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Genetic architecture for yield and its composition in castor (*Ricinus communis* L.)

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ABSTRACT

The genetic architecture of seed yield and related traits was investigated through generation mean analysis for four crosses in six generations in castor. Involvement of both additive and non-additive gene actions with preponderance of non-additive gene actions for seed yield, its major yield components suggested that hybrid breeding can profitably be utilized for improving seed yield in castor by exploiting dominance / non-additive gene action. However, to exploit both additive and non-additive types of gene actions observed for seed yield, its components, cyclic method of breeding involving conventional breeding approaches for selection of superior recombinants and their *inter se* crossing can alternatively be utilized for the development of high yielding inbred and pistillate lines in castor.

Key words : Castor, Genetic architecture, Gene action, Generation mean

INTRODUCTION

Castor (*Ricinus communis* L.) is an important non-edible oil seed crop of arid and semi-arid regions of India, which belongs to the genus *Ricinus* of Euphorbiaceae family. Yield is the ultimate product of action and interaction of number of yield components, which are governed by a large number of genes having small effects and are greatly influenced by environment. Effect of small individual gene cannot be selected, collective effect of the genes can be estimated any of the attributes. The estimation of gene effects involved in the inheritance of yield contributing or quantitative characters are helpful in planning breeding programs. Through gene effects for seed yield and other traits have been estimated in castor, information on epistatic gene effects is negligible. Thus the present investigation, genetic parameters namely additive, dominance and epistatic gene effects were estimated through generation mean study for nine quantitative traits in four crosses of castor.

MATERIALS AND METHODS

The material comprised of four hybrids *viz.,* Geeta x JI-258(Cross-I), SKP-23 x JI-35(Cross-II), VP-1 x 48-1(Cross-III) and VP-1 x JI-35(Cross-IV) involving six diverse parents. The entire experimental material comprised of parents (P_1 and P_2), F_1, F_2, B_1 (F_1 x P_1) and B_2 (F_1 x P_2) generations of all four crosses, which was conducted in compact family block design with three replications at the Main Castor and Mustard Research Station, S.D. Agricultural University, Sardarkrushinagar, Gujarat during *Kharif*, 2004-2005. The four crosses formed the family block, whereas, six generations of each cross-represented individual plots within family. A single replication comprised of one row of parents and F_1s, two rows of the backcrosses and four rows of the F_2s. There were ten plants in a row at inter and intra row spacing of 90 cm x 60 cm, respectively. From each replication data were recorded for nine quantitative characters (Table 1). The data were subjected to different biometrical techniques namely scaling test (Hayman and Mather, 1955) and generation mean analysis by Hayman's six parameter model (Haymen,1958).

RESULTS AND DISCUSSION

Significant scaling test for different traits was observed in almost all crosses indicating the presence of digenic or higher order interactions (Table 1). The estimates of gene effects for days to 50 per cent flowering in cross-I indicated that additive, dominance, additive x additive and dominance x dominance were involved in the expression of this trait. The results further revealed that barring additive x additive and dominance x dominance, all other gene effects were found significant in cross-II. All the gene effects were highly significant in cross-III and IV. Thus, predominance of non-additive gene action was observed in which dominance and dominance x dominance components were in opposite direction in cross-I, II and III, indicating the presence of duplicate type of epistasis. The present findings are in close agreement with the results obtained by Bhatt and Reddy

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Table 1: Estimates of genetic components in castor

Cross	Components of generation mean						Scaling tests			
	m	d	h	i	j	l	A	B	C	D
					Days to 50 per cent flowering					
Cross-I	58.33**	1.00*	-13.50**	-14.00**	-0.50	11.00**	1.000	2.00**	17.00**	7.00**
Cross-II	56.33**	-1.00**	-5.50**	-2.00	2.17**	0.33	3.00**	-1.33	3.67**	1.00
Cross-III	53.67**	-4.33**	-4.83**	-7.33**	0.83*	8.33**	0.33	-1.33	6.33**	3.67**
Cross-IV	56.67**	-4.67**	-5.50**	-5.33**	1.83**	-3.67*	6.33**	2.67**	14.33**	2.67**
					Plant height					
Cross-I	63.30**	25.40**	-0.53	-2.80	12.20**	23.07**	2.07	-22.33**	-17.47**	1.40
Cross-II	55.40**	-5.23**	-12.22**	-2.33	11.78**	-6.37	16.13**	-7.43**	11.03**	1.17
Cross-III	56.20**	-21.03**	-30.05**	-39.67**	2.42**	69.97**	-12.73**	-17.57**	9.37**	19.83**
Cross-IV	58.00**	-14.37**	-7.25*	1.93	12.12**	-51.37**	36.83**	12.60**	47.56**	-0.97
					Number of nodes up to main raceme					
Cross-I	18.50**	2.20**	-4.27**	-5.60**	0.80**	8.67**	-0.73**	-2.33**	2.53**	2.80**
Cross-II	17.70**	-0.87**	-3.85**	-0.53	0.35**	5.30**	-2.03**	-2.73**	-4.23*	0.27
Cross-III	17.17**	-1.67**	-3.47**	-1.73**	0.40**	-1.33**	1.93**	1.13**	4.80**	0.87**
Cross-IV	18.97**	-1.87**	-4.72**	-2.93**	1.88**	-0.30	3.50**	-0.27	6.17**	1.47**
					Length of main raceme					
Cross-I	49.47**	3.03**	2.15	-2.20	-5.72**	12.23**	-10.73**	0.70	-7.83**	1.10
Cross-II	45.37**	1.03	5.90	7.67*	1.80	8.87	-6.47**	-10.07**	-24.20**	-3.83*
Cross-III	59.33**	-6.47**	-9.00**	-22.80**	-6.60**	29.47**	-9.93**	3.27*	16.13**	11.40**
Cross-IV	50.33**	-7.13**	18.98**	12.93**	-8.12**	-6.50	-11.33**	4.90*	-19.37**	-6.47**
					Number of capsules on main raceme					
Cross-I	46.43**	10.47**	38.98**	34.67**	9.45**	-24.10**	4.17*	-14.73**	-45.23**	-17.33**
Cross-II					Not Significant					
Cross-III					Not Significant					
Cross-IV					Not Significant					
					Number of effective branches per plant					
Cross-I	7.63**	2.03**	-6.63**	-5.93**	-0.60**	8.33**	-1.80**	-0.60**	3.53**	2.97**
Cross-II	6.03**	0.50**	0.57**	0.60**	1.13**	-3.40**	2.53**	0.27*	2.20**	-0.30**
Cross-III	7.53**	-1.83**	-0.80**	-1.40**	-0.10**	1.33**	0.07	0.13	1.47**	0.70**
Cross-IV	6.70**	0.03	0.80**	0.07	0.23	-4.13**	2.27**	1.80**	4.00**	-0.03
					Seed yield per plant					
Cross-I	106.06**	25.49**	79.51**	13.17*	14.59**	194.68**	-89.30**	-118.48**	-220.95**	-6.58*
Cross-II	128.37**	-26.44**	-5.13	-44.12**	-5.35**	129.59**	-48.08**	-37.39**	-41.35**	22.06**
Cross-III	88.10**	-23.93**	37.18**	13.60**	-6.66**	84.54**	-55.73**	-42.41**	-111.74**	-6.80**
Cross-IV	120.64**	-25.50**	-29.32**	-54.45**	6.92**	129.53**	-30.62**	-44.46**	-20.62**	27.23**
					100 seed weight					
Cross-I					Not Significant					
Cross-II					Not Significant					
Cross-III	27.06**	-2.57**	-2.27**	-3.85**	-0.09	5.25**	-0.79**	-0.61*	2.45**	1.98**
Cross-IV	24.98**	-0.74**	-0.80**	-1.91**	1.24**	5.54**	-0.58**	-3.05**	-1.73**	0.95**
					Oil content					
Cross-I					Not Significant					
Cross-II					Not Significant					
Cross-III	48.73**	-0.86**	2.69**	1.03**	-0.31*	1.03**	0.083	0.70*	-0.24	-0.51**
Cross-IV	48.44**	-0.92**	0.01	-1.61**	-0.49**	4.23**	-1.80**	-0.82**	-1.02**	0.80**

* and ** indicate significance of values at P=0.05 and 0.01, respectively

(1983) and Solanki *et al.* (2003).

An estimates of gene effects revealed that additive, additive x dominance and dominance x dominance gene effects were involved in the expression of plant height in cross-I. In cross-II, additive, dominance and additive x dominance gene effects were significant, where dominance was higher in magnitude. The estimates of gene effects revealed that all the gene effects were highly significant in the cross-III. This predominance of non-additive gene action was observed in which h and l gene effects were in opposite direction indicated duplicate nature of epistasis. Barring additive x additive, all other type of gene effects were found significant in cross-IV. The present findings are in close agreement with results obtained by Gondaliya *et al.* (2001) and Solanki *et al.* (2003).

The genetic components of variation revealed that all gene effects were involved in the expression of number of nodes up to main raceme in cross-I and III. The opposite signs of dominance and dominance x dominance effects indicated the presence of duplicate epistasis in cross-I and II. Barring dominance x dominance, all other gene effects were found significant in cross-IV. The type of gene action responsible for the inheritance of this trait revealed that homozygous recombinants along with desired number of nodes could be developed by following reciprocal recurrent selection of *inter se* crossing of desired segregants keeping adequate population size. The present findings akin to the results obtained by Gondaliya *et al.* (2001) and Lavanya and Chandramohan (2003).

The estimates of gene effect for length of main raceme in cross-I indicated that additive as well as epistatic (additive x dominance and dominance x dominance) gene effects were involved in the expression of this trait. In cross-II, only additive x additive gene effect governed the expression of length of main raceme. In cross-III, all gene effects *viz.,* additive, dominance and epistatic were found highly significant wherein dominance x dominance gene effect was greater in magnitude. Barring dominance x dominance, all other type of gene effects were found significant in cross-IV. The opposite signs of dominance and dominance x dominance effects indicated the presence of duplicate epistasis in the inheritance of this trait in cross-III and IV. The present findings are in close agreement with the results obtained by Solanki *et al.* (2003).

The estimates of gene effects revealed that all the gene effects *viz.,* additive, dominance and epistatic were involved in the expression of number of capsules on main raceme in cross-I. The opposite signs of h and l gene effects indicated the balance for these interactions and presence of duplicate type of epistasis in nature. In Cross-II, III and IV, scaling tests and genetic components were not carried out as there were non-significant results in analysis of varience. The findings are akin to the results obtained by Gondaliya *et al.* (2001) and Solanki *et al.* (2003).

The estimates of gene effects revealed that all the gene effects were involved in the expression of number of effective branches per plant in the cross-I, II and III. Dominance and dominance x dominance gene effects in cross-IV governed the expression of number of effective branches per plant. The negative sign of h and l in all four crosses indicated the presence of duplicate epistasis. Solanki *et al.* (2003) and Gondaliya *et al.* (2001) obtained the same results.

The estimates of gene effects for seed yield per plant in cross-I and III revealed that all gene effects *viz.*, additive, dominance and epistatic were significant. In cross-II, barring dominance, all other estimates of gene effects were found highly significant. All the gene effects *viz.*, additive, dominance and epistatic were found significant in cross-IV for the expression of seed yield per plant, where dominance x dominance and additive x additive gene effects were of higher magnitude followed by dominance and additive gene effects. In Cross-I and III, the magnitude of dominance and dominance x dominance gene effect were predominant and a duplicate dominant epistasis in nature. Therefore, resorting to heterosis breeding for exploitation of yield would also give fruitful results. The dominance and dominance x dominance gene effects were in opposite direction indicating the involvement of duplicate epistasis in the expression of this trait in cross- II and IV. The results of the present study revealed that seed yield was controlled by both additive as well as non-additive gene effects in all four crosses. Hence, cyclic method of breeding could be profitably utilized to take advantage of both additive and non-additive type of gene actions for the improvement of this trait. The most important components for seed yield are dominance and over dominance, therefore, heterosis breeding should be advocated for the quantum jump in production as always advocated in Gujarat due to developing and release of hybrids. The present findings are akin to the results obtained by Gondaliya *et al.* (2001) and Solanki *et al.* (2003) who reported the role of both additive and non-additive gene effects in the expression of seed yield per plant.

Barring additive x dominance, all other gene effects were found significant in cross-III for 100 seed weight. The opposite signs of dominance and dominance x dominance effects indicated the presence of duplicate

epistasis in the inheritance of this trait. All the gene effects were highly significant in cross-IV, where the magnitude of dominance x dominance was the highest. Thus, predominance of non-additive gene action was observed for the genetic control of 100-seed weight in which dominance and dominance x dominance effects were in opposite direction, indicating the presence of duplicate type of epistasis. These results were in agreement with the results obtained by Solanki *et al.* (2003) and Gondaliya *et al.* (2001).

The estimates on gene effects for oil content revealed that all gene effects were found significant in cross-III for the expression of this trait. Barring, dominance, all other gene effects were found significant in cross-IV, where dominance x dominance gene effect was the highest in magnitude. The dominance and dominance x dominance gene effects were in opposite direction indicating the involvement of duplicate epistasis in the expression of this trait in cross- III and IV. The present findings are akin to the results obtained by Solanki *et al.* (2003) and Gondaliya *et al.* (2001) who reported involvement of both additive and non-additive gene effects for the expression of oil content.

It is, therefore, concluded that heterosis breeding may be used where large magnitude of non- fixable gene effects is observed. However, recurrent selection with *inter se* mating in segregating generation, which utilizes both additive and non-additive types of gene actions would be highly rewarding for the isolation of high yielding pistillate and male inbred lines in castor.

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