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Genetic analysis of yield and its biometric traits in castor (*Ricinus communis* L.)

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Abstract
The P_1, P_2, F_1, F_2, BC_1 and BC_2 of five castor crosses *viz.*, JM-6 x 48-1, JI-433 x SKI-346, JI-436 x PCS-124, SKI-346 x JI-35 and SKI-346 x SKI-215 were studied for twelve metric traits. The scaling tests revealed the importance of additive-dominance model for number of nodes up to primary raceme in JI-436 x PCS-124. The result of rest of the cases depicted the epistatic digenic model including all types of interactions played a major role for the entire cross combinations. The study revealed the importance of additive and non-additive type of gene action for all the characters studied suggesting the use of reciprocal recurrent selection or biparental mating for improving the characters in castor. Duplicate type epistasis played a greater role than complementary epistasis in most of the cases.

Keywords: Castor, generation mean analysis; scaling tests, additive, dominance, epistatic gene

Introduction
Castor (*Ricinus communis* L.) is grown in tropical, sub-tropical and temperate regions of world. Castor is highly cross pollinated crop and being a sexually polymorphic species with different sex forms *viz*., monoecious, pistillate and pistillate with interspersed staminate flowers (ISF). The breeding method to be adopted depends mainly on the nature of gene action involved in the expression of the quantitative traits. Line x tester analysis is used to select the parents based on their combining ability but fails to detect the epistasis which remains the most complex problem and on which it is extremely difficult to obtain reliable results. The epistasis can be detected by the analysis of generation means using the scaling tests, whether it is additive x additive, additive x dominance and dominance x dominance type of gene interaction at the digenic level. After confirmation of epistasis, joint scaling test of six parameter model m, (d), (h), (i), (j) and (l) can be applied. Therefore, in this context, the objective of the present study was to obtain information on the gene effects to provide a basis of selection in a breeding programme for the improvement of castor.

Material and Methods
The experimental material was comprised of five castor crosses *viz.*, JM-6 x 48-1, JI-433 x SKI-346, JI-436 x PCS-124, SKI-346 x JI-35 and SKI-346 x SKI-215, each with six basic generations *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2. The experiment was laid out in Compact Family Block Design with three replications at Main Oilseeds Research Station, Junagadh Agriculture University, Junagadh (Gujarat). The single row plot was sown for both parents and their F_1's, four rows for each F_2 generation and two rows for each backcross during *Kharif* 2018-19. The seed was dibbled with 120 cm and 60 cm as inter and intra row spacing, respectively and with 6 m of row length. All the recommended cultural and plant protection practices were followed to raise good crop. The data were recorded on individual plant basis in each replication on randomly selected five competitive plants in each of parents and F_1's, 10 plants in each of backcross and 20 plants in F_2 generations for 12 characters. The data were first subjected to estimates of individual scaling tests A, B, C and D of Mather (1949) [5] and joint scaling test of Cavalli (1952) [1] to detect the presence of epistasis. The gene effects were estimated using the models suggested by Jinks and Jones (1958) [4]. The significance of the scales and gene effects were tested by using the t-test (Singh and Chaudhary, 2004) [9].

Results and Discussion
The analysis of variance between families revealed that the mean squares due to crosses were significant for all the characters. The analysis of variance revealed significant differences among six basic generation means for all the characters studied in all the five crosses except oil content in JI-433 x SKI-346 (Table 1). This character which failed to show significant variation among the generations was not subjected to further statistical analysis.

The estimates of genetic parameters for different characters recorded in five crosses are presented in Table 2.

The significance of any one, two or all the four individual scaling tests A, B, C or D in all the crosses for all traits indicated adequacy of epistasis model. This was also confirmed by joint scaling test showing significant chi-square values for these cases, indicating involvement of digenic interaction parameters in the inheritance of these characters. The joint scaling test was found to be more efficient in detection of epistasis compared to individual scaling tests. As the simple additive-dominance model failed to explain the variation among generation means for these traits, six parameter model proposed by Jinks and Jones (1958) [5] was employed.

On the basis of six parameter model, primary effects *viz.,* m, (d), (h) and all the three digenic interactions *viz.*, (i), (j) and (l) were significant for days to maturity of primary raceme, plant height up to primary raceme, number of nodes up to primary raceme, number of capsules on primary raceme and 100-seed weight in JM-6 x 48-1; for total length of primary raceme and 100-seed weight in JI-433 x SKI-346; for plant height up to primary raceme, number of effective branches per plant, 100-seed weight and seed yield per plant in JI-436 x PCS-124; for days to flowering of primary raceme, days to maturity of primary raceme, plant height up to primary raceme, total length of primary raceme, effective length of primary raceme, 100-seed weight and seed yield per plant in SKI-346 x JI-35; for days to flowering of primary raceme in SKI-346 x SKI-215 indicated the involvement of additive, dominance as well as epistasis gene action for controlling these traits.

For the characters where evidence of digenic epistatic interaction was obtained, both additive and non-additive effects were significant for days to maturity of primary raceme, plant height up to primary raceme, number of nodes up to primary raceme, total length of primary raceme, effective length of primary raceme, number of effective branches per plant, number of capsules on primary raceme, shelling out turn, 100-seed weight, seed yield per plant and oil content in JM-6 x 48-1; days to flowering of primary raceme, number of nodes up to primary raceme, total length of primary raceme, effective length of primary raceme, number of capsules on primary raceme, shelling out turn, 100-seed weight and seed yield per plant in JI-433 x SKI-346; days to flowering of primary raceme, plant height up to primary raceme, number of effective branches per plant, number of capsules on primary raceme, shelling out turn, 100-seed weight, seed yield per plant and oil content in JI-436 x PCS-124; days to flowering of primary raceme, days to maturity of primary raceme, plant height up to primary raceme, total length of primary raceme, effective length of primary raceme, number of effective branches per plant, shelling out turn, 100-seed weight and seed yield per plant in SKI-346 x JI-35 and days to flowering of primary raceme, days to maturity of primary raceme and number of effective branches per plant in SKI-346 x SKI-215. The importance of additive and dominance effects was also observed by Patel (1996) [6], Gondaliya *et al.* (2001), Golakia *et al.* (2004), Patel (2005) [7], Patel and Pathak (2010) [8] and Virani *et al.* (2013) [10] for days to flowering up to primary raceme, days to maturity of primary raceme, plant height up to primary raceme, number of nodes up to primary raceme, total length of primary raceme, effective length of primary raceme, number of effective branches per plant, number of capsules on primary raceme, shelling out turn, 100-seed weight, seed yield per plant and oil content. The classification of gene action showed importance of duplicate type of gene action for most of the characters in most of the crosses.

Table 1: Analysis of variance (mean squares) between families and between progenies within families of six generations for different characters in castor

Source of variation	d.f	Days to flowering of primary raceme	Days to maturity of primary raceme	Plant height up to primary raceme	Number of nodes up to primary raceme	Total length of primary raceme	Effective length of primary raceme	Number of effective branches per plant	Number of capsules on primary raceme	Shelling out Turn	100-seed weight	Seed yield per plant	Oil content
Analysis of variance between families													
Replications	2	0.256	0.095	0.240	0.012	0.152	0.071	0.004	0.059	0.107	0.011	0.212	0.110**
Crosses	4	618.894**	763.044**	2210.874**	58.982**	118.555**	107.506**	6.828**	1372.452**	20.956**	47.725**	3849.669**	0.121**
Error	8	0.170	0.182	0.665	0.013	0.065	0.034	0.007	0.069	0.126	0.003	0.459	0.006
χ^2		NS	NS	NS	S	NS	NS	NS	NS	NS	NS	NS	NS
Analysis of variance between progenies within families													
JM-6 x 48-1 (cross 1)													
Replications	2	1.151	0.558	3.521	0.043	0.605	0.126	0.101	0.288	0.8593	0.048*	2.192	0.195
Generations	5	3228.665**	5748.868**	4481.674**	203.689**	702.066**	713.111**	18.558**	14732.598**	6.5072**	20.198**	8138.828**	0.178*
Error	10	0.382	0.647	2.263	0.399	0.551	0.443	0.063	0.619	0.4405	0.010	1.769	0.051
JI-433 x SKI-346 (cross 2)													
Replications	2	0.277	1.003	7.196*	0.102	1.101	0.342	0.011	0.055	1.382**	0.015	2.569	0.303
Generations	5	190.260**	267.634**	91.757**	8.401**	105.101**	117.849**	0.770**	2743.851**	64.226**	7.542**	2501.713**	0.287
Error	10	1.034	0.333	1.466	0.050	0.845	0.678	0.069	0.276	0.131	0.061	1.910	0.089
JI-436 x PCS-124 (cross 3)													
Replications	2	0.487	1.426*	1.554	0.051	0.451	0.451	0.077	0.651	0.342	0.002	1.884	0.206*
Generations	5	18.959**	36.712**	68.611**	0.655**	53.213**	53.213**	4.771**	209.042**	29.012**	15.387**	1677.069**	0.620**
Error	10	0.728	0.288	0.453	0.072	0.924	0.924	0.055	0.443	0.441	0.079	2.947	0.034
SKI-346 x JI-35 (cross 4)													
Replications	2	2.512	1.033	1.112	0.167	0.037	0.037	0.003	0.143	0.172	0.058	0.883	0.047
Generations	5	204.561**	372.364**	208.656**	1.738**	307.133**	307.133**	3.687**	4442.898**	5.130**	8.244**	2728.533**	0.173**
Error	10	0.678	0.628	1.128	0.286	0.780	0.780	0.023	0.235	0.164	0.054	1.404	0.028
SKI-346 x SKI-215 (cross 5)													
Replications	2	1.193	0.923	4.012	0.008	0.282	0.282	0.006	0.871*	0.899	0.012	4.767	0.043
Generations	5	141.212**	128.878**	281.097**	1.227**	133.696**	133.696**	11.876**	4006.441**	3.905**	30.513**	4587.552**	0.105*
Error	10	0.522	0.473	2.244	0.062	0.502	0.502	0.032	0.189	0.447	0.054	2.432	0.023

* and ** significant at 5 and 1 per cent levels, respectively

Table 2: Estimate of scaling tests and gene effects for different characters of five crosses in castor

Cross	Individual scaling tests				Joint scaling test	m	(d)	(h)	(i)	(j)	(l)	Type of Epistasis
	A	B	C	D								
Days to flowering of primary raceme												
C_1	**	**	**	*	**	82.37**± 6.33	40.77**± 0.25	1.03 ± 14.65	14.00* ± 6.33	17.47**± 1.66	-8.13 ± 8.54	D
C_2	**	**	**	-	**	58.37**±1.61	-10.50**±0.30	-19.90**±3.92	1.60 ±1.58	5.07**±0.56	13.73**±2.41	D
C_3	**	**	-	**	**	41.17**±2.13	-3.17**±0.20	23.70**±5.23	8.40**±2.12	0.60 ±0.69	-17.47**±3.25	D
C_4	**	*	-	**	**	77.77**±2.11	10.17**±0.23	-55.70**±5.12	-14.13**±2.10	-6.17**±0.68	30.33**±3.13	D
C_5	**	**	-	**	**	85.40**±2.53	7.80**±0.32	-72.33**±5.86	-20.67**±2.51	-5.70**±0.71	42.87**±3.47	D
Days to maturity of primary raceme												
C_1	**	**	**	**	**	92.60**±8.03	51.87**±0.19	122.80**±17.17	65.80**±8.03	23.60**±1.36	-98.47**±9.37	D
C_2	**	**	**	**	**	106.63**±1.76	-12.70**±0.25	-3.10 ±4.27	4.67**±1.74	5.67**±0.58	-3.73 ±2.63	C
C_3	**	-	-	-	**	113.97**±6.78	-2.30**±0.24	-25.77 ±13.78	-6.60 ±6.78	-4.23**±0.57	13.60 ±7.05	D
C_4	**	-	*	**	**	124.17**±2.16	14.17**±0.18	-43.03**±5.05	-11.13**±2.15	-3.00**±0.60	17.53**±3.01	D
C_5	**	**	**	**	**	134.70**±2.50	4.57**±0.22	-64.37**±5.91	-15.40**±2.49	0.83 ±0.73	37.20**±3.52	D
Plant height up to primary raceme												
C_1	**	**	**	**	**	-31.20**±10.85	34.60**±0.90	388.13**±26.97	170.47**±10.81	51.57**±3.64	-232.67**±16.83	D
C_2	**	-	**	-	**	67.30**±4.66	-7.23**±0.55	21.37 ±11.32	1.20 ±4.63	10.53**±1.50	-23.33**±7.06	D
C_3	**	*	**	**	**	39.80**±4.50	-5.13**±0.71	61.60**±11.38	23.53**±4.44	11.10**±1.66	-32.80**±7.25	D
C_4	**	**	**	**	**	41.10**±5.94	-5.30**±0.59	93.03**±14.43	38.80**±5.91	-14.73**±1.88	-47.73**±8.94	D
C_5	-	**	**	-	**	74.63**±6.99	-11.30**±0.66	13.70 ±16.95	11.07 ±6.96	10.33**±2.20	13.73 ±10.45	C
Number of nodes up to primary raceme												
C_1	**	**	**	-	**	6.63**±1.55	9.57**±0.19	37.70**±3.77	20.93**±1.54	5.00**±0.50	-22.80**±2.37	D
C_2	**	**	*	-	**	16.17**±0.88	-2.10**±0.11	-5.30* ±2.13	-1.73* ±0.88	0.03 ±0.28	5.53**±1.31	D
C_3	-	*	-	-	-	12.70**±0.78	0.03 ±0.11	1.83 ±2.08	-	-	-	-
C_4	**	**	**	-	**	15.47**±0.67	0.40**±0.09	-2.87 ±1.64	0.60 ±0.66	0.23 ±0.22	2.27* ±1.06	D
C_5	**	**	**	**	**	16.37**±0.74	-0.10 ±0.14	-4.30* ±1.79	0.07 ±0.72	-0.13 ±0.25	3.67**±1.15	D
Total length of primary raceme												
C_1	**	**	**	-	**	72.10**±5.76	21.83**±0.72	-57.97**±14.45	-10.27 ±5.72	-7.47**±2.03	44.27**±9.13	D
C_2	-	**	-	*	**	64.07**±4.30	-8.67**±0.50	-25.33* ±10.25	-9.73* ±4.27	2.63* ±1.31	17.27**±6.25	D
C_3	**	-	**	-	**	44.47**±2.90	4.93**±0.42	-3.00 ±7.50	-5.27 ±2.87	2.37* ±1.12	0.67 ±4.79	D
C_4	*	**	**	**	**	35.17**±3.50	14.90**±0.48	23.77**±8.36	12.33**±3.47	-4.73**±1.10	-15.00**±5.05	D
C_5	**	*	**	-	**	51.80**±3.67	9.40**±0.66	-13.47 ±9.01	-0.87 ±3.61	-2.93* ±1.29	16.47**±5.65	D
Effective length of primary raceme												
C_1	**	**	**	-	**	68.10**±5.85	21.83**±0.72	-50.63**±14.28	-6.27 ±5.80	-7.27**±1.91	39.33**±8.98	D
C_2	**	**	-	*	**	64.07**±4.07	-8.67**±0.50	-29.93**±9.63	-9.73* ±4.04	0.33 ±1.22	21.87**±5.87	D
C_3	**	-	**	-	**	44.47**±2.90	4.93**±0.42	-3.00 ±7.50	-5.27 ±2.87	2.37* ±1.12	0.67 ±4.79	D
C_4	*	**	**	**	**	35.17**±3.50	14.90**±0.48	23.77**±8.36	12.33**±3.47	-4.73**±1.10	-15.00**±5.05	D
C_5	**	*	**	-	**	51.80**±3.67	9.40**±0.66	-13.47 ±9.01	-0.87 ±3.61	-2.93* ±1.29	16.47**±5.65	D
Cross	**Individual scaling tests**				**Joint scaling test**	**m**	**(d)**	**(h)**	**(i)**	**(j)**	**(l)**	**Type of Epistasis**
	A	**B**	**C**	**D**								
Number of effective braches per plant												
C_1	**	-	-	*	**	7.43**±1.24	-3.30**±0.22	-8.43**±3.01	-3.07* ±1.23	-0.77 ±0.42	4.60* ±1.85	D
C_2	-	-	**	*	**	2.90**±1.10	-0.57**±0.18	4.37 ±2.92	2.20* ±1.08	0.77 ±0.46	-1.47 ±1.92	D
C_3	**	-	-	**	**	10.60**±1.41	-1.13**±0.25	-12.33**±3.44	-5.33**±1.39	-1.27* ±0.49	8.40**±2.10	D
C_4	**	-	*	**	**	3.63**±1.31	0.97**±0.16	7.50* ±3.42	1.20 ±1.30	0.57 ±0.51	-4.87* ±2.18	D
C_5	**	-	**	**	**	3.77**±1.27	-2.30**±0.24	8.83**±3.17	4.40**±1.25	-1.70**±0.47	-3.93 ±2.02	D
Number of capsules on primary raceme												
C_1	-	**	**	**	**	95.17**±3.14	92.70**±0.39	57.57**±7.22	60.67**±3.12	4.67**±0.86	-52.67**±4.25	D
C_2	**	**	**	-	**	139.80**±2.43	-40.00**±0.24	-107.73**±5.69	-1.20 ±2.42	33.33**±0.69	79.47**±3.41	D
C_3	**	**	**	**	**	42.97**±5.00	-4.10**±0.34	49.30**±11.14	29.20**±4.99	-15.70**±1.13	-12.33 ±6.31	D
C_4	**	**	**	**	**	69.63**±4.13	52.70**±0.30	17.63 ±9.72	54.93**±4.12	-18.27**±1.17	29.87**±5.76	C
C_5	**	-	**	**	**	89.23**±3.42	54.10**±0.20	-3.37 ±7.96	32.00**±3.42	-33.20**±0.92	30.80**±4.69	D
Shelling out turn												
C_1	**	-	-	**	**	56.36**±2.03	-1.96**±0.16	17.48**±4.61	7.10**±2.02	0.72 ±0.51	-10.93**±2.70	D
C_2	-	**	*	**	**	49.92**±2.88	-5.47**±0.19	26.50**±6.88	8.81**±2.87	-1.33 ±0.86	-12.34**±4.12	D
C_3	-	*	-	**	*	51.04**±2.37	-3.80**±0.20	20.57**±5.90	6.26**±2.36	0.01 ±0.81	-10.72**±3.63	D
C_4	**	*	-	-	**	60.24**±1.80	1.47**±0.14	11.15* ±4.56	3.12 ±1.79	0.54 ±0.64	-8.63**±2.86	D
C_5	**	-	-	-	**	63.60**±2.13	-1.47**±0.16	7.59 ±5.21	2.55 ±2.12	2.27**±0.68	-6.37* ±3.20	D
100-seed weight												
C_1	**	**	**	**	**	29.03**±0.92	3.65**±0.07	13.63**±2.45	3.73**±0.92	-0.77* ±0.37	-10.05**±1.57	D
C_2	-	**	**	**	**	28.75**±0.95	-1.80**±0.13	-8.54**±2.36	-4.61**±0.94	-1.24**±0.33	3.65* ±1.48	D
C_3	**	-	**	**	**	18.03**±0.68	1.30**±0.12	21.84**±1.75	5.90**±0.67	3.93**±0.27	-14.28**±1.15	D
C_4	**	**	**	**	**	16.29**±0.75	2.09**±0.12	17.62**±1.95	6.95**±0.74	-3.96**±0.29	-9.34**±1.25	D
C_5	-	**	**	**	**	27.37**±0.92	-4.41**±0.09	1.03 ±2.38	2.75**±0.91	0.55 ±0.35	0.01 ±1.50	C
Seed yield per plant												
C_1	**	-	**	-	**	221.90**±23.33	58.83**±0.38	-213.90**±52.15	-19.47 ±23.33	-103.73**±5.30	253.20**±29.61	D
C_2	**	**	-	**	**	60.50**±10.85	-38.97**±0.29	161.47**±25.62	49.93**±10.85	4.02 ±3.05	-90.97**±15.15	D
C_3	**	**	**	**	**	212.83**±12.92	-31.40**±0.23	-157.73**±30.16	-76.17**±12.91	40.43**±3.49	109.77**±17.69	D

C_4	**	**	**	**	**	25.03**±8.70	-9.80**±0.25	421.23**±22.33	142.17**±8.70	9.12**±3.13	-210.93**±13.92	D
C_5	**	**	**	-	**	196.50**±11.39	-38.90**±0.32	-55.23 ±28.64	-1.33 ±11.38	-4.43 ±3.89	122.67**±17.66	D
Oil content												
C_1	**	*	-	**	**	47.02**±0.35	0.17**±0.05	4.61**±0.91	1.64**±0.35	0.17 ±0.23	-3.04**±0.62	D
C_2	-	-	-	-	-	-	-	-	-	-	-	-
C_3	*	-	-	*	**	47.21**±0.45	-.0.64**±0.08	2.83**±1.03	0.96* ±0.44	0.20 ±0.13	-1.60**±0.60	D
C_4	**	*	**	-	**	48.50**±0.33	0.16**±0.05	1.22 ±0.81	-0.07 ±0.33	0.13 ±0.11	-1.04* ±0.51	D
C_5	-	**	**	-	**	48.55**±0.35	-0.21**±0.06	-0.02 ±0.92	0.19 ±0.34	0.21 ±0.14	0.50 ±0.58	D

Conclusion

Seed yield per plant in most of the crosses was observed to be governed by both additive and non-additive gene effects. Reciprocal recurrent selection would be ideal method which would facilitate exploitation of both additive and dominance gene effects simultaneously. Under a situation of duplicate type of gene interaction, it would be difficult for the breeder to get promising segregants better than the parent involved through conventional breeding method such as making simple crosses and their exploitation through straight pedigree method. While in case of complementary type of epistasis interaction namely dominance x dominance (l) along with dominance (h) were found higher in few traits in respective crosses under this study. Such type of non-additive gene effect may be exploited by heterosis breeding for castor.

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