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An assessment of genetic diversity and combining ability of elite castor genotypes suitable for rainfed conditions

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Abstract
A study was conducted to assess the diversity of 72 castor genotypes used as male lines in the hybrid breeding programme in India using multivariate analysis in addition to morphological characterization using DUS (Distinctiveness, Uniformity and Stability) testing guidelines of castor. Fifteen agronomical and three morphological traits were measured in 72 genotypes in field studies conducted for two years. The multivariate data set was subjected to genetic divergence analysis using Mahalonobis' D^2 static and clustered into nine subgroups following Tocher's method in addition to Principal Component Analysis (PCA). The genotypes from Clusters 1 and 5 and Clusters 2 and 5 are genetically diverse with 556.9 and 469.7 units while cluster 7 genotypes with higher mean seed yield are potential candidates as varieties after multilocation testing. In PCA, the first two canonical variants were significant and accounted for 68 per cent of the inter accession variability. Grouping of castor genotypes was also done based on four grouping characteristics of DUS guidelines like stem color, bloom, capsule spines and maturity. Combining ability analysis indicated that DCS-96, DCS-94, DCS-104, DCS-97 were good general combiners for seed yield while M-568 x DCS-96 yielded 21 per cent standard heterosis over the best check DCH-177.

Key words
Principal component analysis, Mahalonobis' analysis, Clusters, genetic distance and DUS guidelines.

INTRODUCTION

In India, the majority (>95%) of the area under irrigated conditions is occupied by castor hybrids while both varieties and hybrids are equally cultivated under rainfed conditions (Lavanya and Varaprasad, 2012). However, there has been stagnation in the magnitude of heterosis of the experimental hybrids due to a gradual decrease in the genotypic diversity of the parental base (AICRP on Castor, DOR, 2006, Lavanya and Solanki, 2010). There is an urgent need to assess and classify the diversity of the working germplasm in order to identify appropriate diverse male lines for the development of castor hybrids. Castor, being a monotypic genus (Moshkin, 1986), diversity is based on geographically diverse germplasm or generation of intra specific diversity through hybridization and selection. In addition, the available literature on genotypic diversity of castor in India and all over the world is limited (Bhatt and Reddy 1987, Chakrabarty and Banu 1999, Sevagaperumal *et al*., 2000, Lakshmamma *et al*., 2002, Durgarani *et al*., 2007, Allan *et al*., 2008, Goodarzi, 2011, Ramesh *et al*., 2012, Ranjitha *et al.,* 2019, Nagarajan *et al.,* 2019).

The main objectives of the study were to assess the genetic diversity in the existing breeding lines and further use them in the generation of hybrids and diverse parental material. An attempt was also made to characterize and group the 72 genotypes based on the grouping characters used for DUS testing in India. Promising male lines selected in the present study were further assessed for their combining ability and heterosis in a line x tester mating design for seed yield and yield components.

MATERIALS AND METHODS

Seventy-two castor genotypes including 67 male lines and five varieties *viz*., DCS-9, 48-1, Kranti, Haritha and Kiran available at ICAR-Indian Institute of Oilseeds Research were used for the study. All the 72 castor genotypes were evaluated in *kharif* season with the onset of monsoon under rainfed conditions for two years in a randomized block design. Each treatment was laid in four row plots of ten plants per row with a spacing of 90 cm between the rows and 45 cm between the plants in two replications. Standard agronomic practices were followed for raising the crop which was harvested when the capsules turned brown. The data was recorded on the traits like days to 50% flowering of the primary spike, the number of nodes up to primary spike, secondary spikes 1 and 2, the plant height up to the base of the primary spike (cm), the total and effective spike length (cm), the number of capsules on the primary spike, the number of effective spikes per plant, the seed yield at first, second and final or total picking (kg/ha) and the hundred seed weight (g) from the net plot (6.48 m^2). The seed yield (g) was recorded from the net plot in three pickings at 90, 120 and 150 days after sowing (DAS) and presented ascumulative seed yield (kg /ha) in the second and final seed yield. After the harvest of the primary spike, the seed oil content of castor genotypes was estimated with Nuclear Magnetic Resonance (NMR) technique (AOAC, 1970).

No significant differences were found for all the characters between the years while interactions between years and genotypes were also not significant. The pooled mean data were subjected to analysis of variance. The genetic divergence was measured by the Mahalonobis' D^2 analysis and genotypes were grouped using Tocher's method (Rao, 1952). The grouping depends on the principle that intra-group distances should be far less than inter-group distances. A principal component analysis based on Mahalonobis' D^2 was carried out using the INDOSTAT statistical software (INDOSTAT Services, Hyderabad, India) to determine the traits most effective in discriminating between accessions. The first two components explaining the maximum variance were selected for the ordination analysis and the correlation between the original traits and the respective principal component was calculated. The principal components with *eigen*values >1.0 were selected.

A set of 13 male lines including nine male lines selected from the present study based on their duration, agronomic adaptability and yielding ability *viz*., DCS-9, DCS-92, DCS-93, DCS-94, DSC-96, DCS-97, DCS-103, DCS-104, Kiran, four other male lines *viz*., DCS-106, DCS-98, DCS-119 and DCS-120 were crossed with three pistillate lines (DPC-9, DPC-17 and M-568) in a line x tester mating design in *rabi* season. All the 39 hybrids along with two standard checks-DCH-177 and DCH-519 were evaluated in a RBD with two replications at ICAR-Indian Institute of Oilseeds Research, Rajendranagar during *kharif* season.

The 41 genotypes were evaluated for 13 characters *viz.,* the number of nodes to primary spike, the number of nodes to secondary spike-1 (S_1), the number of nodes to secondary spike-2 (S_2), plant height up to primary spike (cm), total length of primary spike (cm), effective length of primary spike (cm), the number of capsules per primary spike, the number of effective spikes per plant,100- seed weight (g), cumulative seed yield at first**,** second and final picking (kg/ha) and oil content (%). The data were analysed for estimation of combining ability and heterosis using standard statistical procedures (Cochran and Cox, 1957 and Kempthorne, 1957).

RESULTS AND DISCUSSION

The average performance of the entries along with genetic parameters was presented in **Table 1**. The genotypes varied significantly for all the evaluated 14 characters. The number of days to 50 per cent flowering varied between 26 and 77 days while the number of capsules on the primary spike differed from 3 to 78. The greatest variation was observed in the final or total seed yield (kg/ha) depicted by the high standard deviation value recorded for the parameter. This was followed by the seed yield at second and first picking; the plant height up to the primary spike. The present study indicated an environmental influence in the expression of characters as phenotypic variance (σ^2p) was higher than the corresponding genetic variance (σ^2g) for all the characters presented in **Table 1**. A high variance was observed for seed yield in different pickings and medium variance for the plant height, the number of capsules on primary spike and days to 50 per cent flowering. On the other hand, a low variance was observed in the number of nodes up to secondary spike 1 and 2, primary spike, 100 seed weight and oil content.

High heritability was observed in all the traits, except for oil content while the genetic advance expected in the next generation was high for seed yield at first, second and final picking, plant height up to primary spike, the number of capsules per primary spike and days to 50 per cent flowering of the primary spike (**Table 1**).

High heritability coupled with high genetic advance expected in the next generation for seed yield in first, second and third picking suggested the role of additive or fixable gene effect (Ramu *et al*., 2002, Lavanya and Chandramohan, 2003, Lavanya *et al*., 2006a) to a great extent and the improvement of these traits would be effective through either pedigree or recurrent selection methods. However, the maximum contribution of 100-seed weight (27.9%), seed yield at first (23.2%) and seed yield at second picking (22.3%) to the total divergence indicated that high selection intensity was practiced for these traits.

The characters like the number of nodes to secondary spike 2 (0.2%), effective spikes per plant (0.27%), plant height (0.86%), effective spike length (0.94%), days to

50% flowering (1.8%), total spike length (2.31%) with a minimum contribution to the divergence indicated that scope for further selection in breeding populations. Similar results on the maximum contribution of either seed weight or seed yield towards total divergence were also reported by Bhatt and Reddy (1987), Sevagaperumal *et al*. (2000), Durgarani *et al*. (2007) and Zareena *et al*. (2009).

Table 1. Mean performance and genetic parameters for 14 quantitative characters in 72 castor genotypes

S. No.	Character	Mean	Maximum	Minimum	Standard deviation	Variance		h^2_b	GA	GA as % of mean*	C.V (%)
						σ^2 G	σ^2 p				
1	Days to 50% flowering	51.4	77.5	26	3.8	169	183	0.9208	25.6876	49.9326	10.5
2	Number of nodes to primary spike	14.1	22.9	7.2	0.6	8.61	8.92	0.9647	5.9361	42.2623	5.7
3	Number of nodes to secondary spike 1	4.7	7.0	3.0	0.3	0.41	0.481	0.8440	1.2052	25.8684	8.3
4	Number of nodes to secondary spike 2	5.5	8.4	3.8	0.4	0.52	0.64	0.8076	1.3334	24.4133	9.1
5	Plant height up to primary spike (cm)	78.2	161.3	23.8	8.6	828	901	0.9188	56.8207	72.6647	15.5
6	Total spike length (cm)	34.2	49.9	11.7	2.7	60.9	68.21	0.8936	15.2023	44.4872	11.2
7	Effective spike length (cm)	28.6	44.9	7.6	2.7	63.9	71.29	0.8967	15.5965	54.5386	13.4
8	Number of capsules per primary spike	29.6	78	3.4	5.1	233	259.72	0.8988	29.8403	100.7883	24.5
9	Number of effective spikes per plant	9.8	20.2	3.4	1.3	7.43	9.24	0.8049	5.0390	51.3169	19.3
10	Seed yield at first picking (kg/ha)	97.5	337.5	0	19.9	13283	13678.9	0.9711	233.9692	240.0026	28.8
11	Seed yield at second picking (kg/ha)	153	337.5	0	23.5	7120	7671.9	0.9281	167.4606	109.4564	21.7
12	Seed yield at final picking (kg/ha)	1004	1991	341.5	130	94869	111770	0.8488	584.5619	58.2261	18.3
13	Hundred seed weight (g)	22.5	36.4	10.6	1.1	26.7	27.94	0.9572	10.4220	46.3101	6.9
14	Oil content (%)	45.7	52.5	31.8	2.9	10.0	18.21	0.5503	4.8376	10.5951	8.9

The first principal component (PC 1) explained 45 per cent of the variation of the divergence (**Table 2**). It was positively and strongly correlated with seed yield at second picking and in decreasing importance, with the number of nodes to primary spike, days to 50% flowering, the number of nodes to S_1 and the number of capsules per primary spike; and was negatively correlated with seed yield at first picking. The second component was positively correlated with oil content and number of capsules per primary spike; and negatively correlated with 100 seed weight. Among the 14 traits, 100-seed weight, seed yield at first pick and a second pick contributed the maximum to the total divergence (**Table 2**).

Table 2. Canonical vectors for 14 characters of 72 castor genotypes

S. No.	Character	PC 1	PC-2	PC-3	PC-4
1	Days to 50% flowering	0.31	0.03	0.29	0.1
2	Number of nodes to primary spike	0.39	-0.001	0.40	0.05
3	Number of nodes to secondary spike 1	0.3	-0.02	0.26	0.2
4	Number of nodes to secondary spike 2	0.2	-0.02	0.18	0.01
5	Plant height up to primary spike	0.11	0.01	0.06	0.22
6	Total spike length	0.13	0.07	-0.006	0.40
7	Effective spike length	-0.06	0.02	-0.09	0.10
8	Number of capsules per primary spike	0.2	0.3	-0.02	0.4
9	Number of effective spikes per plant	-0.02	-0.05	-0.06	-0.25
10	Seed yield at first picking	-0.53	0.17	-0.03	0.6
11	Seed yield at second picking	0.5	-0.13	-0.73	0.05
12	Seed yield at final picking	0.06	-0.20	-0.06	0.3
13	Hundred seed weight	-0.2	-0.82	0.18	0.1
14	Oil content	-0.1	0.37	0.14	-0.3
	Eigen value	3.38	1.76	0.74	0.38
	Variance (%)	44.9	23.4	9.82	5.03
	Cumulative variance (%)	44.9	68.3	78.11	83.14

Clustering pattern based on Mahalonobis' method of nine groups indicated that the intra-cluster distance was minimum in Cluster 3 and maximum in Cluster 8 followed by Cluster 4 and 9 (**Table 3**). Among the nine clusters, genotypes from cluster 1 and cluster 5 recorded maximum inter cluster distance followed by genotypes from cluster 2 and 5; cluster 1 and 7. This pattern of clustering was also confirmed by a grouping of genotypes in the same cluster in the dendrogram formed by Mahalonobis' D^2 analysis. The details of the members of each of the nine clusters with their pedigree along with the mean values of the 14 characteristics of the nine clusters calculated by Tocher's method were given in **Table 4**.

Castor is a monotype genus and all the six subspecies based on morphological characters (Weiss, 1971, Kulkarni and Ramanamurthy, 1977, Lavanya *et al*., 2018) can be easily crossed with each other. However, the available morphological diversity was wide varying from indeterminate to determinate, divergent to convergent branching, tall to dwarf, early to late, monoecious to pistillate forms etc in the existing germplasm (Moshkin, 1986, Rao *et al*., 2003, Anjani and Jain, 2004 and Anjani, 2010).

The presence of wide diversity in castor reported by earlier workers (Bhatt and Reddy, 1987,

Table 3. Intra and inter cluster distances (D^2 value) in 72 castor genotypes

Cluster	Genotypes	Cluster								
		1	2	3	4	5	6	7	8	9
1	DCS-16, DCS-7, DCS-2, DCS-3, DCS-28, DCS-1, DCS-17, DCS-18	**55.5**	123.8	99.2	282.3	556.9	326.4	409.4	345.7	369.8
2	DCS-37, DCS-85, DCS-94, DCS-21, DCS-92, DCS-22, DCS-96		**51.1**	81.6	249.4	469.7	198.8	305.8	230.2	186.2
3	DCS-5, DCS-84, DCS-9, DCS-93, DCS-104, DCS-103, DCS-71, DCS-67, DCS-13, DCS-78, DCS-64, Kranthi, Kiran			**44.1**	167.5	388.7	236.4	290.8	218.9	236.0
4	DCS-26, DCS-23, DCS-25, DCS-74, DCS-66, DCS-51, DCS-97, DCS-45, DCS-52, DCS-50, DCS-59, DCS-63				**91.9**	199.4	311.8	254.5	185.1	311.9
5	DCS-52, DCS-50, DCS-59, DCS-63					**66.9**	282.8	147.6	192.8	369.2
6	DCS-41, DCS-95, DCS-91, DCS-86, DCS-102, DCS-100, DCS-12, DCS-79, DCS-80, DCS-81, 48-1						**79.3**	112.1	134.3	129.3
7	DCS-89, DCS-53, DCS-68, DCS-36, DCS-42, Haritha							**63.9**	129.6	211.4
8	DCS-54, DCS-29, DCS-49, DCS-57, DCS-46, DCS-47, DCS-60, DCS-33, DCS-65, DCS-27								**93.8**	134.7
9	DCS-101, DCS-99, DCS-70, DCS-86-1, DCS-38									**85.2**

Table 4. Cluster means of 72 castor genotypes for 14 characters

S. No.	Characters	Cluster								
		1	2	3	4	5	6	7	8	9
1	Days to 50% flowering	28.6	43.8	41.2	56.6	66	53.8	57.3	64.7	66.7
2	Number of nodes to primary	8.9	11.6	12.2	14.6	16.9	15.2	15.7	16.9	16.9
3	Number of nodes to S1	3.7	4.2	4.5	4.6	5.2	4.9	5.1	4.9	5.4
4	Number of nodes to S2	4.4	5.0	5.1	5.3	6.0	5.7	5.9	5.9	6.6
5	Plant height up to primary (cm)	30.5	60.6	59.0	82.8	108.9	86.5	99.1	100.2	109.9
6	Total spike length (cm)	17.2	36.0	30.9	38.1	42.9	36.8	41.1	36.0	36.3
7	Effective spike length (cm)	12.3	30.5	24.8	32.6	38.9	31.7	35.3	29.6	30.4
8	Number of capsules / primary spike	15.2	22.7	27.6	45.2	67.5	26.6	34.0	27.7	17.6
9	Number of effective spikes /plant	15.6	9.0	10.4	9.1	7.0	9.6	8.3	9.5	6.6
10	Seed yield at first picking (kg/ha)	226	153.5	242	123.6	0	0	0	0	0
11	Seed yield at second picking (kg/ha)	226	153.5	242.2	142.4	169.4	122	179.3	61.3	27.6
12	Seed yield at final picking (kg/ha)	839	921	1067	816	792	1152	1406	893.5	1103.5
13	Hundred seed weight (g)	22.3	25.8	22.7	13.8	14.8	27.4	21.1	21.9	29.7
14	Oil content (%)	49.6	45.8	45.3	46.9	43.4	43.3	43.3	46.1	46.9

Sevagaperumal *et al*., 2000, Durgarani *et al.,* 2007) was not dependent on geographical distance. Genetic drift, selection in different environments and the free exchange of seed material also played a role in creating genetic diversity (Bhatt and Reddy, 1987). In the present study, all the 72 genotypes were the end products of the crop improvement programme aimed at generating high yielding genotypes with resistance to major diseases like *Fusarium* wilt, *Botrytis*, leaf hoppers *etc*. (Lavanya *et al*., 2006a). The majority of the genotypes were derived from hybridization between exotic germplasm (EC-169803, Baker, 240) and native germplasm (H-86, HC-8, Aruna, Bhagya, Sowbhagya, TMV-5 *etc.*).

The cluster analysis grouped together, genotypes with greater genetic similarity while the genotypes sharing a common pedigree like EC-169803 x Aruna (as one of the original cross) were grouped into different clusters (Clusters 3, 4, 5, 8, 9) indicating that artificial selection for the duration, plant height, the number of capsules per primary and hundred seed weight and breaking of linkages led to sister lines with diverse morphological characters. The genetic distance between cluster 3 and 5 was high, while the genotypes differed in their yielding ability and flowering duration. Minimum intra cluster distance was found in cluster 3 which included 3 released varieties *viz*., DCS-9, Kranti, Kiran and 2 male lines-DCS-5 and DCS-78 of two hybrids with almost similar morphological characters like red stem color, double bloom, spiny capsules, short height and early maturity (Lavanya and Mukta, 2008). Thus, the mere emphasis on early duration (< 90 DAS) and emphasis on morphological characters like stem color, bloom led to the narrow genetic base and heterosis levels. Instead, the characters *viz*. seed yield, days to 50 per cent flowering and number of capsules on primary spike contributed maximum towards genetic divergence in the present study.

The present study confirmed the earlier findings of the presence of high genetic diversity (Chakrabarty and Banu, 1999, Lakshmamma *et al.,* 2002). Artificial selection, exchange of breeding material, environmental variation in addition to breaking of linkages and independent inheritance of morphological characters played a greater role in generating genotypic diversity.

On the contrary, Allan *et al.* (2008) and Goodarzi *et al*. (2011) reported low genetic diversity in 41 and 12 castor bean germplasm accessions respectively. The authors discussed in length about the probable reasons like use of DNA from open pollinated plants in the wild, genetic drift during rejuvenation, small sample sizes, selective

Table 5. Estimates of general combining ability (*gca)* effect for 3 lines and 13 testers for seed yield and yield component in castor

	Number of nodes to			Plant height	Primary spike length		Number of capsules/ primary	Number of effective spikes	100-seed weight	Seed yield at different pickings			Oil content
	Primary	(S_1)	(S_2)		Total	Effective				First	Second	Final	
Lines													
DPC-9	-1.01 **	-0.25	-0.2	-6.77 **	-1.58	-1.41	-1.79	0.21	0.31	-20.07	-13.98	71.94**	0.54
DPC-17	0.32	0.27	0.25	-7.11 **	-1.93 *	-1.62	-8.19 **	-0.14	-0.16	-8.20	-1.30	0.84	-1.02
M-568	0.69 *	-0.02	-0.05	13.88 **	3.52 **	3.03**	9.98 **	-0.07	-0.15	28.27*	15.28	-72.78	0.48
Testers													
DCS 91	0.28	0.09	-0.14	-6.71	-1.18	-0.90	-2.04	0.03	-0.60	108.02**	153.22**	197.17**	1.19
DCS 92	-0.39	0.04	-0.07	-0.89	-1.45	0.20	-0.71	0.23	0.92	-7.57	12.01	-36.91	1.43
DCS 93	-0.16	-0.11	-0.29	3.44	1.15	1.70	-3.28	-0.29	0.99	73.7**	-19.35	-19.15	-0.61
DCS 94	-0.39	0.20	-0.24	1.64	2.05	0.84	0.66	-0.75	-3.15	55.44*	44.87	210.16**	0.78
DCS 96	-0.76	-0.30	0.25	-0.82	1.25	-2.71	2.92	0.81	-1.25	120.97**	132.36**	259.61**	-0.02
DCS 97	-1.32	-0.20	-0.12	-3.09	0.32	2.02	-2.91	0.38	-0.68	-13.94	-30.88	117.83**	-0.29
DCS 98	1.38	-0.10	-0.05	9.41	3.32	4.49*	-0.84	-0.27	-1.18	131.97**	-186.26	-537.8	1.53
DCS 103	0.24	-0.10	0.03	-2.29	-0.35	0.20	-0.91	-0.22	3.42*	-32.35	-134.44	-217.39	-2.20
DCS 104	-0.62	-0.03	0.10	-4.42	-0.78	-0.76	2.01	-0.49	-3.00	53.45*	-20.63	239.03**	0.50
KIRAN	-0.52	0.37	0.38	2.14	-0.11	0.07	-2.43	-0.54	0.20	-16.41	41.79	-73.81	1.07
DCS 106	0.34	-0.10	0.63	6.01	-1.05	-0.21	-5.38	-0.19	-0.48	62.96*	46.07	-108.77	-0.40
DCS-119	3.14	0.12	0.00	2.48	-4.71	-5.03	11.52**	1.20*	-0.33	51.49*	-44.50	18.08	-1.36
DCS-120	-1.22	0.10	-0.47	-6.92	1.52	0.10	1.41	0.10	5.14**	33.50	5.74	-48.05	-1.60

* Significant at 5 per cent level; ** Significant at 1 per cent level

cultivation, domestication, and anthropogenic influence. Similar reports on low genetic variation following domestication due to intense selection for favorable traits were also reported by Hyten *et al*. (2006), Zhu *et al*. (2007), Harlan, (1987) in soybean, rice and hard red winter wheat, respectively. Similar results on low genetic diversity which was not geographically structured were also reported in 8 castor cultivars using SNP markers (Foster *et al.,* 2010) as a consequence of a genetic bottleneck due to domestication. Reports on such low genetic diversity in a monotypic genus like castor bean throw a challenge to the plant breeders worldwide for intensification of research efforts on the creation of inter generic diversity using related genera of the *Euphorbiaceae* family like *Manihot esculenta* (Gedil *et al*., 2009) and *Jatropha curcus.*

Nine male lines were selected from the Cluster 2 to 4 based on their medium duration (44-57 days to 50% flowering), plant height (59-83 cm), total spike length (31-38 cm), the higher number of spikes per plant (9-11) and seed yield (816-1067 kg/ha) and used in the line x tester study. The analysis of variance for combining ability revealed significant differences among the lines, testers and line x testers for all the traits except for the number of nodes to secondary spike 1, secondary spike 2 and effective spikes per plant. The present study indicated non additive or dominance type of gene action for all the 13 characters under study (**Table 5**). Earlier studies by Solanki and Joshi, 2000, Lavanya and Chandramohan 2003, Tank *et al*., 2003, Solanki *et al*., 2004, Chandramohan *et al*., 2006 and Kanwal *et al.,* 2006, Ramya *et al.,* 2018 reported non-additive or dominant gene action mostly for all components and especially for 100 seed weight and seed yield which were identified as the traits of interest based on the genetic diversity study.

The estimates of *gca* effects revealed that among the 13 testers, DCS-91 and DCS-96 were the best general combiners for seed yield in all the three pickings while DCS-94, DCS-104, DCS-97 were good combiners for seed yield in final picking alone (**Table 6**). The majority of the testers were average combiners for yield contributing characters except for DCS-98 for effective spike length, DCS-119 for the number of capsules per primary spike and the number of effective spikes per plant, DCS-103 and DCS-120 for 100- seed weight. The present study indicated none of the parental lines is good combiners for oil content.

Table 6. Estimates of general and specific combining variances and proportionate gene action for thirteen characters in castor

Character	σ^2gca	σ^2sca	σ^2gca/ σ^2sca
Number of nodes to primary spike	-0.04	7.76	0.01
Number of nodes to secondary spike-1 (S_1)	0.01	0.09	0.11
Number of nodes to secondaryspike-2 (S_2)	0.02	0.14	0.14
Plant height	3.23	126.25	0.02
Total length of primary spike	0.27	11.16	0.02
Effective length of primary spike	0.21	13.20	0.01
Number of capsules per primary spike	1.54	106.02	0.01
Number of effective spike per plant	-0.04	1.14	-0.03
100- Seed weight	0.01	12.68	0.01
Seed yield (First picking)	-84.08	20187.89	-0.01
Seed yield (Second picking)	-204.23	35229.00	-0.01
Seed yield (Final picking)	510.66	102220.00	0.01
Oil content	0.02	3.42	0.01

Among the three lines, DPC-9 was a good general combiner for final seed yield and short plant height. The line M-568 was a good general combiner for the number of nodes to the primary spike, plant height, total and effective primary spike length, the number of capsules per primary spike and seed yield in first picking while DPC-17 was a poor combiner for plant height, total spike length and the number of capsules per primary spike.

The hybrid M-568 x DCS-96 recorded maximum standard heterosis for seed yield over both the checks *viz*., DCH-177 (21%) and DCH-519 (31%) and were also heterotic for the number of capsules per primary spike and oil content. Three other hybrids *viz*., DPC-9 x DCS-94, DPC-9 x DCS-104 and DPC-17 x DCS-91 were significantly superior to high yielding check DCH-177 for cumulative final seed yield. Standard heterosis for seed yield ranged from -59.5 (DPC-9 x DCS-98) to 21 per cent (M-568 x DCS-96) over the best check DCH-177. It is well established in castor that the magnitude of heterosis for seed yield depends on both genetic diversity and individual combining ability of the parents (Liv *et al*., 2012).

The main conclusions from the study are (i) the genotypes from clusters with maximum seed yield (Cluster 7) will be of immediate use and relevance compared to the early

duration checks (DCS-9, Kranti, Kiran) (ii) grouping of genotypes based on grouping characters of DUS testing are independent of the present clustering pattern based on Mahalanobis D^2 and principal component analysis (iii) good general male combiners for seed yield *viz.,* DCS-96, DCS-94, DCS-104, DCS-97 identified from cluster 2 to 5 yielded a heterotic hybrid M-568 x DCS-96 hybrid with 21 per cent standard heterosis over the best check DCH-177.

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