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Identification of Promising Castor Hybrid Combinations by Principal Component Analysis

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A B S T R A C T

In order to find out the selection criteria thirty three genotypes were evaluated during *kharif* 2019-20 which includes 20 hybrids, 12 parents and a check (ICH-66). Data was subjected to principal component analysis (PCA) to reduce the number of variables in the original data set to a more significant set of variables, while maintaining maximum information. In the present investigation PCA was performed for 12 quantitative traits which yielded five PCs among them only four PCs exhibited more than 1.0 eigen values and showed about 84.34% variability. The PC 1 explained total variation 33.88% followed by PC 2 with 27.53%, PC 3 with 13.12% and PC 4 with 9.81%.The whole thirty three genotypes divided into eight main clusters. Cluster I consist of 19 genotype which was found to be a largest cluster had sub clusters from A to O followed by Cluster II had seven genotypes which divided into five sub clusters. Whereas, cluster III, IV, VI, VII and VIII consists of one genotype in each clusters and they had solitary entries Viz. DCS-120, DCS-102, ICH-66, DCS-108 and DCS-89 respectively. Cluster V also grouped as solitary but had ICH-1090 and ICH-326 genotypes. Based on values of inter cluster distance, it was found that the highest divergence occurred between cluster II and V (156.96) followed by cluster V and VIII (138.08),cluster I and VIII (110.42) indicating the wider genetic diversity between genotypes of these groups.

Introduction

Castor bean (*Ricinus communis* L.) is a tropical plant with high tolerance to drought and high-temperatures. It is one of the most important non-edible oilseed crops in the world. It is generally distributed in the tropical, sub-tropical and warm temperate zones (Weiss, 2000), it plays an important economic and social role, particularly due to its oil production potential (Costa *et al.*, 2010). Castor oil is obtained by pressing its seeds, which is used in the manufacturing of several products such as soaps, lubricants, hydraulic and brake fluids, dyes, and pharmaceuticals (Scholz and Silva, 2008). Oil content varies between 48 and 60% and is comprised of 80 to 90% ricinoleic acid, a monounsaturated, 18-carbon fatty acid with a hydroxyl functional group on the 12th carbon, which makes it more polar than most fats (Beltrão *et al.*, 2008). There has been

increasing interest in castor oil production due to its market value. As a result, cultivation has expanded to different regions in the country creating the need for the development of cultivars more adapted to a wide range of environmental condition, which allows farmers to better exploit the crop commercially (Costa *et al.,* 2006).

However, the identification of superior genotypes in a breeding program is not a quick and simple task, and breeders should be aware of more suitable and efficient methods for evaluating crop performance. Genotype-based selection studies are traditionally described through univariate statistical analyses. Nevertheless, such approach may compromise interpretations and conclusions by not exploiting the dependence among variables. Moreover, selection based on one or a few traits often leads to failure since univariate approach is often too narrow for the scope of plant breeding (Fikdalski *et al.*, 2007). Breeding a crop for a particular trait involves a complex system of several interacting factors which give rise to several variables which may or not be of interest for breeding. On the other hand, multivariate analysis allows researchers to obtain more information from a data set by considering not only each variable by itself but also the relation among them (Grobe, 2005). According to Beebe, Pell, and Seasholt (1998), multivariate techniques are a key tool in plant breeding programs as it increases selection efficiency.

Among these techniques, principal components analysis (PCA) aims at reducing the set of traits and thus simplifying structurally the data set so that differences between treatments, in principle influenced by a larger set of traits, can be evaluated in two- or three-dimensional spaces of easy geometric interpretation (Cruz *et al.*, 2012). The technique creates orthogonal axes called principal components (PCs), which are linear combinations of the original variables (Leite *et al.*, 2016). Despite the importance of such a tool, application of multivariate methods in castor breeding programs are lacking. One of the few studies which address the topic was Sartori, Silva, and Zanotto (2018), who investigated the efficiency of multivariate methods such as clustering methods (complete link, Euclidian distance and the nearest neighbour method) and PCA to select short-height, high-yielding castor bean cultivars. While dendrograms in clustering methods yielded contrasting results, PCA allowed to efficiently select genotypes based on all desired traits concomitantly. Therefore, the objective of this study was to evaluate PCA as a tool to identify the promising cross combination for commercial cultivation.

Materials and Methods

The experimental material consists of 33 entries, which includes 20 hybrids, 12 parents and a check (ICH-66) were obtained from the ICAR-IIOR, Hyderabad, India. The present investigation was laid out by randomized complete block design (RCBD) with three replications during *kharif*, 2019-20 at All India Co-ordinated Research Project on Castor, Zonal Agricultural Research Station, GKVK, Bengaluru.

The complete set of thirty three entries was sown in a single row of 6.0 meter length was assigned to each genotype with 10 dibbles having 60 cm intra row spacing and 90 cm inter row spacing. All recommended agronomic practices (dose of NPK (40:40:20 N: P_2O_5: K_2O Kg/ha) and plant protection (Sprayed Larvin @ 1g/l and propiconazole @ 0.5 ml/l for the control of capsule borer and gray mold disease respectively) measures were followed for raising normal crop. The observations were recorded on five randomly selected plants for twelve traits *viz.,* DFF: Days to 50 per cent flowering, DMPS: Days

to maturity of primary spike, PH: Plant height (cm), NN: Number of nodes up to primary spike, TLPS: Total Length of primary spike (cm), ELPS: Effective Length of primary spike (cm), NC: Number of capsules on primary spike, NES/P: Number of effective spikes per plant, HSW: 100 seed weight (g), HVW: 100 Volume weight (g), SY: Seed yield per plant (g), OC: Oil content (%). The observations for days to 50 per cent flowering and maturity were recorded on plot basis.

Data was subjected to principal component analysis (PCA) to reduce the number of variables in the original dataset to a more significant set of variables, while maintaining maximum information. Since the original variables do not have the same unit, the correlation matrix was used as a way of prior standardization of the data (cantering on the mean and reducing to the unit of standard deviation). If standardization is not, variables having higher variances would be emphasized in the first components (Wilks, 2006). Eigenvectors, which are coefficients associated positively or negatively with each original variable, were compared to identify how much each PC was explained by each variable and to define those that contributed the most to the formation of each selected PCs. Scores, which are assumed values of each PC for the studied hybrids, are then obtained from the eigenvectors. Finally, such information allows the identification of those hybrids that best stood out in relation to each PC. Data analysis was performed using statistic package Windost at Version 9.3 from indostat services, Hyderaba (India).

Results and Discussion

The analysis of variance was performed to test the difference amongst parents and hybrids for twelve traits. The results revealed that, highly significant differences among the 33 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), Anjani (2012), Gabriela *et al.*, (2019) and Jawahar *et al*., (2019).

Principal component analysis is a simple non parametric method for extracting relevant information from confusing data sets. With minimum efforts, this provides a roadmap for how to reduce the complex data to a lower dimension to sometimes hidden, simplified structures that often underlines it. Principal component analysis converts a set of correlated variables into a set of values of linearly uncorrelated variables called principal component. In general, plant breeder is interested in keeping only those principal components whose values are greater than 1. Components with an eigen values of less than 1 account for less variance.

In the present investigation PCA was performed for 12 quantitative traits which yielded five PCs among them only four PCs exhibited more than 1.0 eigen values and showed about 84.34% variability. Therefore, these four PCs were given due importance for the further explanation. Out of five, the first four principal component having eigen values greater than one with 84.34% of the total variation among the thirty-three genotype.

The PC 1 explained total variation 33.88% followed by PC 2 with 27.53%, PC 3 with 13.12% and PC 4 with 9.81%. PC 1 and PC 2 showed maximum contribution to the total variation are presented in the table 2 and figure 1. In the figure-1, line diagram explains the percentage of variation associated with each principal component obtained by drawing a graph between Eigen value and principal component number.

Table.1 ANOVA and Estimates of genetic parameters for twelve morphological descriptors evaluated by 33 castor genotypes

Source of Variations	DF	DFF	DMPS	PH	NN	TLPS	ELPS	NC	NES/P	SY	HSW	HVW	OC
Replicate	2	18.575**	56.030**	60.246	2.064	124.492*	91.384**	174.139	11.368**	562.131	13.427	16.945	4.262
Treatments	32	98.896**	306.884**	476.006**	9.583**	119.179**	74.358**	126.379**	13.502**	4240.164**	72.81**	88.938**	29.412**
Error	64	2.096	6.488	19.443	0.919	29.567	15.473	57.443	1.232	474.967	6.512	5.816	5.609
Genetic Parameters													
Var Environmental		2.10	6.49	19.44	0.92	29.57	15.47	57.44	1.23	474.97	6.51	5.82	5.61
ECV		3.22	2.72	10.71	9.63	14.40	12.70	18.04	15.72	18.63	9.90	4.33	5.37
Var Genotypical		32.27	100.13	152.19	2.89	29.87	19.63	22.98	4.09	1255.07	22.10	27.71	7.93
GCV		12.62	10.68	29.96	17.06	14.47	14.30	11.41	28.64	30.29	18.23	9.45	6.39
Var Phenotypical		34.36	106.62	171.63	3.81	59.44	35.10	80.42	5.32	1730.03	28.62	33.52	13.54
PCV		13.03	11.02	31.82	19.59	20.42	19.12	21.34	32.67	35.56	20.74	10.39	8.35
h^2 (Broad Sense)		0.94	0.94	0.89	0.76	0.50	0.56	0.29	0.77	0.73	0.77	0.83	0.59
Genetic Advancement 5%		11.34	19.98	23.93	3.05	7.98	6.83	5.28	3.65	62.16	8.51	9.86	4.44
Genetic Advancement 1%>		14.53	25.60	30.67	3.91	10.23	8.75	6.77	4.68	79.66	10.91	12.63	5.69
Gen.Adv as % of Mean 5%		25.20	21.31	58.12	30.60	21.14	22.03	12.56	51.72	53.14	33.01	17.70	10.08
Gen.Adv as % of Mean 1%		32.29	27.31	74.48	39.22	27.09	28.23	16.10	66.28	68.10	42.30	22.68	12.91
C.V.		3.22	2.72	10.71	9.63	14.40	12.69	18.03	15.72	18.63	9.90	4.33	5.37
S.E.		0.84	1.47	2.55	0.55	3.14	2.27	4.38	0.64	12.58	1.47	1.39	1.37
C.D. 5%		2.36	4.16	7.19	1.56	8.87	6.42	12.36	1.81	35.55	4.16	3.93	3.86
C.D. 1%		3.14	5.52	9.56	2.08	11.79	8.53	16.43	2.41	47.24	5.53	5.23	5.13
General Mean		45.00	93.73	41.18	9.96	37.76	30.99	42.03	7.06	116.98	25.79	55.71	44.08
Range Lowest		35.33	81.33	25.74	8.00	22.33	21.30	28.15	3.78	33.78	13.16	42.85	35.23
Range Highest		57.33	110.67	77.78	14.22	52.29	43.67	54.66	14.34	189.41	36.09	64.17	49.18
Exp Mean next Generation		56.34	113.70	65.11	13.01	45.74	37.81	47.30	10.71	179.14	34.30	65.56	48.52

[*, ** Significant at 5 % and 1 % levels of probability, respectively. DF: Degree of freedom, DFF: Days to 50 per cent flowering, DMPS: Days to maturity of primary spike, PH: Plant height (cm), NN: Number of nodes up to primary spike, TLPS: Total Length of primary spike (cm), ELPS: Effective Length of primary spike (cm), NC: Number of capsules on primary spike, NES/P: Number of effective spikes per plant, SY: Seed yield per plant (g), HSW: 100 seed weight (g), HVW: 100 Volume weight (g), OC: Oil content (%).].

Table.2 Eigen value and percentage of total variance of various principal components

Component	Eigen vector	% Variance explained	Cumulative percentage
PC1	4.066	33.88	33.88
PC2	3.303	27.53	61.41
PC3	1.574	13.12	74.53
PC4	1.177	9.81	84.34
PC5	0.608	5.07	89.41

Table.3 Component matrix showing latent vectors associated with the five principal components

CHARACTERS	COMPONENTS				
	PC1	**PC2**	**PC3**	**PC4**	**PC5**
Days to 50 per cent flowering	0.43778	0.04314	0.18520	0.03821	0.36322
Days to maturity of primary spike	0.01120	-0.49475	0.18096	0.11762	-0.17140
Plant height (cm)	0.42835	0.10129	0.08406	-0.24815	-0.18600
Number of nodes up to primary spike	0.35549	-0.09826	-0.03456	0.29145	-0.71760
Total Length of primary spike (cm)	0.21364	-0.33558	0.40836	-0.00107	0.16805
Effective Length of primary spike (cm)	0.23900	-0.40027	0.20601	-0.19738	0.22183
Number of capsules on primary spike	0.07091	0.23706	0.45040	-0.43024	-0.30048
Number of effective spikes per plant	0.30227	0.14479	-0.43840	-0.36372	-0.09676
Seed yield per plant (g)	-0.37167	-0.14007	0.22993	-0.29447	-0.30542
100 seed weight (g)	-0.20366	0.36861	0.34958	-0.22345	0.05921
100 Volume weight (g)	-0.34380	-0.35045	-0.08096	-0.11361	-0.10265
Oil content (%)	0.03733	-0.32426	-0.37257	-0.57643	0.06873

Table.4 Cluster composition of Castor germplasm based on quantitative characters

Clusters	Sub clusters	No. of genotypes	Name of Genotypes
I	A	2	ICH-1099, ICH-1100
	B	1	ICH-404
	C	1	ICH-1106
	D	1	ICH-1104
	E	1	ICH-1097
	F	1	DPC-15
	G	2	DCS-104, ICH-824
	H	2	ICH-1101, ICH-1098
	I	2	DPC-9, ICH-1094
	J	1	ICH-1107
	K	1	ICH-1089
	L	1	ICH-1087
	M	1	ICH-1380
	N	1	ICH-1093
	O	1	DCS-94

	TOTAL	**19**	
II	A	2	DCS-107, DCS-112
	B	1	ICH-1086
	C	1	DCS-119
	D	1	DCS-105
	E	2	ICH-823, ICH-1092
	TOTAL	**7**	
III	A	1	DCS-120
IV	A	1	DCS-102
V	A	2	ICH-1090, ICH-326
VI	A	1	ICH-66
VII	A	1	DCS-108
VIII	A	1	DCS-89
GRAND TOTAL		**33**	

Fig.1 Line diagram showing eigen value for each Principal components

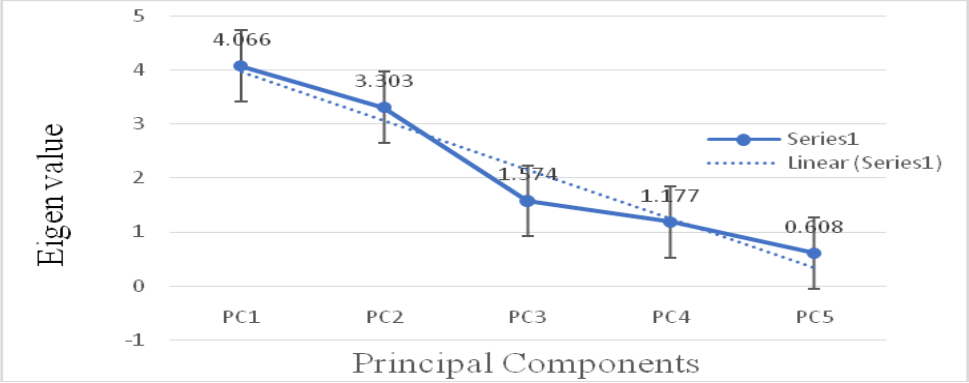
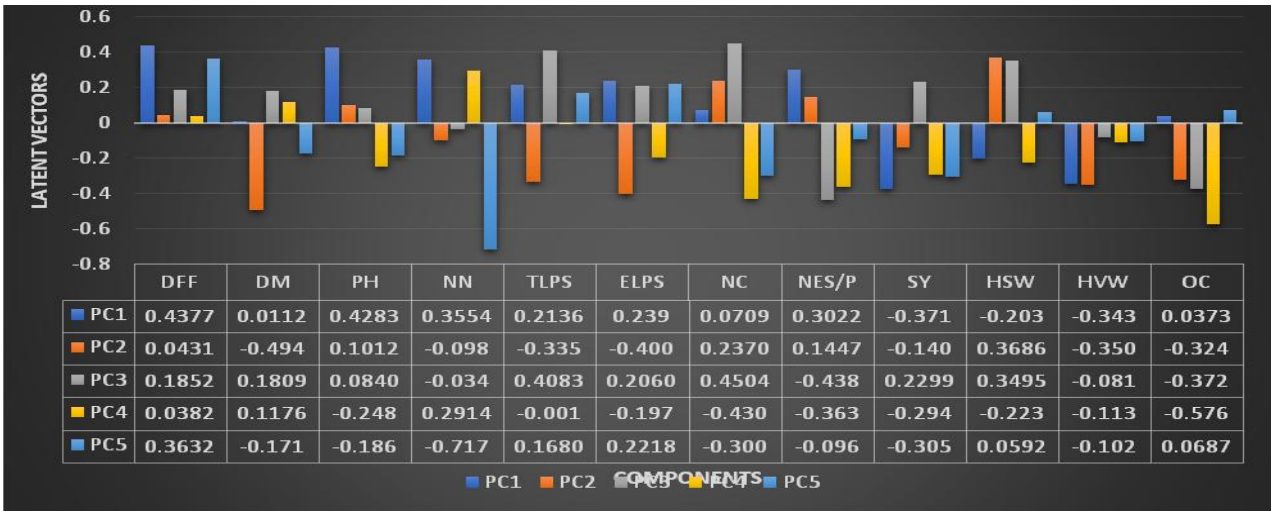


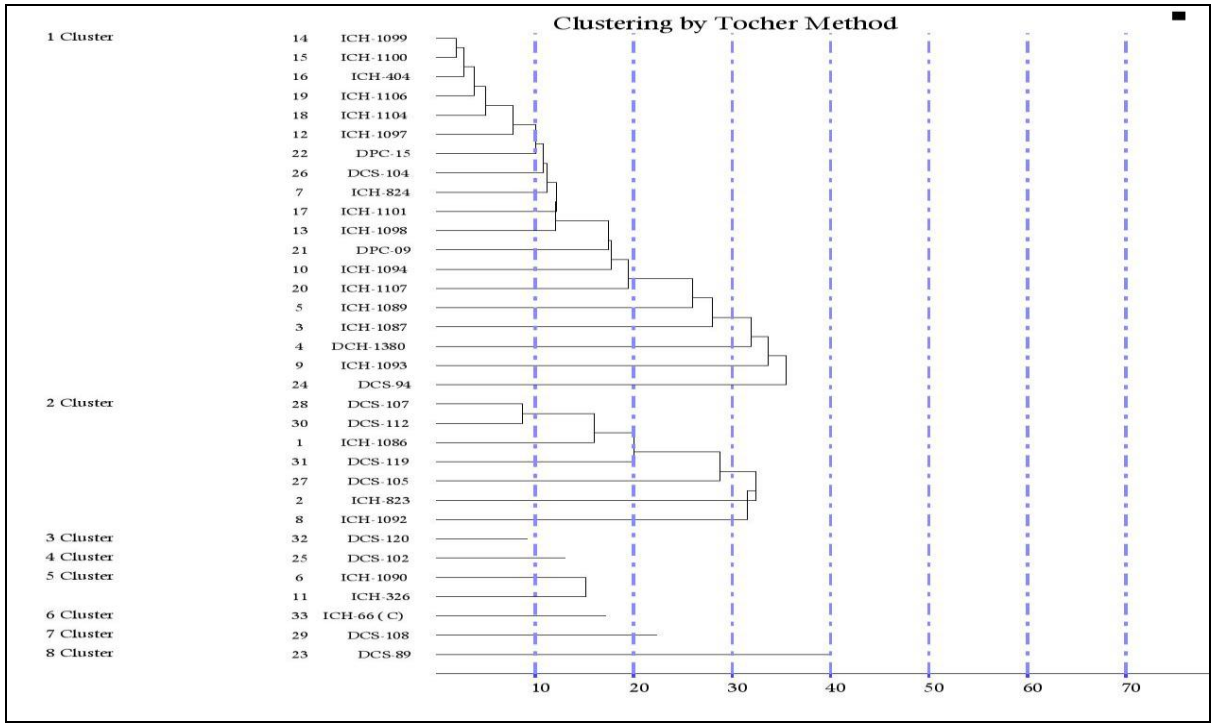
Fig.2 Component matrix showing latent vectors associated with the five principal components



	DFF	DM	PH	NN	TLPS	ELPS	NC	NES/P	SY	HSW	HVW	OC
PC1	0.4377	0.0112	0.4283	0.3554	0.2136	0.239	0.0709	0.3022	-0.371	-0.203	-0.343	0.0373
PC2	0.0431	-0.494	0.1012	-0.098	-0.335	-0.400	0.2370	0.1447	-0.140	0.3686	-0.350	-0.324
PC3	0.1852	0.1809	0.0840	-0.034	0.4083	0.2060	0.4504	-0.438	0.2299	0.3495	-0.081	-0.372
PC4	0.0382	0.1176	-0.248	0.2914	-0.001	-0.197	-0.430	-0.363	-0.294	-0.223	-0.113	-0.576
PC5	0.3632	-0.171	-0.186	-0.717	0.1680	0.2218	-0.300	-0.096	-0.305	0.0592	-0.102	0.0687

DFF: Days to 50 per cent flowering, DMPS: Days to maturity of primary spike, PH: Plant height (cm), NN: Number of nodes up to primary spike, TLPS: Total Length of primary spike (cm), ELPS: Effective Length of primary spike (cm), NC: Number of capsules on primary spike, NES/P: Number of effective spikes per plant, SY: Seed yield per plant (g), HSW: 100 seed weight (g), HVW: 100 Volume weight (g), OC: Oil content (%)

Fig.3 Clustering by toucher Method for twelve quantitative characters of Castor



The objective of the principal component analysis is to identify the minimum number of components, which explains maximum variability out of the total variability. PC1 is the most important component, explained 33.88% of the total variation and the characters which contributed high on the component were days to 50 per cent flowering, Plant height, number of effective spikes per plant, number of nodes up to primary spike, total Length of primary spike, effective Length of primary spike (cm), number of capsules on primary spike, days to primary spike maturity and percent oil content contributed more towards total variation. The plant traits that separate genotypes along PC1 were major yield contributing characters presented in Table 3 and figure 2. PC2, which is the second important component, explained 27.53% of total variability and the characters which contribute high on the components were100 seed weight, Number of capsules on primary spike, Number of effective spikes per plant, Plant height and days to 50 per cent flowering. The third component (PC3), explained 13.12% of total variability and the characters *viz.*,Number of capsules on primary spike, Total Length of primary spike, 100 seed weight, Seed yield per plant, Effective Length of primary spike, Days to 50 per cent flowering, Days to maturity of primary spike and plant height were contributed more for the component. PC4, which is the fourth component, explained 9.81% of total variability and the characters which contributed high on the component were Number of nodes up to primary spike, Days to maturity of primary spike and Days to 50 per cent flowering. These finding are in confirmation with the earlier findings of Bhand and Patel (1999), Shaheen (2002), Sunil *et al.*, (2005), Amar *et al.*, (2010), Sreelakshmi (2015) reported the first three principal component analysis attributed 95.48% of variation towards total divergence. Manyasa *et al.*, (2008), Husna *et al.*, (2011), Shivwanshi and Babbar (2017)reported similar traits contributing more to diversity in

pigeonpea. Similar results were reported by Jawahar *et al.,* (2019) that 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 havean important implication for castor genotype characterization, improvement, agro-morphological evaluation and conservation.

Clustering analysis

Genetic diversity within the castor genotypes was done by Toucher Method for twelve quantitative traitsusing statistic package Windostat Version 9.3. Based on the cluster analysis, thirty three genotypes were grouped into different clusters and sub clusters which is presented in Table 4 and Figure 3. The whole thirty three genotypes divided into eight main clusters. Cluster I consist of 19 genotype which was found to be a largest cluster had sub clusters from A to O followed by Cluster II had seven genotypes which divided into five sub clusters. Whereas, cluster III, IV, VI, VII and VIII consists of one genotype in each clusters and they had solitary entries Viz. DCS-120, DCS-102, ICH-66, DCS-108 and DCS-89 respectively. Cluster V also grouped as solitary but had ICH-1090 and ICH-326 genotypes.

Based on values of inter cluster distance, it was found that the highest divergence occurred between cluster II and V (156.96) followed by cluster V and VIII (138.08), cluster I and VIII (110.42) indicating the wider genetic diversity between genotypes of these groups. The cluster VIII involved DCS-89which high yielding, cluster II involves DCS-105, DCS-107, DCS-112, and DCS-119 genotypes 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 (Jawahar *et al.,* 2019). 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 III and IV (16.70) 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 these results were in agreement with Ramesh *et al.,* (2012), Jawahara *et al.,* (2019) which indicates the existence of substantial diversity among the genotypes.

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