster V with only genotype RG 43 recorded resistance to reniform nematodes and leaf hoppers (DOR, 2013). Cluster VII

which consisted of only one genotype SKI 215 showed superior mean values for number of laterals (43), root length (226 cm), total root length (1342 cm), plant height (74 cm) and CID (-19.33 %) (Table 4). The superior root architectural traits of SKI-215 point towards its ability to mine water. SKI 215 at present is used as a male line in breeding programmes (DOR, 2013). In contrast, cluster IV genotype namely RG 1354 recorded low values for as many as seven characters (Table 4). RG 1354 was found to be wilt resistant (DOR, 2013). Castor being monospecific genus, diversity is based on geographical, genetic and morphological characters (Mallesha, 2007). The genotypes belonging to these clusters separated by high statistical distance have been attributed with greater genetic divergence. The genotypes of cluster I were highly divergent to those of cluster VII indicating the scope of generating heterotic hybrids in a crossing programme. SKI 215 of cluster VII, PCS 106 of cluster II as female lines and Haritha, Kranthi as male lines of cluster I can be utilized in line × tester or diallel analysis. All the elite lines which occurred randomly in clusters can be considered as potential divergent lines for future breeding programme.

Table 4. Cluster means for evaluated traits of 27 castor accessions

	Root diameter (cm)	No. of laterals	Root length (cm)	Total root length (cm)	Root dry weight (g)	Total dry matter (g)	RWC (%)	SCMR	Fluorescence	Plant height (cm)	No. of nodes	Effective spike length (cm)	100-seed weight (g)	Yield (kg/ha)	CID (kg/ha %)
Cluster I	8.60	21	164	1138	32	127	83	52	0.66	55	13	29	28.00	1508	-18.73
Cluster II	5.86	18	115	778	10	57	74	50	0.58	48	10	19	22.31	704	-18.66
Cluster III	7.50	28	132	1011	24	98	78	49	0.61	48	10	19	19.63	645	-18.57
Cluster IV	4.50	24	89	909	3	14	79	47	0.59	36	10	13	19.00	595	-17.80
Cluster V	7.70	21	142	1292	8	19	81	49	0.66	52	10	12	25.50	858	-17.56
Cluster VI	8.35	40	158	1025	39	134	77	48	0.63	56	10	13	19.50	876	-17.57
Cluster VII	8.30	43	226	1342	29	89	76	51	0.63	74	11	27	26.50	1288	-19.33
Range	3.68 - 8.75	16.3- 74.8	74.5 - 226	503 - 1341	1.8 - 38.9	26.8 - 138	67.3 - 83.3	45.9 - 51.8	0.52 - 0.68	33.5- 85.5	9-14	12-30.3	17.5- 28.6	517- 1622	-17.6- 19.3
Mean	6.58	35.5	128	906	15	71.7	76.2	49.7	0.6	49.6	10	19.7	22.5	814	-18.6

CID: carbon isotope discrimination; RWC: relative water content; SCMR: SPAD chlorophyll meter reading

The contribution of individual character towards the divergence was maximum for seed yield (31.19%) followed by total dry matter (23.36 %), fluorescence (13.96 %), 100-seed weight (13.96%) and root dry weight (5.70 %). Root traits together contributed to 8.54%. Four root characters showed significant correlation with seed yield and included root diameter (0.5838), root length (0.5626), total root length (0.5393) and root dry weight (0.5785). In other studies, oil content, seed yield and 100 seed weight recorded higher contribution (Ramesh, 2008). Least contributors for divergence included, root diameter, number of laterals and plant height (Table 5). Genetic drift and selection in different environments have been reported to cause greater diversity than geographic distance (Murty and Arunachalam, 1966). In the present study, crossing between genotypes of cluster I with cluster II and VII could be better for obtaining high heterosis.

The new information generated through this research for identification of the genetically divergent material as per the need of breeder, which was hitherto lacking, has significant bearing on the development of new heterotic hybrids aimed towards the improvement of yield traits in castor. Haritha, RG 48, Kranthi and SKI 215 showed superior root and shoot characters which make them likely candidates in breeding for drought tolerance.

Table 5. Contribution of characters towards genetic divergence

Character	Time ranked first	Contribution (%)
Root diameter (cm)	0	0.00
No. of laterals	0	0.00
Root length (cm)	7	1.99
Total root length (cm)	3	0.85
Root dry weight (g)	20	5.70
Total dry weight (g)	82	23.36
Relative water content (%)	10	2.85
SPAD chlorophyll meter reading (SCMR)	1	0.28
Fluorescence	49	13.96
Plant height (cm)	0	0.00
No. of nodes	1	0.28
Effective spike length (cm)	8	2.28
100-Seed weight (g)	49	13.96
Yield (Kg/ha)	112	31.19

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