

Gene effects for earliness and seed yield 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 characters related to earliness and seed yield in castor. On simple additive-dominance model, three parameters viz., 'm', additive [d] and dominance [h] were significant for days to 50 % flowering in JP 96 x JI 368. The $\chi^2_{(1)}$ at nine degrees of freedom was found non-significant for days to 50% flowering in cross JP 96 x JI 368 proving adequacy of additive-dominance model. Under six-parameters model of Hill (1966), the components 'm', additive [d], dominance [h] and digenic ([i] and [j]) were found significant for days to 50 % flowering in cross JP 96 x JI 372. The $\chi^2_{(2)}$ at six degrees of freedom was found non-significant for days to 50% flowering in cross JP 96 x JI 372 proving six-parameters model as the best fit model. For all traits in all crosses (except days to 50 % flowering in JP 96 x JI 3 and JP 96 x JI 372) were found significant for $\chi^2_{(2)}$ and were subjected to trigenic ten-parameter model. The trigenic ten-parameter model was found adequate for days to maturity in crosses JP 96 x JI 368 and JP 101 x SKI 215 along with non-significant $\chi^2_{(3)}$ with two degrees of freedom indicating major role of trigenic interaction for the inheritance of above said traits. On the other hand, $\chi^2_{(3)}$ with two degrees of freedom was found significant for remaining traits in all the three crosses showing the presence of higher order epistasis and/or linkage. Besides, all the ten-parameters were significant for seed yield per plant in all the three crosses.

Key words: Scaling tests, trigenic 10-parameters model, gene effects, trigenic interaction

The information on the nature and magnitude of gene actions could be helpful in predicting the effectiveness of selection in a population. A distinct knowledge of three types of gene actions, its magnitude and composition of genetic variance are of fundamental importance to a plant breeder, which helps in formulating effective, sound and appropriate breeding procedures. In this context, genetic analysis of generation means is very useful in testing the adequacy of different type of genetic models and then estimating the genetic parameters in the form of the components of means (Marther and Jinks,

1971). The parameters obtained are useful to the plant breeders to understand the genetical structure of populations, their variation and prediction of response to selection. For these objects, the present experiment was carried out.

MATERIALS AND METHODS

The basic set of twelve generations viz., P_1 , P_2 , F_1 , F_2 , B_1 , B_2 , B_{1S} , B_{11} , B_{12} , B_{2S} , B_{21} and B_{22} derived from three castor crosses namely JP 96 x JI 368 (cross 1), JP 96 x JI 372 (cross 2) and JP 101 x SKI 215 (cross 3) were sown in Compact Family Block Design with three replications at Instructional Farm, College of

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Agriculture, J.A.U., Junagadh during Kharif, 2011-12. 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_{1s} , B_{11} , B_{12} , B_{2s} , B_{21} and B_{22} in four rows. Each row was of 7.2 m in length with 90 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 condition. The observations were recorded on individual plant basis in each replication on randomly selected five plants from P_1 , P_2 and F_1 , ten plants from first backcross (B_1 and B_2) and twenty plants of F_2 , B_{1s} , B_{11} , B_{12} , B_{2s} , B_{21} , B_{22} generations for number of nodes upto main raceme, plant height upto main raceme and seed yield per plant; days to 50% flowering and days to maturity of main raceme on plot basis.

The inheritance of traits under present investigation was computed through generation mean analysis methods (Mather, 1949; Hayman and Mather, 1955; Hayman, 1958 and Hill, 1966). The $\chi^2_{(1)}$ of joint scaling test under three-parameters model gives idea about fitness of additive-dominance model. In addition to six generations and six-parameters model (Hayman, 1958), the data were subjected to ten-parameters model given by Hill (1966). 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-parameters model at six degrees of freedom and for ten-parameters model at two degrees of freedom, respectively. This is an additional advantage of using twelve generations and ten-parameters 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) and Hill (1966) were compared, whenever six-parameters model was satisfactory for inheritance of the trait.

RESULTS AND DISCUSSION

The data of all the twelve generations viz., P_1 , P_2 , F_1 , F_2 , B_1 , B_2 , B_{11} , B_{12} , B_{21} , B_{22} , B_{1s} and B_{2s} were analyzed for five characters of three crosses. The gene effects were estimated in those cases where mean sum of

squares for a trait was found significant. 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_{1s} and B_{2s} (Hill, 1966) and X and Y (Van Der Veen, 1959) were also computed. Significant estimates of the test(s) given by Hill (1966) showed contribution of particular generation to higher order epistasis, which is indirectly indicating presence of epistasis. If any of the Van Der Veen's tests significantly deviates from zero, it also indicated presence of trigenic or higher order epistasis. The results of simple scaling tests were further confirmed by joint scaling test (Cavalli, 1952), 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-parameters model, six-parameters model and ten-parameters model, respectively. The ten-parameters model was used to estimate higher order epistasis (Hill, 1966). To draw inference on adequacy of ten-parameters model, chi-square test $[\chi^2_{(3)}]$ at two degrees of freedom was applied. The character and cross-wise results of scaling tests and gene effects are presented in Table 1 to 5.

The application of individual scaling test (Table 1 to 5) A, B, C and D of Mather (1949) as well as joint scaling test of Cavalli (1952) were non-significant for days to 50% flowering, days to maturity of main raceme and plant height in cross 1 and for number of nodes upto main raceme in cross 2, while special scaling tests viz., B_{11} , B_{12} , B_{21} , B_{22} , B_{1s} and B_{2s} of which, B_{21} and B_{22} were significant for days to 50% flowering in Cross 1; only B_{1s} in cross 2 and B_{11} , B_{21} , B_{22} , B_{1s} and B_{2s} in cross 3. Whereas for days to maturity of main raceme, B_{12} , B_{22} and B_{2s} were significant in cross 1; B_{11} , B_{21} , B_{1s} and B_{2s} in cross 2 and B_{11} , B_{12} , B_{21} and B_{1s} in cross 3. For plant height, B_{11} , B_{12} , B_{21} , B_{22} , B_{1s} and B_{2s} were significant in cross 1; B_{11} , B_{1s} and B_{2s}

Table 1 Scaling tests and estimation of gene effects for days to 50 % flowering of main raceme in three crosses of castor

Scaling tests / gene effects	JP 96 x JI 368 (Cross 1)	JP 96 x JI 372 (Cross 2)	JP 101 x SKI 215 (Cross 3)
A	-0.66 ± 1.24	2.60 ± 1.52	6.06** ± 1.76
B	-1.86 ± 1.53	-3.46* ± 1.41	1.06 ± 1.79
C	-1.06 ± 2.02	5.20** ± 1.98	7.93** ± 2.72
D	0.43 ± 1.28	3.03* ± 1.28	0.40 ± 1.63
B ₁₁	-1.85 ± 2.41	-1.71 ± 2.38	-22.87** ± 2.23
B ₁₂	0.40 ± 2.55	-1.68 ± 2.65	-4.93 ± 3.17
B ₂₁	-6.91** ± 2.30	-3.21 ± 2.55	-11.61** ± 2.97
B ₂₂	11.60** ± 2.52	-1.12 ± 2.18	-10.15** ± 2.49
B _{1S}	-7.79 ± 4.47	-23.21** ± 4.35	-17.58** ± 4.66
B _{2S}	1.53 ± 4.34	-6.29 ± 4.29	-18.30** ± 5.05
X	283.76** ± 1.10	281.13** ± 1.07	287.25** ± 1.12
Y	138.40** ± 1.18	139.35** ± 1.18	139.72** ± 1.31
Three parameter s model (Cavalli)			
m	71.21** ± 0.17	70.14** ± 0.14	68.45** ± 0.14
(d)	-2.68** ± 0.17	-2.10** ± 0.14	-1.24** ± 0.13
(h)	1.03** ± 0.38	1.42** ± 0.37	5.03** ± 0.42
X ² ₍₁₎ (9 df)	7.36	45.29**	129.84**
Six parameter s model (Hayman)			
m	71.58** ± 0.44	71.67** ± 0.42	71.15** ± 0.58
(d)	-1.93* ± 0.91	0.76 ± 0.96	0.70 ± 1.15
(h)	0.36 ± 2.60	-5.19* ± 2.62	1.93 ± 3.35
(i)	-0.86 ± 2.56	-6.06* ± 2.57	-0.80 ± 3.27
(j)	0.89 ± 0.93	3.03** ± 0.98	2.50* ± 1.16
(l)	2.79 ± 4.19	6.93 ± 4.35	-6.33 ± 5.35
Digenic and trigenic interactions (Hill)			
m	72.80** ± 1.27	74.79** ± 1.27	64.81** ± 1.44
(d)	-2.78** ± 0.19	-2.26** ± 0.15	-1.71** ± 0.15
(h)	-3.33 ± 3.47	-7.84* ± 3.55	23.74** ± 3.99
(i)	-1.55 ± 1.27	-4.84** ± 1.28	3.10* ± 1.44
(j)	1.33 ± 1.16	3.43** ± 1.14	5.43** ± 1.22
(l)	2.91 ± 2.44	3.98 ± 2.55	-18.99** ± 2.95
X ² ₍₂₎ (6 df)	4.57	11.45	34.38**
m	73.77** ± 3.41	76.76** ± 3.35	64.41** ± 3.92
(d)	-1.45 ± 2.72	2.73 ± 2.72	-8.77** ± 2.98
(h)	-7.55 ± 17.37	-18.13 ± 16.96	30.45 ± 20.34
(i)	-2.53 ± 3.41	-6.81 ± 4.35	3.41 ± 3.92
(j)	2.21 ± 7.50	-8.18 ± 7.52	24.43** ± 8.01
(l)	6.53 ± 26.89	19.48 ± 26.26	-43.88 ± 31.38
(w)	-1.38 ± 2.71	-5.01 ± 2.72	6.99* ± 2.98
(x)	4.55 ± 9.46	5.72 ± 9.15	4.56 ± 11.54
(y)	-6.66 ± 7.39	6.66 ± 7.28	-15.43* ± 7.61
(z)	-0.24 ± 13.16	-7.19 ± 12.93	19.96 ± 15.34
X ² ₍₃₎ (2 df)	0.41	5.42	12.01**
Type of epistasis	Duplicate	Duplicate	Duplicate

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

Table 2 Scaling tests and estimation of gene effects for days to maturity of main raceme in three crosses of castor

Scaling tests / gene effects	JP 96 x JI 368 (Cross 1)	JP 96 x JI 372 (Cross 2)	JP 101 x SKI 215 (Cross 3)
A	3.06 ± 1.93	4.46** ± 1.40	6.40** ± 1.56
B	-3.00 ± 1.75	-2.86 ± 1.51	4.26** ± 1.57
C	1.20 ± 2.44	3.40 ± 2.21	11.33** ± 2.67
D	0.56 ± 1.52	0.90 ± 1.33	0.33 ± 1.55
B ₁₁	-1.89 ± 3.02	-6.14** ± 2.26	-18.18** ± 2.58
B ₁₂	7.13* ± 2.77	-3.26 ± 3.03	-8.2** ± 2.78
B ₂₁	-0.19 ± 2.87	-13.34** ± 2.69	-13.74** ± 2.86
B ₂₂	12.47** ± 2.76	-3.98 ± 2.68	-1.36 ± 2.55
B ₁₅	-1.42 ± 5.63	-13.96** ± 4.32	-32.86** ± 4.66
B ₂₅	24.02** ± 5.18	-11.48* ± 5.33	-9.42 ± 5.36
X	639.78** ± 1.16	645.88** ± 1.17	642.6** ± 1.14
Y	324.35** ± 1.28	318.92** ± 1.29	317.2** ± 1.29
Three parameter s model (Cavalli)			
m	161.91** ± 0.28	160.51** ± 0.17	159.43** ± 0.18
(d)	-2.39** ± 0.28	-0.99** ± 0.17	-1.83** ± 0.18
(h)	-0.99 ± 0.56	1.07* ± 0.42	1.97** ± 0.44
X ² ₍₁₎ (9 df)	41.74**	51.14**	103.30**
Six parameter s model (Hayman)			
m	162.32** ± 0.49	160.95** ± 0.47	161.45** ± 0.59
(d)	-0.86 ± 1.16	2.46** ± 0.94	-1.16 ± 1.00
(h)	-2.36 ± 3.13	-2.13 ± 2.73	-1.23 ± 3.16
(i)	-1.13 ± 3.05	-1.79 ± 2.67	-0.66 ± 3.10
(j)	3.03* ± 1.24	3.66** ± 0.96	1.06 ± 1.02
(l)	1.06 ± 5.25	0.19 ± 4.37	-10.00* ± 4.82
Digenic and trigenic interactions (Hill)			
m	161.85** ± 1.36	160.95** ± 1.36	159.72** ± 1.44
(d)	-3.59** ± 0.40	-1.30** ± 0.19	-2.08** ± 0.20
(h)	-2.51 ± 3.91	3.08 ± 3.74	9.97* ± 3.94
(i)	0.33 ± 1.36	-0.63 ± 1.36	-0.84 ± 1.45
(j)	6.91** ± 1.59	5.32** ± 1.23	5.74** ± 1.24
(l)	2.11 ± 2.89	-3.63 ± 2.69	-11.12** ± 2.86
X ² ₍₂₎ (6 df)	19.28* 	18.53**	15.84*
m	154.48** ± 3.55	168.17** ± 3.69	162.92** ± 4.00
(d)	-0.99 ± 2.80	-2.44 ± 2.97	-0.16 ± 3.07
(h)	33.81 ± 18.28	-34.72 ± 18.73	-8.03 ± 20.59
(i)	7.69** ± 3.56	-7.87* ± 3.69	-4.02 ± 4.00
(j)	5.57 ± 7.90	2.65 ± 8.15	8.60 ± 8.34
(l)	-47.85 ± 28.36	54.42 ± 29.00	17.07 ± 31.51
(w)	-2.90 ± 2.77	1.22 ± 2.96	-2.04 ± 3.06
(x)	-25.91* ± 10.20	20.57* ± 10.14	20.48* ± 9.60
(y)	-6.25 ± 7.69	9.51 ± 7.97	-12.44 ± 7.86
(z)	-20.48 ± 13.94	-27.75 ± 14.25	-13.42 ± 15.22
X ² ₍₃₎ (2 df)	4.86	9.80**	5.96
Type of epistasis	Duplicate	Duplicate	Duplicate

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

Table 3 Scaling tests and estimation of gene effects for plant height upto main raceme in three crosses of castor

Scaling tests / gene effects	JP 96 x JI 368 (Cross 1)	JP 96 x JI 372 (Cross 2)	JP 101 x SKI 215 (Cross 3)
A	-0.0067 ± 2.25	20.34** ± 3.08	17.22** ± 4.37
B	0.16 ± 2.21	-14.08** ± 3.53	29.62** ± 2.42
C	0.68 ± 4.25	23.76** ± 6.40	56.42** ± 7.62
D	0.26 ± 2.12	8.75** ± 3.37	4.78 ± 4.35
B ₁₁	-27.75** ± 3.56	56.44** ± 6.37	-40.79** ± 5.92
B ₁₂	-12.53* ± 5.72	-5.29 ± 11.44	-44.25** ± 6.34
B ₂₁	-44.65** ± 5.21	-4.00 ± 7.61	-25.01** ± 6.22
B ₂₂	-11.99* ± 4.65	3.93 ± 8.33	-11.83 ± 9.64
B ₁₅	-54.66** ± 7.98	-43.89** ± 13.26	-124.66** ± 11.91
B ₂₅	-41.78** ± 9.33	42.71** ± 14.25	-129.86** ± 16.48
X	-242.19** ± 1.96	287.58** ± 3.88	239.99** ± 3.38
Y	107.64** ± 2.28	135.91** ± 4.17	103.26** ± 3.50
Three parameter s model (Cavalli)			
m	58.42** ± 0.35	65.01** ± 0.54	57.67** ± 0.45
(d)	-5.30** ± 0.34	-8.89** ± 0.53	-4.48** ± 0.45
(h)	2.57** ± 0.86	17.48** ± 1.27	4.29** ± 0.91
$\chi^2_{(1)}$ (9 df)	183.73**	154.00**	339.69**
Six parameter s model (Hayman)			
m	56.53** ± 0.85	77.17** ± 1.36	68.09** ± 1.83
(d)	-7.54** ± 1.25	4.43* ± 1.97	-12.62** ± 2.35
(h)	0.18 ± 4.44	-0.15 ± 6.95	-9.02 ± 8.77
(i)	-0.52 ± 4.25	-17.49** ± 6.74	-9.57 ± 8.71
(j)	-0.086 ± 1.35	17.20** ± 2.08	-62.00** ± 2.41
(l)	0.36 ± 6.59	11.23 ± 10.17	-37.27** ± 12.11
Digenic and trigenic interactions (Hill)			
m	60.21** ± 2.16	59.85** ± 3.70	73.46** ± 3.80
(d)	-6.87** ± 0.45	-12.00** ± 0.62	-5.99** ± 0.53
(h)	4.19 ± 5.84	38.00** ± 9.90	8.98 ± 9.61
(i)	-3.24 ± 2.15	3.30 ± 3.72	-19.45** ± 3.82
(j)	9.03** ± 2.07	29.32** ± 3.30	-7.41* ± 3.02
(l)	-5.83 ± 4.37	-20.30** ± 7.08	-28.35** ± 6.35
$\chi^2_{(2)}$ (6 df)	150.91**	55.03**	18.98**
m	89.91** ± 6.29	16.43 ± 10.82	91.72** ± 11.86
(d)	-9.22 ± 4.87	-16.11 ± 8.40	-13.56 ± 8.87
(h)	-149.19** ± 32.23	272.94** ± 55.69	-89.75 ± 61.12
(i)	-33.37** ± 6.29	46.15** ± 10.82	-38.00** ± 11.87
(j)	10.01 ± 12.99	72.13** ± 23.74	32.92 ± 23.59
(l)	211.23** ± 49.99	-396.86** ± 87.59	117.10 ± 92.14
(w)	2.22 ± 4.86	3.28 ± 8.39	7.20 ± 8.86
(x)	98.70** ± 17.82	-117.97** ± 29.58	58.11 ± 34.91
(y)	4.97 ± 12.91	-75.29** ± 25.14	-56.61* ± 22.15
(z)	-92.84** ± 24.66	187.75** ± 43.50	-65.49 ± 43.29
$\chi^2_{(3)}$ (2 df)	112.97**	7.32*	7.40*
Type of epistasis	Duplicate	Duplicate	Duplicate

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

in cross 2 and B_{11} , B_{12} , B_{21} , B_{15} and B_{25} in cross 3. Likewise, for number of nodes, B_{11} , B_{12} , B_{15} and B_{25} were significant in cross 1; B_{11} , B_{21} , B_{22} and B_{15} in cross 2 and B_{11} , B_{12} , B_{21} , B_{22} and B_{15} in cross 3. On other hand, all special scaling tests viz., B_{11} , B_{12} , B_{21} , B_{22} , B_{15} and B_{25} were significant in all the three crosses for seed yield per plant. Similarly, the special scaling tests viz., X and Y were found significant for all the above traits in all the three crosses.

As non-significant $\chi^2_{(1)}$ values with nine degrees of freedom of joint scaling test of Cavalli (1952) was more reliable because of involvement of all twelve generations means at a time and hence one can concluded that additive-dominance model was found satisfactory only for days to 50% flowering in cross 1. The results revealed that all the three gene effects i.e., 'm', additive [d] and dominance [h] were found significant for days to 50% flowering in cross 1. The additive-dominance model was not found adequate for days to 50% flowering in cross 2 and cross 3. The failure of additive-dominance model was attributed mainly to the epistasis. Cockerham (1959) postulated that epistatic gene action was common in the inheritance of quantitative traits and there was no sound biological reason why this type of gene action should be less common for yield and yield related traits. Studies have also been reported in castor, which showed evidence of non-allelic interaction of economically important traits (Pathak *et al.*, 1988; Solanki *et al.*, 2003 and Golakiya *et al.*, 2004, Monpara, 2010).

When the simple additive-dominance model failed to explain the variation among generation means, a six-parameters perfect fit model involving three digenic interactions ([i], [j] and [l]) proposed by Hayman (1958) was applied. This model utilized only six basic generations viz., P1, P2, F1, F2, B1 and B2. On other hand, based on weighted least square technique, digenic interaction model of Hill (1966) 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 six-parameter model was adequate for days to 50% flowering in the Cross 2.

The results obtained from six-parameters model of Hayman (1958) revealed that 'm', dominance [h] and digenic [i] and [j] interactions were significant for days to 50% flowering of main raceme in cross 2, while, 'm', additive [d], dominance [h] and digenic ([i] and [j]) interactions were found significant under six-parameter model of Hill (1966) for days to 50% flowering in cross 2. Irrespective of nature, the high magnitude of dominance effect ([h] and [l]) was observed in cross 2 for days to 50% flowering. The results of present findings were in accordance with the results obtained by Pathak *et al.*, (1988) for days to flowering. The goodness of fit for six-parameters model of Hayman (1958) could not, however, be tested in the present study owing to no degrees of freedom left for testing chi-square estimates for various characters. Hence, the present study was planned and executed with means of twelve generations. The model of Hill (1966) was tested in which six degrees of freedom left for testing the adequacy of six-parameter model of Hill (1966). Chi-square test with six degrees of freedom was non-significant suggesting adequacy of six-parameters model of Hill (1966) for days to 50% flowering in Cross 2.

The additive [d] gene effect (Table 1 to 5) found significant and negative in Cross 3 for days to 50% flowering and in Cross 1 for nodes upto main raceme. Likewise, additive [d] gene effect was found significant in all the three crosses for seed yield per plant. The dominance [h] gene effect were important for inheritance of the traits like plant height in the crosses 1 and 2; number of nodes upto main raceme in Cross 2 and seed yield per plant in all the three crosses. As in the present study, the importance of additive and dominance effects was also reported by Solanki *et al.* (2003) for plant height up to main raceme and number of nodes up to main raceme and Golakiya *et al.* (2004) for number of nodes up to main raceme and seed yield per plant. Among digenic interactions, additive x additive [i] gene effect found significant in the cross 1 and cross 2 for days to maturity; in the cross 3 for number of nodes upto main raceme and in all the three crosses for plant height and seed yield per plant. Likewise, the estimates of additive x dominance [j] gene effect was

Table 4 Scaling tests and estimation of gene effects for number of nodes upto main raceme in three crosses of castor

Scaling tests / gene effects	JP 96 x JI 368 (Cross 1)	JP 96 x JI 372 (Cross 2)	JP 101 x SKI 215 (Cross 3)
A	2.86* $\pm$ 1.18	1.20 $\pm$ 1.19	10.73** $\pm$ 1.00
B	-3.33** $\pm$ 1.08	-1.60 $\pm$ 1.07	3.06* $\pm$ 1.39
C	3.53 $\pm$ 2.04	3.26 $\pm$ 2.07	6.93** $\pm$ 2.03
D	2.00 $\pm$ 1.10	1.83 $\pm$ 1.13	-3.43** $\pm$ 1.24
B ₁₁	-13.40** $\pm$ 1.94	-10.67** $\pm$ 1.68	-29.69** $\pm$ 2.09
B ₁₂	-6.60** $\pm$ 2.16	2.99 $\pm$ 2.26	-6.47** $\pm$ 1.76
B ₂₁	-2.20 $\pm$ 2.01	-7.41** $\pm$ 2.19	-16.27** $\pm$ 1.92
B ₂₂	-4.44 $\pm$ 2.38	-8.27** $\pm$ 1.65	7.67** $\pm$ 2.02
B _{1S}	-10.68** $\pm$ 3.55	-9.22* $\pm$ 3.82	-43.42** $\pm$ 3.81
B _{2S}	-23.80** $\pm$ 3.95	3.42 $\pm$ 3.86	2.18 $\pm$ 3.42
X	67.64** $\pm$ 0.87	63.48** $\pm$ 0.78	61.75** $\pm$ 0.88
Y	33.40** $\pm$ 0.97	33.97** $\pm$ 0.92	28.68** $\pm$ 0.91
Three parameters model (Cavalli)			
m	16.72** $\pm$ 0.19	15.80** $\pm$ 0.16	17.35** $\pm$ 0.16
(d)	-0.83** $\pm$ 0.19	1.18** $\pm$ 0.15	-0.68** $\pm$ 0.17
(h)	-0.77* $\pm$ 0.39	-0.72* $\pm$ 0.36	-3.42** $\pm$ 0.29
$\chi^2_{(1)}$ (9 df)	131.91**	97.38**	308.70**
Six parameters model (Hayman)			
m	16.30** $\pm$ 0.43	15.60** $\pm$ 0.44	15.35** $\pm$ 0.47
(d)	2.40** $\pm$ 0.67	-0.10 $\pm$ 0.70	-0.06 $\pm$ 0.79
(h)	-4.29* $\pm$ 2.07	-4.43* $\pm$ 2.13	5.23* $\pm$ 2.51
(i)	-3.99 $\pm$ 2.22	-3.66 $\pm$ 2.27	6.86** $\pm$ 2.48
(j)	3.09** $\pm$ 0.74	-1.39* $\pm$ 0.62	3.83** $\pm$ 0.84
(l)	4.46 $\pm$ 3.39	4.06 $\pm$ 3.48	-20.66** $\pm$ 3.78
Digenic and trigenic interactions (Hill)			
m	19.67** $\pm$ 0.95	12.59** $\pm$ 1.04	13.65** $\pm$ 0.98
(d)	-1.01** $\pm$ 0.27	1.62** $\pm$ 0.18	-2.91** $\pm$ 0.23
(h)	-5.12* $\pm$ 2.50	10.66** $\pm$ 2.78	12.66** $\pm$ 2.68
(i)	-3.54** $\pm$ 0.97	2.86** $\pm$ 1.04	1.56 $\pm$ 1.00
(j)	2.98** $\pm$ 1.05	4.19** $\pm$ 0.92	11.54** $\pm$ 1.04
(l)	0.65 $\pm$ 2.02	-9.59** $\pm$ 2.02	-13.47** $\pm$ 1.85
$\chi^2_{(2)}$ (6 df)	90.01**	53.26**	104.03**
m	21.17** $\pm$ 2.76	6.52* $\pm$ 2.92	20.99** $\pm$ 2.90
(d)	-12.82** $\pm$ 2.01	2.54 $\pm$ 2.17	-3.16 $\pm$ 2.09
(h)	-14.17 $\pm$ 14.60	46.85** $\pm$ 15.13	-27.56 $\pm$ 15.41
(i)	-5.31 $\pm$ 2.76	8.70** $\pm$ 2.92	-6.43* $\pm$ 2.91
(j)	37.76** $\pm$ 5.83	-9.56 $\pm$ 5.59	29.38** $\pm$ 6.00
(l)	9.05 $\pm$ 22.62	-76.24** $\pm$ 23.16	45.71 $\pm$ 23.65
(w)	11.86** $\pm$ 1.99	-4.04 $\pm$ 2.17	-0.58 $\pm$ 2.08
(x)	12.66 $\pm$ 8.32	-14.37 $\pm$ 8.75	26.55** $\pm$ 8.91
(y)	-30.73** $\pm$ 5.79	15.00** $\pm$ 5.27	-35.78** $\pm$ 5.90
(z)	-0.38 $\pm$ 11.00	37.66** $\pm$ 11.19	-26.28* $\pm$ 11.26
$\chi^2_{(3)}$ (2 df)	39.31**	21.55**	20.55**
Type of epistasis	Duplicate	Duplicate	Duplicate

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

Table 5 Scaling tests and estimation of gene effects for seed yield per plant in three crosses of castor

Scaling tests / gene effects	JP 96 x JI 368 (Cross 1)	JP 96 x JI 372 (Cross 2)	JP 101 x SKI 215 (Cross 3)
A	-11.86** $\pm$ 3.23	-8.90** $\pm$ 2.95	52.20** $\pm$ 3.05
B	-15.40** $\pm$ 3.49	68.86** $\pm$ 3.83	37.60** $\pm$ 2.87
C	29.46** $\pm$ 5.80	113.73** $\pm$ 5.09	144.00** $\pm$ 5.94
D	28.36** $\pm$ 2.52	26.88** $\pm$ 2.59	27.10** $\pm$ 2.45
B ₁₁	144.14** $\pm$ 6.29	1.46 $\pm$ 5.51	-212.08** $\pm$ 4.99
B ₁₂	143.80** $\pm$ 7.42	-53.94** $\pm$ 6.52	-81.62** $\pm$ 7.17
B ₂₁	163.86** $\pm$ 6.47	-107.58** $\pm$ 6.61	-103.60** $\pm$ 6.92
B ₂₂	-15.12* $\pm$ 6.79	-267.02** $\pm$ 4.35	28.42* $\pm$ 6.23
B ₁₅	46.02** $\pm$ 9.38	-75.08** $\pm$ 8.21	-147.38** $\pm$ 10.61
B ₂₅	-55.02** $\pm$ 12.74	-284.52** $\pm$ 8.80	-163.22** $\pm$ 12.12
X	647.10** $\pm$ 2.27	740.57** $\pm$ 1.96	662.81** $\pm$ 2.08
Y	388.66** $\pm$ 2.93	336.67** $\pm$ 2.66	296.01** $\pm$ 2.79
Three parameter s model (Cavalli)			
m	179.43** $\pm$ 0.57	172.18** $\pm$ 0.44	163.64** $\pm$ 0.57
(d)	10.07** $\pm$ 0.53	12.05** $\pm$ 0.42	-0.24 $\pm$ 0.49
(h)	-19.81** $\pm$ 1.19	-0.53 $\pm$ 1.01	12.39** $\pm$ 1.23
$\chi^2_{(1)}$ (9 df)	2033.90**	4695.12**	2511.51**
Six parameter s model (Hayman)			
m	191.00** $\pm$ 0.96	179.03** $\pm$ 0.84	183.31** $\pm$ 1.04
(d)	23.50** $\pm$ 1.63	-7.48** $\pm$ 1.96	-10.76** $\pm$ 1.28
(h)	-33.46** $\pm$ 5.49	-63.23** $\pm$ 5.52	-56.26** $\pm$ 5.34
(i)	-56.73** $\pm$ 5.04	-53.76** $\pm$ 5.18	-54.20** $\pm$ 4.90
(j)	1.76 $\pm$ 1.98	-38.88** $\pm$ 2.05	-7.30** $\pm$ 1.63
(l)	84.00** $\pm$ 8.74	-61.99** $\pm$ 9.37	-35.60** $\pm$ 7.86
Digenic and trigenic interactions (Hill)			
m	221.15** $\pm$ 2.35	142.10** $\pm$ 2.25	144.52** $\pm$ 2.40
(d)	14.45** $\pm$ 0.90	22.93** $\pm$ 0.56	-4.13** $\pm$ 0.83
(h)	-123.30** $\pm$ 7.37	157.11** $\pm$ 6.84	128.03** $\pm$ 6.77
(i)	-49.45** $\pm$ 2.33	17.35** $\pm$ 2.23	1.64 $\pm$ 2.38
(j)	-25.11** $\pm$ 3.02	-66.93** $\pm$ 2.37	23.99** $\pm$ 2.72
(l)	67.36** $\pm$ 6.18	-166.04** $\pm$ 5.63	-127.63** $\pm$ 5.50
$\chi^2_{(2)}$ (6 df)	1521.26**	2567.01**	21.77**
m	90.22** $\pm$ 6.38	118.53** $\pm$ 5.91	99.76** $\pm$ 6.84
(d)	32.70** $\pm$ 4.74	104.66** $\pm$ 4.45	-131.08** $\pm$ 5.02
(h)	625.98** $\pm$ 34.03	329.43** $\pm$ 31.30	377.41** $\pm$ 35.87
(i)	77.89** $\pm$ 6.41	37.71** $\pm$ 5.92	48.49** $\pm$ 6.85
(j)	-114.14** $\pm$ 14.28	-455.37** $\pm$ 13.01	433.09** $\pm$ 13.51
(l)	-1163.00** $\pm$ 54.28	-539.76** $\pm$ 50.26	-515.46** $\pm$ 55.99
(w)	-11.86* $\pm$ 4.65	-73.02** $\pm$ 4.42	116.36** $\pm$ 4.96
(x)	-398.67** $\pm$ 19.03	-79.51** $\pm$ 17.25	-158.22** $\pm$ 20.50
(y)	126.59** $\pm$ 14.33	523.23** $\pm$ 12.92	-421.93** $\pm$ 13.33
(z)	628.29** $\pm$ 27.85	245.72** $\pm$ 26.10	188.24** $\pm$ 28.06
$\chi^2_{(3)}$ (2 df)	922.42**	314.30**	450.14**
Type of epistasis	Duplicate	Duplicate	Duplicate

*, ** Significant at 5 and 1 % levels, respectively.

significant for days to 50% flowering of main raceme in cross 3; plant height in cross 2; number of nodes upto main raceme in cross 1 and cross 3 and for seed yield per plant in all the three crosses. Similarly, dominance x dominance [l] gene effect was significant for plant height in cross 1 and cross 2; number of nodes upto main raceme in cross 2 and seed yield per plant in all the three crosses. This indicated that digenic epistatic interactions had also contributed a sizeable portion of variation in the genetic make up of various traits. These findings were further confirmed from the investigation done Pathak *et al.* (1988) for inheritance of days to flowering and seed yield in castor.

Trigenic epistasis additive x additive x additive [w] gene effects were significant in cross 3 for days to 50% flowering; cross 1 for number of nodes upto main raceme and all the three crosses for seed yield per plant. Additive x additive x dominance [x] was observed to be significant for plant height and number of nodes upto main raceme in the cross 3 and for days to maturity and seed yield per plant in all the three crosses. On the other hand, additive x dominance x dominance [y] gene effects were found significant for days to 50% flowering in the cross 3; plant height in the cross 2 and cross 3 and for number of nodes upto main raceme and seed yield per plant in all the three crosses. In case of dominance x dominance x dominance [z] gene effects, it was significant for plant height in the cross 1 and cross 2; number of nodes upto main raceme in cross 2 and cross 3 and for seed yield per plant in all the three crosses. Interestingly, all the types of digenic and trigenic interactions were significant in all the crosses for seed yield per plant. While, fitting trigenic epistatic model, the χ^2 (3) value at two degrees of freedom were non-significant in ten-parameter model for days to maturity in cross 1 and cross 3 suggesting the adequacy of the trigenic interaction model of Hill (1966) and Van Der Veen (1959) for days to maturity.

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 suggested presence of duplicate type of epistasis. In present study, duplicate epistasis

was observed in all the crosses for all the characters. Duplicate type of epistasis for plant height, number of nodes and seed yield per plant was also reported by Golakiya *et al.* (2004). Solanki *et al.* (2003) observed additive, dominance and all the epistasis with high magnitude of (l) for plant height and number of nodes up to main raceme. Singh and Yadava (1981) also reported partial and over dominance for days to flowering of main raceme and seed yield per plant, respectively.

It can be concluded from the present study that seed yield per plant and traits related to earliness in three 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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