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Genetic architecture for seed yield and oil content in castor (*Ricinus communis* L.)

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Abstract
The present investigation was undertaken with a view to generate genetic information on gene effects for seed yield and oil content in Castor (*Ricinus communis* L.). The experimental materials consisted of twelve generations, namely P_1, P_2, F_1, F_2, B_1, B_2, B_{11}, B_{12}, B_{21}, B_{22}, $B_{1(s)}$ and $B_{2(s)}$ of five crosses *viz*., JM 6 x 48-1 (cross I), JI 433 x SKI 346 (cross II), JI 436 x PCS 124 (cross III), SKI 346 x JI 35 (cross IV) and SKI 346 x SKI 215 (cross V). Significance of simple scaling tests and Cavali's joint scaling test indicated the presence of gene interactions for seed yield per plant (g) and oil content (%) in all five crosses. Based on six-parameter model, significant $\chi^2_{(2)}$ pointed out the presence of trigenic or higher order epistasis in all the crosses for seed yield per plant and oil content. The trigenic ten-parameter model was found to be adequate for seed yield per plant in cross III and cross IV; and for oil content in cross IV. On other hand, $\chi^2_{(3)}$ with two degrees of freedom was found significant for seed yield per plant in cross I, II and V; and for oil content in cross I, II, III and V showing the presence of higher order epistasis and/or linkage.

Keywords: Castor, epistasis, gene effect, linkage, seed yield, oil content

Introduction
Castor is short-lived small tree or shrub with soft wood and hollow stems which can grow to 5 m or more. Its bark is greenish to reddish brown and smooth. Leaves are palmately and deeply lobed with serrate leaf margins; long-stalked, alternate, dark green or even reddish. Its flowers are crowded on upright spikes up to 40 cm long; both sexes occur on the same plant; the upper female flowers appear before the lower male ones. Its fruits are round, deep red, prickly capsules, in dense clusters; containing three tick-like, brown or reddish-brown marbled, very poisonous seeds with high oil content (Rana *et al*., 2012) [10].

Traditionally, the plant has been used for the treatment of various diseases in traditional or folk remedies throughout the world. The extracted oil has been used for many centuries as a purgative (strongly laxative). It is one of the safest and most reliable purgatives which relieve obstinate constipation. The leaves have been also recommended in the form of a decoction or poultice, as an application to the breasts of women to increase the secretion of milk. In traditional medicine, the leaves and seeds are used as a laxative, for wound dressing, against rheumatism and mental illness (Singh & Geetanjali, 2015) [12].

The individual parts of the plant such as the seed, seed oil, leaves and the roots showed their importance in pharmacology. Due to the presence of important phytochemical constituents like flavonoids, glycosides, alkaloids, steroids, terpenoids, etc., this plant is reported to possess antioxidant, anti-inflammatory, anti-diabetic, central analgesic, anti-tumor, anti-nociceptive, anti-asthmatic activity and other medicinal properties (Jombog & Enenebeaku, 2008; Singh & Geetanjali, 2015) [7, 12]. Castor seed is the source of castor oil, colourless to a very pale yellow liquid with mild or no odour or taste, which has over 1000 industrial uses and because of this its demand increases with increase in industrialization (Ojo & Bello, 2004) [9].

The information on the nature of gene action could be helpful in predicting the effectiveness of selection in a population. A distinct knowledge of the type of gene action, its magnitude and composition of genetic variance are of fundamental importance to a plant breeder which helps in formulating an effective and sound breeding programme. The assessment of the magnitude of gene action for seed yield and oil content in castor is helpful in deciding the appropriate breeding procedures. Hence, experiment was planned to study the gene effects in castor with 12 generations.

Material and Method

The experimental material was comprised of five crosses *viz*., JM 6 x 48-1 (cross I), JI 433 x SKI 346 (cross II), JI 436 x PCS 124 (cross III), SKI 346 x JI 35 (cross IV) and SKI 346 x SKI 215 (cross V) each with twelve basic generations *viz*., P_1, P_2, F_1, F_2, B_1, B_2, B_{11}, B_{12}, B_{21},B_{22}, $B_{1(s)}$ and $B_{2(s)}$ were sown in compact family block design with three replications during *Kharif* -2019-20. The plots of various generations contained different number of rows i.e. parents and F_1 in single row; B_1 and B_2 in two rows and F_2, $B_{1(s)}$, B_{11}, B_{12}, $B_{2(s)}$, B_{21} and B_{22} in four rows. Each row was of 6.0 m in length with 120 cm and 60 cm inter and intra row spacing, respectively. All the recommended agronomical practices and necessary plant protection measures were followed timely to raise good crop of castor. The observations were recorded on individual plant basis in each replication on five competitive and randomly selected plants from P_1, P_2 and F_1, ten plants from backcross (B_1 and B_2) and twenty plants from F_2, B_{11}, B_{12}, B_{21}, B_{22}, $B_{1(s)}$and $B_{2(s)}$ generations for seed yield per plant (g) and oil content (%). The oil content was estimated by Nuclear Magnetic Resonance (NMR) technique. The inheritance of seed yield per plant and oil content was computed through generation mean analysis methods (Mather, 1949; Hayman & Mather, 1955; Hayman, 1958 and Hill, 1966) [8, 5, 4, 6]. The $\chi^2_{(1)}$ of joint scaling test under three-parameter model gives idea about fitness of additive-dominance model. In addition to six generations and six parameter model given by Hayman (1958) [4], the data were subjected to ten-parameter model given by Hill (1966) [6]. He proposed estimation of first order and second order epistasis utilizing twelve generations including double backcross generations. The $\chi^2_{(2)}$ and $\chi^2_{(3)}$ values were estimated under six-parameter model at six degrees of freedom and for ten-parameter model at two degrees of freedom, respectively. This is an additional advantage of using twelve generations and ten-parameter model as it provides sufficient degree of freedom for testing validity and goodness of fit for different models. The results of models given by Hayman (1958) [4] and Hill (1966) [6] were compared whenever six-parameter model was satisfactory for inheritance of the trait.

Results and Discussion

The data were initially subjected to simple scaling tests A, B, C and D. Significant estimates of any one or more of these tests indicate the presence of digenic interactions. Further, simple scaling tests B_{11}, B_{12}, B_{21}, B_{22}, $B_{1(s)}$ and $B_{2(s)}$ given by (Hill, 1966) [6] and X and Y given by (Van Der Veen, 1959) [13] were also computed. Significant estimate of the test(s) given by Hill (1966) [6] shows the contribution of particular generation to higher order epistasis which is indirectly indicating the presence of epistasis. If any of the Van Der Veen's tests deviate significantly from zero indicates the presence of trigenic or higher order epistasis. The results of simple scaling tests were further confirmed by joint scaling test (Cavalli, 1952) [2], which effectively combines the whole set of simple scaling tests. Thus, it offers a more general, convenient, adoptable and informative approach for estimating gene effects and also for testing adequacy of additive-dominance model. The $\chi^2_{(1)}$ test with nine degrees of freedom; $\chi^2_{(2)}$ at six degrees of freedom and $\chi^2_{(3)}$ at two degrees of freedom was applied to test the fitness of three parameter model, six parameter model and ten parameter model, respectively. The ten parameter model was used to estimate higher order epistasis (Hill, 1966) [6]. To draw inference on adequacy of ten parameter model, chi-square test $\chi^2_{(3)}$ at two degrees of freedom was applied. The character and cross wise results of seed yield per plant and oil content presented in Table 1 and 2.

Out of all the scaling tests such as A, B, D, B_{11} B_{21}, B_{22} and $B_{1(s)}$ were significant in

cross I; B_{11}, B_{12}, B_{22} and $B_{2(s)}$ were significant in cross II; B_{11} $B_{1(s)}$, X and Y were significant in cross III; A, D, B_{22}, $B_{2(s)}$, X and Y were significant in cross IV and A, B, C, D, B_{11}, B_{12}, B_{21}, $B_{1(s)}$ and Y were significant in cross V for seed yield per plant and for oil content scaling tests such as A, D, B_{22}, X and Y were significant in cross I; C, D, B_{22}, B_{1s}, B_{2s}, X and Y were significant in cross II; B, D, B_{11}, $B_{1(s)}$ and $B_{2(s)}$ were significant in cross III; A, B, D, B_{11}, B_{21}, B_{22}, $B_{1(s)}$, $B_{2(s)}$, X and Y were significant in cross IV and A, B, C, B_{11}, B_{12}, B_{21}, B_{22}, $B_{1(s)}$, X and Y were significant in cross V indicating the presence of digenic and trigenic interactions. Under additive-dominance model estimates of 'm' and additive [d] gene effects were found significant in cross I and cross V; only 'm' were found significant in cross II and cross III; 'm' and dominance [h] were found significant in cross IV for seed yield per plant and for oil content all the three parameter 'm', additive [d] and dominance [h] of three-parameter model were significant in all five crosses. The $\chi^2_{(1)}$ values with nine degrees of freedom of joint scaling test was significant in all the five crosses in both character resulting to the failure of additive-dominance model which indirectly pointed out the presence of epistasis. Cockerham (1959) [3] postulated that the epistatic gene action is common in the inheritance of quantitative traits and there is no sound biological reason why this type of gene action should be less common for these traits.

When the simple additive-dominance model failed to explain the variation among generation means, a six-parameter perfect fit model involving three digenic interactions ([i], [j] and [l]) proposed by Hayman (1958) [4] was applied. This model utilized only six basic generations *viz*., P_1, P_2, F_1, F_2, B_1 and B_2. On the other hand, based on weighted least square technique, digenic interaction model of Hill (1966) [6] was also tested which had provision of testing the adequacy of model with six degrees of freedom besides being utilizing means of all the twelve generations. The goodness of fit for six-parameter model of Hayman (1958) [4] could not, however, be tested in the present study owing to no degrees of freedom left for testing chi-square estimates for seed yield per plant and oil content. Hence, the present study was planned and executed with means of twelve generations and model of Hill (1966) [6] was tested in which six degrees of freedom left for testing the adequacy of six-parameter model of Hill (1966) [6]. According to the six-parameter model of Hill, 'm', dominance [h] and digenic ([j] and [l]) gene effects were found significant in cross I; 'm', additive [d] and digenic [j] were found significant in cross II; 'm' and digenic [l] were found significant in cross III; 'm', dominance [h] and digenic [l] were found significant in cross IV and 'm', additive [d], dominance [h], digenic [i] and [l] were found significant in cross V for seed yield per plant and for oil content gene effects 'm', additive [d] and digenic [j] were found significant in cross I; 'm' and digenic [i] and [l] were found significant in cross II; 'm', additive [d], dominance [h] and digenic [l] were found significant in cross III; 'm', additive [d], dominance [h] and digenic [j] and [l] were found significant in cross IV and

'm', dominance [h] and digenic [i], [j] and [l] were found significant in cross V. The $\chi^2_{(2)}$ value at six degrees of freedom were found significant in all the five crosses for both characters supporting the presence of higher order epistasis.

In ten parameter model, 'm', additive [d], additive x additive [i], additive x additive x additive [w] and additive x dominance x dominance [y] were found significant in cross I; dominance [h], additive x additive [i], dominance x dominance [l], additive x additive x dominance [x] and dominance x dominance x dominance [z] were found significant in cross II; 'm', dominance x dominance [l], additive x additive x dominance [x] and additive x dominance x dominance [y] were found significant in cross III; 'm', additive x additive [i] and additive x dominance x dominance [y] were found significant in cross IV and dominance [h], dominance x dominance [l], additive x additive x dominance [x] and additive x dominance x dominance [y] were found significant in cross V for seed yield per plant. The $\chi^2_{(3)}$ value was significant at two degrees of freedom indicating the presence of higher order epistasis and/or linkage in cross I, II and V, while non- significant in cross III and IV indicated the adequacy of ten parameter model and absence of higher order epistasis for seed yield per plant. Ten parameter model, 'm', additive [d], dominance [h], additive x dominance [j], dominance x dominance [l], additive x dominance x dominance [y] and dominance x dominance x dominance [z] were found significant in cross I; all the ten parameter were found significant in cross II and V; 'm', additive [d], additive x dominance [j], additive x additive x additive [w] and additive x additive x dominance [x] were found significant in cross III and 'm', dominance [h], additive x additive [i], dominance x dominance [l], additive x additive x dominance [x], additive x dominance x dominance [y] and dominance x dominance x dominance [z] were found significant in cross IV for oil content. The $\chi^2_{(3)}$ value was significant at two degrees of freedom indicating the presence of higher order epistasis and/or linkage in cross I, II, III and V, while non-significant in cross IV indicated the adequacy of ten parameter model and absence of higher order epistasis for oil content

These findings were further confirmed from the investigations done by several researchers who worked on different kind of gene effects in castor. Bhapkar and D' cruz (1967) [1], Singh *et al.* (2013) [1] and Virani *et al*. (1959) [14] reported that epistasis played a major role in castor beans with high seed yield and oil content. The opposite signs of either two or all the three gene effects *viz*., dominance [h], dominance x dominance [l] and dominance x dominance x dominance [z] gene effects suggests the presence of duplicate type of epistasis. In present study, duplicate epistasis was observed in all the crosses for seed yield per plant and oil content.

Table 1: Scaling tests and estimation of gene effects for seed yield per plant (g) in five crosses of castor

Scaling tests / gene effects	JM - 6 x 48-1 (cross 1)			JI-433 x SKI-346 (cross 2)			JI-436 x PCS-124 (cross 3)			SKI-346 x JI-35 (cross 4)			SKI-346 x SKI-215 (cross 5)		
A	140.81**	±	50.44	-5.09	±	20.14	32.15	±	28.13	82.34*	±	38.68	-163.24**	±	48.03
B	106.94**	±	36.20	-10.06	±	21.41	-10.89	±	25.25	29.46	±	32.99	-182.36**	±	42.82
C	49.26	±	59.17	-22.69	±	33.19	65.44	±	51.90	-14.70	±	39.82	-228.61*	±	87.19
D	-99.24**	±	35.15	-3.77	±	16.30	22.09	±	27.90	-63.25*	±	25.33	58.49*	±	27.17
B_{11}	-154.85*	±	63.58	-64.06*	±	28.68	107.45*	±	44.82	10.06	±	51.90	239.75**	±	61.31
B_{12}	37.69	±	55.07	91.76**	±	32.06	-49.42	±	49.64	21.18	±	48.30	447.26**	±	116.34
B_{21}	-168.45*	±	66.88	-4.45	±	30.83	-46.37	±	38.86	-22.33	±	50.25	544.09**	±	116.25
B_{22}	-95.00*	±	43.38	109.47**	±	41.35	-22.19	±	42.15	-193.39**	±	45.40	110.23	±	88.16
B_{1S}	-430.98**	±	144.33	1.08	±	55.54	182.30*	±	80.58	43.94	±	91.48	389.72**	±	141.53
B_{2S}	-75.87	±	86.76	214.31**	±	70.93	-146.16	±	89.34	-384.46**	±	91.26	39.34	±	118.39
X	36.57	±	18.75	-19.33	±	10.13	31.65*	±	15.87	61.74**	±	16.69	8.17	±	24.26
Y	29.77	±	25.11	10.48	±	13.52	-45.26*	±	19.36	45.54*	±	21.17	160.34**	±	44.56
Three parameter model															
m	155.64**	±	6.22	106.45**	±	5.31	112.77**	±	4.97	117.42**	±	6.07	130.82**	±	5.74
(d)	31.48**	±	5.99	-6.34	±	5.36	-1.61	±	4.67	5.20	±	5.63	11.09*	±	5.21
(h)	-22.62	±	11.96	10.28	±	10.18	6.37	±	9.99	34.90**	±	12.23	2.47	±	11.44
$\chi^2_{(1)}$ (9 df)	29.39**			16.06*			21.44*			39.31**			23.17**		
Six parameter model (Hayman 1958) [4]															
m	156.97**	±	11.22	110.14**	±	5.97	142.82**	±	11.45	119.27*	±	6.19	165.43**	±	10.63
(d)	29.64	±	27.05	-23.73*	±	11.10	35.04*	±	15.93	56.63*	±	22.09	36.44*	±	16.90
(h)	205.29**	±	72.89	20.58	±	34.59	-60.17	±	57.12	179.03**	±	53.01	27.00	±	66.34
(i)	198.47**	±	70.29	32.61**	±	7.54	-44.17**	±	15.81	126.50*	±	50.66	-116.98*	±	54.34
(j)	16.93	±	28.71	2.48	±	13.26	21.51	±	17.67	26.43	±	23.69	9.55	±	18.35
(l)	-446.21**	±	123.33	7.60	±	55.45	22.91	±	82.19	-238.30*	±	96.93	462.58**	±	110.33
Digenic and trigenic interactions															
m	108.57**	±	25.91	83.45**	±	11.22	122.44**	±	19.63	82.09**	±	20.69	267.81**	±	29.22
(d)	6.82	±	8.04	-13.98**	±	4.60	-1.81	±	6.51	11.32	±	7.03	26.19**	±	6.52
(h)	244.31**	±	76.55	50.96	±	36.75	18.23	±	55.86	151.78*	±	63.86	-347.94**	±	85.95
(i)	34.58	±	24.98	20.02	±	10.95	-0.19	±	19.80	21.79	±	20.09	-115.53**	±	28.69
(j)	105.00**	±	28.69	46.50**	±	14.32	2.90	±	23.64	-2.46	±	25.00	-44.69	±	23.29
(l)	-232.69**	±	60.95	-22.74	±	31.70	-10.57**	±	3.79	-103.86*	±	51.55	250.13**	±	71.47
$\chi^2_{(2)}$ (6 df)	19.99**			18.62**			24.29**			41.33**			22.78**		
m	220.45**	±	73.92	37.29	±	32.70	120.99*	±	58.68	163.18**	±	49.86	63.92	±	81.65
(d)	132.05*	±	57.06	-15.80	±	21.95	-67.02	±	40.60	-48.12	±	41.89	-70.76	±	62.16
(h)	-286.48	±	378.55	322.42*	±	140.83	56.33	±	340.42	-192.47	±	251.59	808.76*	±	400.74

(i)	-80.92*	±	40.11	67.42*	±	32.95	12.59	±	62.83	-67.89*	±	30.11	84.65	±	81.73
(j)	-264.21	±	146.40	83.64	±	66.65	57.46	±	111.87	-36.31	±	118.41	142.54	±	169.34
(l)	432.40	±	577.32	-466.46**	±	178.75	58.89**	±	21.51	241.81	±	394.77	-1808.17**	±	697.81
(w)	-118.85*	±	56.37	-4.30	±	21.00	78.11	±	40.06	75.98	±	41.17	95.48	±	62.00
(x)	360.74	±	220.83	-160.66*	±	80.51	-152.11	±	206.26	302.53*	±	137.63	-530.33*	±	226.22
(y)	332.97**	±	126.25	-57.62	±	62.03	89.59*	±	40.41	237.66*	±	109.46	-90.47	±	149.48
(z)	-226.73	±	283.33	226.03**	±	87.64	-68.49	±	248.37	-65.01	±	202.20	1193.30**	±	382.70
$\chi^2_{(3)}$ (2 df)	7.24*			13.99**			5.49			5.34			8.47*		
Type of epistasis	Duplicate			Duplicate			Duplicate			Duplicate			Duplicate		

*, ** Significant at 5 and 1 percent levels, respectively

Table 2: Scaling tests and estimation of gene effects for oil content (%) in five crosses of castor

Scaling tests / gene effects	JM 6 x 48-1 (cross I)			JI 433 x SKI 346 (cross II)			JI 436 x PCS 124 (cross III)			SKI 346 x JI 35 (cross IV)			SKI 346 x SKI 215 (cross V)		
A	-0.71**	±	0.22	-0.37	±	0.21	-0.09	±	0.22	0.98**	±	0.22	0.41*	±	0.16
B	0.04	±	0.31	-0.20	±	0.15	0.49*	±	0.21	0.89**	±	0.20	-1.50**	±	0.28
C	0.13	±	0.48	-2.36**	±	0.23	-0.33	±	0.40	0.71	±	0.39	-1.42**	±	0.32
D	0.40*	±	0.19	-0.90**	±	0.14	-0.36*	±	0.16	-0.58**	±	0.17	-0.16	±	0.21
B_{11}	0.52	±	0.41	0.13	±	0.40	-1.24**	±	0.33	-1.92**	±	0.39	-0.69*	±	0.27
B_{12}	0.96	±	0.52	0.27	±	0.31	-0.36	±	0.49	-0.80	±	0.46	-0.68*	±	0.31
B_{21}	-0.06	±	0.48	0.47	±	0.35	-0.36	±	0.49	-1.84**	±	0.45	1.24**	±	0.35
B_{22}	-2.21**	±	0.65	1.87**	±	0.32	-0.45	±	0.36	-2.46**	±	0.46	5.96**	±	0.28
B_{1S}	0.55	±	0.76	1.83**	±	0.59	-3.22**	±	0.56	-4.92**	±	0.64	-2.08**	±	0.66
B_{2S}	-2.27	±	1.27	1.69**	±	0.54	1.23*	±	0.62	-5.43**	±	0.75	1.06	±	0.56
X	0.94**	±	0.16	-0.48**	±	0.15	-0.20	±	0.12	0.39*	±	0.15	-2.14**	±	0.13
Y	0.65**	±	0.21	-0.32*	±	0.16	0.24	±	0.19	0.44*	±	0.20	-1.18**	±	0.14
Three parameter model															
m	47.82**	±	0.04	47.94**	±	0.03	48.54**	±	0.03	48.32**	±	0.04	47.69**	±	0.03
(d)	0.60**	±	0.03	-0.10**	±	0.03	-0.52**	±	0.03	-0.40**	±	0.04	0.31**	±	0.03
(h)	0.58**	±	0.08	0.41**	±	0.06	0.61**	±	0.07	0.78**	±	0.08	0.40**	±	0.05
$\chi^2_{(1)}$ (9 df)	65.28**			139.53**			93.65**			121.22**			645.66**		
Six parameter model (Hayman 1958) [4]															
m	48.13**	±	0.08	47.75**	±	0.04	48.66**	±	0.06	48.50**	±	0.07	47.74**	±	0.07
(d)	0.59**	±	0.11	-0.20	±	0.11	-0.94**	±	0.10	-0.32**	±	0.10	0.69**	±	0.15
(h)	0.28	±	0.42	2.17**	±	0.30	1.37**	±	0.35	2.00**	±	0.37	0.40	±	0.42
(i)	-0.80*	±	0.38	1.80**	±	0.29	0.73*	±	0.32	1.16**	±	0.34	0.33	±	0.42
(j)	-0.38*	±	0.16	-0.09	±	0.12	-0.29*	±	0.11	0.04	±	0.12	0.95**	±	0.16
(l)	1.47*	±	0.65	-1.23*	±	0.51	-1.12*	±	0.56	-3.03**	±	0.57	0.77	±	0.67
Digenic and trigenic interactions															
m	47.95**	±	0.16	47.68**	±	0.14	48.36**	±	0.14	48.33**	±	0.17	49.56**	±	0.15
(d)	0.44**	±	0.07	-0.02	±	0.05	-0.52**	±	0.04	-0.45**	±	0.05	0.03	±	0.04
(h)	-0.23	±	0.52	0.25	±	0.42	1.44**	±	0.44	1.90**	±	0.50	-4.96**	±	0.41
(i)	0.05	±	0.15	0.54**	±	0.14	0.11	±	0.14	-0.29	±	0.17	-1.70**	±	0.15
(j)	0.57*	±	0.23	-0.09	±	0.18	0.01	±	0.16	0.40*	±	0.18	1.69**	±	0.18
(l)	0.84	±	0.45	0.63*	±	0.31	-0.83*	±	0.38	-1.60**	±	0.41	3.67**	±	0.29
$\chi^2_{(2)}$ (6 df)	55.53**			63.61**			87.53**			56.65**			411.22**		
m	46.95**	±	0.48	49.77**	±	0.37	48.95**	±	0.38	50.23**	±	0.46	52.28**	±	0.44
(d)	1.36**	±	0.35	-0.83**	±	0.30	0.99**	±	0.26	-0.29	±	0.35	-2.65**	±	0.31
(h)	5.83*	±	2.51	-10.90**	±	1.90	-2.05	±	2.10	-8.02**	±	2.44	-21.47**	±	2.36
(i)	0.70	±	0.48	-1.61**	±	0.37	-0.53	±	0.39	-2.32**	±	0.46	-4.24**	±	0.45
(j)	-3.91**	±	0.99	2.88**	±	0.93	-2.91**	±	0.80	-1.00	±	1.02	12.06**	±	0.82
(l)	-9.91*	±	3.91	17.85**	±	3.04	3.59	±	3.40	11.66**	±	3.85	32.24**	±	3.63
(w)	-0.40	±	0.34	0.73*	±	0.30	-1.62**	±	0.26	-0.07	±	0.34	2.37**	±	0.31
(x)	-1.91	±	1.48	6.50**	±	0.99	3.03*	±	1.19	7.42**	±	1.34	8.06**	±	1.40
(y)	5.34**	±	0.93	-3.20**	±	0.97	0.81	±	0.79	2.12*	±	1.00	-13.35**	±	0.82
(z)	5.92**	±	1.97	-8.20**	±	1.53	-1.36	±	1.79	-5.07**	±	1.95	-14.93**	±	1.74
$\chi^2_{(3)}$ (2 df)	12.73**			8.67*			13.38**			2.52			10.93**		
Type of epistasis	Duplicate			Duplicate			Duplicate			Duplicate			Duplicate		

*, ** Significant at 5 and 1 percent levels, respectively

Conclusion

It can be concluded from the present study that seed yield per plant and oil content recorded in five castor crosses were governed by additive, dominance and digenic and/or trigenic epistasis gene effects along with duplicate type of gene action. When additive as well as non-additive effects are involved, a breeding scheme efficient in exploiting both types of gene effects should be employed. Reciprocal recurrent selection could be followed which would facilitate exploitation of both additive and non-additive gene effects simultaneously.

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