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Genetic variability and diversity analysis in castor (*Ricinus communis* L.)

CM Godhani, RS Bhakta and HR Patel

Abstract
The experiment was carried out using 32 genotypes for various variability parameters, correlation analysis, path analysis for ten quantitative characters in castor. The high heritability along with high genetic advance was found for yield per plot, branches per plant, capsules per primary spike, primary spike length, plant height, 100 seed weight and nodes per plant. Yield per plot was found highly significant and positively correlated with days to 50% flowering, primary spike length, capsules per primary spike and 100 seed weight. Path analysis revealed the highest positive direct effect of capsules per primary spike on yield per plot, followed by oil content, 100 seed weight, plant height and days to maturity. The maximum intra cluster distance observed in cluster II (D = 8.99) followed by cluster I (D = 8.24), suggesting that crosses should be attempted between the genotypes belonging to clusters separated by large inter cluster distance.

Keywords: Variability, heritability, correlation, path analysis, diversity, castor

Introduction
Castor (*Ricinus communis* L.) (2n = 2x = 20) is an industrially important non-edible oilseeds crop widely cultivated in the arid and semi-arid regions of the world (Govaerts *et al*., 2000) [10]. Cross pollination in castor is due to its monoecious nature which favours up to 50 percent out crossing. It is essentially a semi-tropical, intermediate perennial plant, but it has naturalized as seasonal crop or annual plant throughout the world in frost free zones. It has an ability to grow under low rainfall and low fertility conditions, hence it is most suitable for dry land farming. Castor is most probably originated in Ethiopian-East African region. There are four centres of diversity *viz*., South-West, North-West, Ethiopian-Eastern African and Arabian Peninsula as well as sub-continent of India and China. In India, it is known from very early days and is referred in the Susruta Samhita written over 2,000 years ago (Gangaiah, 2005) [8].
Castor is grown in sub-tropical and tropical regions of the world. It is cultivated in about 30 countries on commercial scale. India, China, Brazil, Thailand, Russia and Philippines are the principle castor growing countries. In Gujarat, Banaskantha, Mehsana and Sabarkantha are major castor growing districts.
Castor seed contains more than 45 percent oil, this oil is rich in ricinoleic acid and unusual hydroxyl fatty acid. Castor oil is the only oil soluble in alcohol and during the production of biodiesel requiring less heating than other oils and presenting high viscosity. Due to its unique physical and chemical properties, the oil is used as raw material for varied and numerous industrial applications like, the production of hydraulic fluids, plastics, nylon, rubber substitutes, artificial leather, printing ink, fast drying oils, soaps, paints, waxes, recinolyl, varnishes and medicines. Castor oil has extra properties than other vegetable oils, as it does not freeze even under -12 ºC to -18 ºC temperature therefore, considered as the best lubricating agent particularly for aeroplanes and high-speed engines. The castor plant itself may be used as a source of pulp for card board, cellulose and news print. The leaves may be used for rearing ‘eri’ silkworm for the production of ‘eri silk’. The castor oil cake is poisonous for cattle due to the presence of a protein “ricin” (blood coagulating factor) and a toxic alkaloid “ricinine”, but it is a valuable source of nitrogen (5.5%) as organic manure.
Presence of variability in the population is pre-requisite for the selection in crop improvement programme. Selection of populations or superior varieties will be possible only when adequate variability present in the gene pool. The coefficient of variation expressed at genotypic and phenotypic levels are used to compare the variability observed among different characters. Hence, knowledge about the variability using parameters like, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are importance for an effective

breeding programme in crops like castor. The heritability estimates aid in determining the relative amount of heritable part in variation and thus helps the plant breeder in selecting the best genotypes from a diverse population.

The phenotypic correlation indicates the extent of observed relationship between the two characters while genotypic correlation provides information about linkage for the gene controlling the pair of characters. Therefore, the correlation coefficient at genotypic and phenotypic levels were considered. However, they do not provide the exact picture of direct and indirect cause of such association, which can be cleared through path analysis. Thus, path analysis and character association provide the information of yield contributing characters and breeder can practice selection using this information for the isolation of superior succession from germplasm.

An assessment of genetic diversity can lead to classification and identification of diverse heterotic groups with potential breeding values. Progenies derived from diverse crosses determined using genetic divergence analysis should display a broad range of genetic variability. Among the available methods of multivariate analysis, Mahalanobis D^2 analysis appears to be most suitable for divergence study because it permits precise comparison among all possible pairs of population in any given group before affecting actual crosses. Hence, the aim of present experiment was to assess the variability parameters, correlation coefficient analysis, path analysis and Mahalanobis D^2 analysis among the various traits in diverse genotypes of castor.

Materials and Methods

The experimental material comprised of 32 genotypes of castor obtained from Pulses and Castor Research Station, Navsari Agricultural University, Navsari. The present investigation was laid out by Randomized Block Design (RBD) with three replications during late *Kharif*, 2021-22 at Pulses and Castor Research Station, Navsari Agricultural University, Navsari. Each entry (genotype) was accommodated in a single row of 7.2 m length with a spacing of 120 cm × 60 cm. A line of 12 plants were grown as a gross plot and from both sides 1 plant each were excluded to consider 10 plants as net plot. Observations were taken for ten characters *viz*., days to 50% flowering, days to maturity, plant height (cm), nodes per plant, branches per plant, primary spike length (cm), capsules per primary spike, 100 seed weight, yield per plot (kg) and oil content (%). The observations were recorded on five competitive plants randomly selected from each experimental unit in all the replications for seed yield as well as its components characters except days to 50% flowering and days to maturity. The traits days to 50% flowering and days to maturity were recorded on plot basis.

The data were subjected to analysis of variance for character estimated on the basis of mean value (Panse and Sukhatme, 1985). The estimates of PCV and GCV were classified as given by Shivasubramanian and Madhavamenon (1973) [22]. The phenotypic and genotypic coefficient of variation were calculated as Burton and De Vane (1953) [1]. Heritability estimates in broad sense and genetic advance were worked out as per Johnson *et al*. (1955) [3]. Genetic divergence was calculated using Mahalanobis D^2 statistics (1936) [11]. Grouping of the genotypes in different clusters was done by using Tocher's method. The statistical analysis was performed as per randomized block design (RBD) using statistical package R studio and Indostat.

Results and Discussion

Analysis of variance

The data recorded over ten characters were subjected to analysis of variance and results represented in Table 1. The results revealed that mean sum of squares were highly significantly differed for ten characters among the genotypes indicating presence of sufficient amount of variability in the population. A wide range of variation for agronomic parameters in castor was reported by Movaliya *et al.* (2018) [13], Rukhsar *et al*. (2018) [20] and Yamanura and Kumar (2020) [26].

Genetic variability

The mean values of 32 genotypes of castor for ten characters along with the standard error of mean (S.Em.), coefficient of variation (CV %) and variability parameters are given in Table 1. The magnitude of variation for days to 50% flowering ranged from 56.67 days (GP-705) to 79.67 days (NAUCI-10). Genotype GP-705 was earliest to flowering followed by RG-3568 (58.00 days) and DCS 85 (63.33 days). Range of variation for days to maturity was observed between 98.00 days (GP-705) to 125.33 days (JI-422). The data for plant height ranged from 73.78 cm (DCS 84) to 144.44 cm (GP-705) and for nodes per plant ranged from 12.78 (RG-3568) to 23.33 (NAUCI-10). The variation for branches per plant ranged from 2.33 (NCGP-4) to 8.83 (NCGP-2). Mainly three types of spikes *viz*., loose, semi compact and compact were observed, which affect number of capsules on spike. Primary spike length ranged from 36.00 cm (RG-3568) to 90.33 cm (JI-422) and capsules per primary spike ranged from 47.33 (DCS 84) to 149.00 (NAUCI-7). The seed quality parameters are the most important characters which determine the price of seeds at the time of sale and 100 seed weight gives an idea about boldness of seeds, so higher mean performance is desirable. 100 seed weight was highest in RG-3568 (20.93 g) and lowest in NAUCI-8 (35.80 g). The variability in oil content ranged from 44.20% (RG-631) to 48.60% (NAUCI-8) and for yield per plot ranged from 0.32 kg (RG-3568) to 3.18 kg (NAUCI-7).

Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV)

Genotypic and phenotypic coefficient of variation are used to compare the variability observed among different traits. Hence, knowledge about the variability using parameters like GCV and PCV are of paramount importance for an effective breeding programme in crops like castor. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) could be partitioned as high (>20%), moderate (10-20%) and low (<10%) as per Shivasubramanian and Menon (1973) [22]. Based on this, high GCV and PCV were observed for branches per plant, primary spike length, capsules per primary spike and yield per plot, which offering good scope for selection as there was less influence of environment and suggesting that potential variability available in germplasm for these traits (Table 1). Similar results were observed by Mehta and Vashi (1997) [12] and Movaliya *et al.* (2018) [13] for primary spike length; by Patel *et al.* (2010) [18], Movaliya *et al*. (2018) [13] and Sowmya *et al.* (2019) [23] for branches per plant, capsules per primary spike and yield per

plot. Moderate GCV and PCV were showed for nodes per plant and 100 seed weight whereas, moderate GCV and high PCV were observed for plant height. Low GCV and PCV were perceived for days to 50% flowering, days to maturity and oil content.

Heritability

High heritability was observed for days to 50% flowering (75.43%), days to maturity (65.33%), plant height (66.62%), nodes per plant (84.08%), branches per plant (91.75%), primary spike length (89.03%), capsules per primary spike (83.77%), 100 seed weight (80.80%) and yield per plot (90.27%) indicating that all the traits were majorly governed by additive genes and thus have the least environmental influence (Table 1). Similar results were reported by Patel *et al.* (2010) [18], Movaliya *et al.* (2018) [13] and Yamanura and Kumar (2020) [26] for days to 50% flowering, days to maturity, branches per plant, 100 seed weight and yield per plot; by Patel and Patel (2014) [17] for plant height and nodes per plant; by Mehta and Vashi (1997) [12] and Chaudhari *et al*. (2018) [5] for primary spike length and capsules per primary spike; by Alemaw *et al*. (2014) and Sowmya *et al*. (2019) [23] for nodes per plant, capsules per primary spike and 100 seed weight. Moderate heritability was observed for oil content (50.66%), similar results were reported by Yamanura and Kumar (2020) [26].

Genetic advance expressed as percent of mean

The genetic advance as percent of mean was recorded highest for yield per plot (93.32%) followed by branches per plant (72.24%), capsules per primary spike (45.90%), primary spike length (41.39%), plant height (28.81%), 100 seed weight (27.97%) and nodes per plant (25.70%) (Table 1). Similar results were observed by Chaudhari *et al*. (2018) [5] and Movaliya *et al*. (2018) [13] for all above traits. Medium genetic advance as percent of mean was observed for days to 50% flowering (14.15%). Similar results were observed for these characters by Chaudhari *et al.* (2018) [5]. Low genetic advance as percent of mean was observed for days to maturity (9.42%) and oil content (3.25%) indicating higher non additive gene action over the characters.

Higher heritability coupled with high genetic advance as percent of mean was observed for yield per plot, branches per plant, capsules per primary spike, primary spike length, plant height, 100 seed weight and nodes per plant. This confirms higher additive gene action and thus improvement could be brought about by direct phenotypic selection over the genotypes. These findings are similar to the results obtained by Dhapke *et al*. (1992) and Mehta and Vashi (1997) [12] for primary spike length, capsules per primary spike and yield per plot; by Patel *et al*. (2010) [18] and Yamanura and Kumar (2020) [26] for plant height, branches per plant, 100 seed weight and yield per plot; by Chaudhari *et al.* (2018) [5] and Movaliya *et al.* (2018) [13] for plant height, nodes per plant, branches per plant, primary spike length, capsules per primary spike and yield per plot.

Correlation coefficient analysis

Yield is a complex quantitative character governed by a large number of genes and is greatly affected by the environment. As a result, selecting superior genotypes based on yield will not be fruitful. Based on the correlation between yield and yield components, we selected the desired genotypes. Therefore, in the present experiment genotypic (r_g) and phenotypic (r_p) correlation coefficient were computed and are presented in Table 2.

In many cases, the direction of the phenotypic and genotypic correlation between several characters remained more or less similar. Generally, genotypic correlation was higher than phenotypic correlation indicating narrow environment effect and inherent association between traits. Yield per plant showed highly significant positive correlation with days to 50% flowering (r_g = 0.458 and r_p = 0.428), primary spike length (r_g = 0.625 and r_p = 0.572), capsules per primary spike (r_g = 0.974 and r_p = 0.870) and 100 seed weight (r_g = 0.832 and r_p = 0.696) at both genotypic and phenotypic levels. It had positive and significant correlation with oil content (r_g = 0.401 and r_p = 0.214) at both genotypic and phenotypic levels. It showed positive and significant correlation with days to maturity (r_g = 0.440 and r_p = 0.329), plant height (r_g = 0.362 and r_p = 0.326) and nodes per plant (r_g = 0.433 and r_p = 0.409) at genotypic level and positive highly significant at phenotypic level. It had positive and non-significant correlation with branches per plant (r_g = 0.183 and r_p = 0.168) at both genotypic and phenotypic levels.

These findings are in confirmation with Golakia *et al.* (2007) [9] for branches per plant; Tewari and Mishra (2013) [24] for oil content at genotypic level; Dapke *et al*. (2016) [6] for plant height, primary spike length and capsules per primary spike; Nagarajan *et al.* (2019a) [14] for capsules per primary spike; Yamanura and Kumar (2020) [26] for primary spike length, branches per plant, capsules per primary spike, 100 seed weight and oil content. According to the results of the present study, characters such as medium plant height, more number capsules per spikes and long primary spike would greatly improve the yield per plant.

Path coefficient analysis

Correlation studies provide information only on the magnitude and direction of association of yield with its components. But to know the direct effects of each independent variable on yield and indirect effects of it through other characters, path coefficient analysis has to be performed. In the present study, yield per plot was considered as the dependent variable and nine other characters were taken as independent variables. In accordance with Dewey and Lu (1959) [2], a genotypic path analysis was conducted. The direct and indirect effects of these independent variables on yield per plot are demonstrated in Table 3.

Highest positive direct effect was exhibited by capsules per primary spike (0.918) followed by oil content (0.252), 100 seed weight (0.187), plant height (0.035) and days to maturity (0.017), while highest negative direct effect on yield per plot was shown by days to 50% flowering (-0.192) followed by primary spike length (-0.112), branches per plant (-0.103) and nodes per plant (-0.013). Similar results were observed for days to 50% flowering, primary spike length, capsules per primary spike by Dapke *et al.* (2016) [6] and Nagarajan *et al.* (2019a) [14]; for days to maturity and oil content by Dapke *et al.* (2016) [6]; for plant height and 100 seed weight by Thatikunta *et al*. (2001), Golakia *et al*. (2007) [9], Dapke *et al*. (2016) [6] and Nagarajan *et al.* (2019a) [14]; for nodes per plant by Sevugaperumal *et al*. (2000) [21], Thatikunta *et al.* (2001) and Golakia *et al*. (2007) [99]; for branches per plant by Rukhsar *et al*. (2018) [20]; for direct effect on yield per plot.

In plant breeding, it is very difficult to have complete

knowledge of all component traits of yield. The residual effect, permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures the role of other possible independent variables which were not included in the study on the dependent variables. The residual effect is estimated with the help of direct effects and simple correlation coefficients. The residual effect being 0.012 suggested that only few other excluded components being effective over yield per plot.

Genetic Diversity Analysis

Genetic diversity studies are helpful in determining whether a cross has the capacity to produce heterosis. Hence, in this experiment 32 genotypes were analysed through cluster analysis, grouping them into five clusters based on mean values for different quantitative characters. Different clusters by using Tocher's method was presented in Table 4. Among the five clusters, cluster I was the largest with 22 genotypes followed by cluster II with 7 genotypes. Cluster III, IV and V had one genotypes each The average D^2 values of intra and inter cluster distances are given in Table 5. The maximum intra cluster distance was in cluster II (D = 8.99) followed by cluster I (D = 8.24). The maximum inter cluster distance was between cluster IV and V (D = 20.42) included only single genotype in each cluster followed by cluster III and IV (D = 20.41) included one genotype each. Cluster III, IV and V had no intra cluster distances as they were represented by only single genotype in each cluster. The minimum inter cluster distance was showed among cluster I and II (D = 11.29) indicate that closer relation among the genotypes included.

Genetic diversity presented by intra and inter cluster distance values revealed that genotypes of the same cluster had little divergence from each other with respect to aggregate effect of ten characters. Therefore, the chances of obtaining good recombination in segregating generation by crossing the members of the same clusters are low. Thus, suggested that crosses should be attempted between the genotypes belonging to clusters separated by large inter cluster distance.

Cluster means analysed for ten characters in castor clearly indicates appreciable differences for most of the characters as shown in Table 6. Cluster II had maximum value for oil content (47.46). Cluster III revealed maximum value for days to 50% flowering (79.00), days to maturity (125.33), plant height (121.56), nodes per plant (20.55), primary spike length (90.33) and 100 seed weight (35.77). Cluster IV showed maximum value for branches per plant (7.67). Cluster V had maximum value for capsules per primary spike (149.00) and yield per plot (3.18).

The present study revealed that highest genetic divergence contributing characters were branches per plant (33.67%) followed by primary spike length (17.64%), yield per plot (15.12%), 100 seed weight (8.67%), nodes per plant (7.86%), capsules per primary spike (5.24%), days to 50% flowering (4.64%), plant height (4.03%) and oil content (2.82%) contributed to maximum divergence. The analysis of percent contribution of various characters to divergence was presented in Table 6. The higher contribution of branches per plant, primary spike length and yield per plot was showed by Chaudhari *et al*. (2018) [5]; for yield per plot, 100 seed weight, capsules per primary spike and plant height by Nagarajan *et al*. (2019b) [15] and Ranjitha *et al*. (2019) [19].

Therefore, the results indicated that capsules per primary spike, oil content, 100 seed weight, plant height and days to maturity were the traits to be emphasized upon due to their significant positive correlation with yield per plot coupled with positive direct effect for developing the selection indices and would be useful in a further breeding program for improving seed yield in castor.

Table 1: ANOVA and Estimates of genetic parameters for ten characters evaluated by 32 castor genotypes

Source of variation	DF	Mean sum of square									
		DFF	DM	PH	NPP	BPP	PSL	CPS	SW	OC (%)	YP (kg)
Replication	2	19.16	54.09	153.29	1.31	0.89	50.38	6.32	2.80	2.88	0.11
Genotype	31	104.82**	147.86**	987.92**	19.43**	10.18**	483.13**	1680.59**	59.84**	4.23**	1.10**
Error	62	10.26	22.22	141.41	1.15	0.30	19.05	101.94	4.39	1.04	0.04
Genetic variability parameters											
General mean		71.00	114.44	98.05	18.14	4.96	58.41	94.23	28.46	46.61	1.24
Range Lowest		56.67	98.00	73.78	12.78	2.33	36.00	47.33	20.93	44.20	0.32
Range Highest		79.67	125.33	144.44	23.33	8.83	90.33	149.00	35.80	48.60	3.18
S.Em.±		1.85	2.72	6.87	0.62	0.31	2.52	5.83	1.21	0.59	0.11
C.D. (5%)		5.23	7.69	19.41	1.75	0.89	7.12	16.48	3.42	1.66	0.32
C.V. (%)		4.51	4.12	12.13	5.92	10.98	7.47	10.71	7.36	2.18	15.66
Environmental variance (σ^2_e)		10.26	22.22	141.41	1.15	0.3	19.05	101.94	4.39	1.04	0.04
Environmental Coefficient of Variance (ECV %)		4.51	4.12	12.13	5.92	10.98	7.47	10.71	7.36	2.19	15.66
Genotypic variance (σ^2_g)		31.52	41.88	282.17	6.09	3.30	154.69	526.22	18.48	1.06	0.35
Genotypic coefficient of variation (GCV %)		7.91	5.65	17.13	13.61	36.61	21.30	24.34	15.11	2.21	47.68
Phenotypic variance (σ^2_p)		41.78	64.10	423.58	7.25	3.59	173.75	628.15	22.88	2.10	0.39
Phenotypic coefficient of variation (PCV %)		9.10	7.00	20.99	14.84	38.22	22.57	26.60	16.80	3.11	50.19
Heritability (broad sense) %		75.43	65.33	66.62	84.08	91.75	89.03	83.77	80.80	50.66	90.27
Genetic advance		10.04	10.78	28.24	4.66	3.58	24.18	43.25	7.96	1.51	1.16
Genetic advance as percent of mean (%)		14.15	9.42	28.81	25.70	72.24	41.39	45.90	27.97	3.25	93.32

[*, ** Significant at 5% and 1% levels, respectively. DF: degrees of freedom, DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPP: Nodes per plant, BPP: Branches per plant, PSL: Primary spike length (cm), CPS: Capsules per primary spike, SW: 100 seed weight (g), OC (%): Oil content (%), YP: Yield per plot (kg)]

Table 2: Genotypic (r_g) and Phenotypic (r_p) correlation coefficients among 10 characters in castor

Characters		DFF	DM	PH	NPP	BPP	PSL	CPS	SW	OC (%)	YP (kg)
Days to 50% flowering	r_g	1.000									
	r_p	1.000									
Days to maturity	r_g	0.984**	1.000								
	r_p	0.730**	1.000								
Plant height (cm)	r_g	0.415*	0.418*	1.000							
	r_p	0.263**	0.324**	1.000							
Nodes per plant	r_g	0.649**	0.600**	0.695**	1.000						
	r_p	0.526**	0.460**	0.601**	1.000						
Branches per plant	r_g	-0.012	-0.072	-0.127	0.069	1.000					
	r_p	-0.021	-0.063	-0.105	0.052	1.000					
Primary spike length (cm)	r_g	0.710**	0.699**	0.621**	0.672**	-0.056	1.000				
	r_p	0.617**	0.559**	0.506**	0.575**	-0.045	1.000				
Capsules per primary spike	r_g	0.441*	0.395*	0.350*	0.447*	0.270	0.615**	1.000			
	r_p	0.347**	0.309**	0.333**	0.383**	0.257*	0.545**	1.000			
100 seed weight (g)	r_g	0.684**	0.814**	0.499**	0.569**	0.006	0.780**	0.808**	1.000		
	r_p	0.521**	0.555**	0.350**	0.466**	0.028	0.661**	0.688**	1.000		
Oil content (%)	r_g	0.685**	0.641**	0.202	0.402*	0.143	0.525**	0.292	0.392*	1.000	
	r_p	0.347**	0.339**	0.080	0.234*	0.057	0.352**	0.186	0.302**	1.000	
Yield per plot (kg)	r_g	0.458**	0.440*	0.362*	0.433*	0.183	0.625**	0.974**	0.832**	0.401*	1.000
	r_p	0.428**	0.329**	0.326**	0.409**	0.168	0.572**	0.870**	0.696**	0.214*	1.000

[*, ** Significant at 5% and 1% levels, respectively. DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPP: Nodes per plant, BPP: Branches per plant, PSL: Primary spike length (cm), CPS: Capsules per primary spike, SW: 100 seed weight (g), OC (%): Oil content (%), YP: Yield per plot (kg)]

Table 3: Genotypic path analysis of component characters towards yield per plot in thirty two genotypes

Characters	DFF	DM	PH	NPP	BPP	PSL	CPS	SW	OC	Correlation with yield per plot
DFF	-0.192	0.016	0.015	-0.008	0.001	-0.080	0.405	0.128	0.172	0.458**
DM	-0.189	0.017	0.015	-0.008	0.008	-0.079	0.363	0.152	0.161	0.440*
PH	-0.080	0.007	0.035	-0.009	0.013	-0.070	0.321	0.093	0.051	0.362*
NPP	-0.124	0.010	0.025	-0.013	-0.007	-0.076	0.411	0.106	0.101	0.433*
BPP	0.002	-0.001	-0.005	-0.001	-0.103	0.006	0.248	0.001	0.036	0.183
PSL	-0.136	0.012	0.022	-0.009	0.006	-0.112	0.565	0.146	0.132	0.625**
CPS	-0.085	0.007	0.012	-0.006	-0.028	-0.069	0.918	0.151	0.073	0.974**
SW	-0.131	0.014	0.018	-0.007	-0.001	-0.088	0.742	0.187	0.099	0.832**
OC	-0.131	0.011	0.007	-0.005	-0.015	-0.059	0.268	0.073	0.252	0.401*

[*, ** Significant at 5% and 1% levels, respectively. Residual effect = 0.012. Diagonal (bold) values indicate direct effect. DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPP: Nodes per plant, BPP: Branches per plant, PSL: Primary spike length (cm), CPS: Capsules per primary spike, SW: 100 seed weight (g), OC (%): Oil content (%), YP: Yield per plot (kg)]

Table 4: Distribution of thirty two castor genotypes into five different clusters as per Mahalanobis D^2 statistics

Clusters	No. of genotypes included	Genotypes
Cluster I	22	NAUCI-9, NAUCI-11, NAUCI-12, NAUCI-13, NCGP-3, NCGP-4, NCGP-5, NCGP-6, NCGP-7, ANDCI8-1, GAC-11, DCS 9, DCS 84, DCS 85, DCS 95, GP-525, GP-664, GP-705, RG-631, JI-423, JI-436, DCS 107
Cluster II	7	NAUCI-5, NAUCI-6, NAUCI-8, NAUCI-10, NCGP-1, NCGP-2, 48-1
Cluster III	1	JI-422
Cluster IV	1	RG – 3568
Cluster V	1	NAUCI – 7

Table 5: Average D^2 values of intra and inter cluster distance among thirty two genotypes of castor

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	8.24	11.29	11.57	12.60	15.12
Cluster II		8.99	12.41	14.74	13.98
Cluster III			0.00	20.41	14.68
Cluster IV				0.00	20.42
Cluster V					0.00
* - Diagonal (bold) values indicate intra cluster distance					

Table 6: Cluster means and percent contribution of characters towards total genetic divergence of ten characters in castor

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Contribution (%)
DFF	70.20	74.19	79.00	58.00	71.33	4.64
DM	113.68	117.48	125.33	100.67	112.67	0.00
PH	94.96	107.10	121.56	81.89	95.22	4.03
NPP	17.66	20.24	20.55	12.78	17.00	7.86
BPP	4.19	7.21	3.33	7.67	5.00	33.67
PSL	56.23	64.05	90.33	36.00	57.33	17.94
CPS	86.20	113.52	108.00	67.33	149.00	5.24
SW	27.61	30.30	35.77	20.93	34.57	8.67
OC (%)	46.38	47.46	47.13	45.30	46.50	2.82
YP	1.04	1.68	1.65	0.32	3.18	15.12

[DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPP: Nodes per plant, BPP: Branches per plant, PSL: Primary spike length (cm), CPS: Capsules per primary spike, SW: 100 seed weight (g), OC (%): Oil content (%), YP: Yield per plot (kg)]

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