

GENETIC ANALYSIS IN CASTOR (*Ricinus communis* L.)

VIRANI, H. P., DHADUK, H. L., MEHTA, D. R. AND PATEL, N. B*.

DEPARTMENT OF GENETICS AND PLANT BREEDING
JUNAGADH AGRICULTURAL UNIVERSITY
JUNAGADH - 362 001, GUJARAT, INDIA

**E-mail: nitinpatel@jau.in*

ABSTRACT

*Inheritance studies to understand the genetics of seed yield and its components was conducted in castor (*Ricinus communis* L.) utilizing three crosses viz., JP 96 x JI 368 (C₁); JP 96 x JI 372 (C₂) and JP 101 x SKI 215 (C₃) following six parameter model of generation mean analysis. On the basis of individual scaling test A, B and C, the additive-dominance model was found adequate for description of variation in generation means for days to flowering of main raceme and number of nodes up to main raceme in cross 1 (JP 96 x JI 368); number of effective branches per plant in cross 1 (JP 96 x JI 368) and cross 2 (JP 96 x JI 372) and shelling out turn in cross 3 (JP 101 x SKI 215). All the six parameters viz., m, (d), (h), (i), (j) and (l) were significant for length of main raceme and effective length of main raceme in cross 1 (JP 96 x JI 368) and for 100-seed weight in cross 2 (JP 96 x JI 372) indicated the involvement of additive, dominance as well as epistasis gene interaction controlling these traits. For the characters where evidence of digenic epistatic interaction was obtained, both main effects viz., additive (d) and non-additive (h) gene effects were significant for days to maturity of main raceme, plant height up to main raceme, length of main raceme, effective length of main raceme, shelling out turn and 100-seed weight in cross 1 (JP 96 x JI 368); days to maturity of main raceme, plant height up to main raceme, shelling out turn, 100 seed weight and seed yield per plant in cross 2 (JP 96 x JI 372); and for days to flowering of main raceme, length of main raceme, effective length of main raceme and number of capsule on main raceme in cross 3 (JP 101 x SKI 215). Only additive (d) component was found significant for number of capsule on main raceme and oil content in cross 1 (JP 96 x JI 368); oil content in cross 2 (JP 96 x JI 372); and for plant height up to main raceme, number of nodes up to main raceme, 100-seed weight, oil content and seed yield per plant in cross 3 (JP 101 x SKI 215), while only dominance (h) component was found significant for seed yield per plant in cross 1 (JP 96 x JI 368); and for length of main raceme, effective length of main raceme and number of capsule on main raceme in cross 2 (JP 96 x JI 372). Looking to the interaction components, any one or any two or all the three interaction parameters were found significant for most of the traits in all the three crosses indicating interaction parameters also played an important role in the inheritance of majority of the characters in all the three crosses. The classification of gene action showed importance of duplicate type of gene action for most of the characters in all the three crosses. Breeding procedures involving either multiple crosses or biparental crosses may be restored to get transgressive segregants. This is especially important to develop inbred lines having superiority in different characters.*

KEY WORDS: Castor, generation mean analysis, inheritance, scaling test

INTRODUCTION

Castor (*Ricinus communis* L., $2n=20$, Family: Euphorbiaceae) is a highly cross pollinated crop in which most of the cultivars have been developed through hybridization followed by selection. The exploitation of heterosis has been an important breeding tool in castor, which became feasible due to availability of 100% pistillate lines (Gopani *et al.*, 1968). In Gujarat, real breakthrough in castor production has come with the development and release of hybrids for commercial cultivation. Still there is potential to further increase in yield level of castor through genetic improvement.

Seed yield in any field crops, is due to interaction of many genes with environment, thus, direct selection for it will not be successful. Selection for yield components has been suggested as a solution for further advance in increasing yield. In breeding to increase the inherent yielding potential of a crop plant, the selection criterion may be yield or some of the morphological components of yield. An understanding of the mode of inheritance of the yield components, the correlations among them, and the association between each component with yield is necessary for the intelligent choice of breeding procedures for developing high yielding varieties. One of the best methods for the estimation of genetic parameters is generation mean analysis, in which epistatic effects could also be estimated. Six basic generations' variance components can give accurate information in relating average dominance ratio and inheritance. Thus, these components can complete the derived information from means (Mather and Jinks, 1982; Kearsey and Pooni, 1996). The choice of an efficient breeding procedure depends on the knowledge of the genetic controlling system of the character to be selected (Azizi *et al.*, 2006) and therefore, it is always essential to evaluate available promising lines in their hybrid combinations for seed yield and yield

attributing characters (Giriraj *et al.*, 1973). Keeping in view, an experiment was laid out to estimate the nature and magnitude of gene effects for yield and its components using six basic generations of three cross combinations in castor.

MATERIAL AND METHODS

P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 generations of three crosses viz., JP 96 x JI 368 (C_1); JP 96 x JI 372 (C_2) and JP 101 x SKI 215 (C_3) were used as the genetic materials in the present study. The experiment was laid out in Compact Family Block Design with three replications at Main Oilseeds Research Station Junagadh Agricultural University, Junagadh. Each replication was divided into three compact blocks, each consists of single cross and each block was consisted of six plots comprised of six basic generations of each cross. The single row plot was sown for both parents and its F_1 ; five rows plot for each F_2 generation and three rows plot for each backcross generations during *kharif* 2010-2011. The experiment plot possessed row length of 7.2 m with 90 cm and 60 cm inter and intra row spacing, respectively. All the recommended cultural and plant protection practices were followed to raise good crop of castor. Observations were recorded on seed yield and other component traits viz., days to flowering and maturity of main raceme, plant height up to main raceme, nodes up to main raceme, length and effective length of main raceme, effective branches per plant, number of capsules on main raceme, 100-seed weight, shelling outturn and oil content on five plants from P_1 , P_2 and F_1 , forty plants from F_2 and twenty plants from BC_1 and BC_2 generations in each replication.

The mean values, standard errors and variances of the different generations were subjected to weighed least-squares analysis using the scaling test (Mather 1949) to estimate the gene effects. The genetic effects were estimated using the models suggested by Jinks and Jones (1958) and Mather and Jinks

(1982). The significance of the scaling test and gene effects were tested by using the t-test (Singh and Chaudhary, 2004). The type of epistasis was determined only when dominance (*h*) and dominance x dominance (*l*) effects were significant; when these effects had the same sign the effects were complementary, while different signs indicated duplicate epistasis.

RESULTS AND DISCUSSION

The analysis of variance between families (crosses) revealed that the mean squares due to crosses were significant for all the characters except plant height up to main raceme and number of effective branches per plant. The analysis of variance among progenies within each family indicated significant differences among six generation means for all the characters studied in all the three crosses except number of nodes up to main raceme in cross 1 (JP 96 x JI 368) and number of effective branches per plant in cross 1 (JP 96 x JI 368) and cross 2 (JP 96 x JI 372).

On the basis of individual scaling test A, B and C and joint scaling test (Table 1), the additive-dominance model was found adequate for description of variation in generation means for days to flowering of main raceme and number of nodes up to main raceme in cross 1 (JP 96 x JI 368); number of effective branches per plant in cross 1 (JP 96 x JI 368) and cross 2 (JP 96 x JI 372) and shelling out turn in cross 3 (JP 101 x SKI 215). For remaining crosses, any one or two or all the three individual scaling tests A, B or C were found significant. 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.

On the basis of perfect fit solution of six parameter model, all the six parameters viz., *m*, (*d*), (*h*), (*i*), (*j*) and (*l*) were significant for length of main raceme and effective length of main raceme in cross 1 (JP 96 x JI 368) and for 100-seed weight in cross 2 (JP 96 x JI 372)

indicated the involvement of additive, dominance as well as epistasis gene interaction controlling these traits. For the characters where evidence of digenic epistatic interaction was obtained, both main effects viz., additive (*d*) and non-additive (*h*) gene effects were significant for days to maturity of main raceme, plant height up to main raceme, length of main raceme, effective length of main raceme, shelling out turn and 100-seed weight in cross 1 (JP 96 x JI 368); days to maturity of main raceme, plant height up to main raceme, shelling out turn, 100 seed weight and seed yield per plant in cross 2 (JP 96 x JI 372); and for days to flowering of main raceme, length of main raceme, effective length of main raceme and number of capsule on main raceme in cross 3 (JP 101 x SKI 215). Only additive (*d*) component was found significant for number of capsule on main raceme and oil content in cross 1 (JP 96 x JI 368); oil content in cross 2 (JP 96 x JI 372); and for plant height up to main raceme, number of nodes up to main raceme, 100-seed weight, oil content and seed yield per plant in cross 3 (JP 101 x SKI 215), while only dominance (*h*) component was found significant for seed yield per plant in cross 1 (JP 96 x JI 368); and for length of main raceme, effective length of main raceme and number of capsule on main raceme in cross 2 (JP 96 x JI 372). Looking to the interaction components, any one or any two or all the three interaction parameters were found significant for most of the traits in all the three crosses indicating interaction parameters also played an important role in the inheritance of majority of the characters in all the three crosses.

The classification of gene action showed importance of duplicate type of gene action for most of the characters in all the three crosses except number of capsules on main raceme in cross 1, where complementary type of gene action operated. In case of duplicate type of gene action, breeding procedures involving either multiple crosses or

biparental crosses may be restored to get transgressive segregants. This is especially important to develop inbred lines having superiority in different characters. Such lines can give better hybrids. While in case of complementary type of epistasis, material can be utilized directly in breeding programme.

The evidence of non-allelic interactions was reported by Pathak *et al.* (1988) for days to flowering of main raceme, plant height up to main raceme, total length of main raceme, number of capsules on main raceme, 100-seed weight, oil content and seed yield per plant. While studying the genetic architecture of seed yield and related traits through generation mean analysis for three crosses in six generations, Gondaliya *et al.* (2001) reported that additive and non-additive gene effects for seed yield and majority of the traits were significant. However, magnitude of dominance and epistasis components were higher than additive components. Solanki *et al.* (2003) estimated the gene effects based on analysis of generation mean for eight characters in five crosses of castor and observed the presence of additive, dominance and epistatic gene effects. Among non-allelic interaction dominance x dominance (I) interactions was of greater magnitude than main gene effects for almost all the characters, indicating the importance of heterosis breeding to utilize non-additive gene effects. Golakia *et al.* (2004) advocated presence of additive, dominance and epistasis gene effects for number of nodes up to main raceme, total length of main raceme, effective length of main raceme and seed yield per plant.

CONCLUSION

The results showed the presence of additive, dominance and epistatic gene interactions for seed yield per plant and its components in all the three crosses, which could be utilized by attempting biparental crosses to get desirable transgressive segregants in castor. The additive dominance model was adequate for days to flowering of

main raceme and number of nodes up to main raceme in cross 1 (JP 96 x JI 368); number of effective branches per plant in cross 1 (JP 96 x JI 368) and cross 2 (JP 96 x JI 372) and shelling out turn in cross 3 (JP 101 x SKI 215). Duplicate type epistasis gene effects played a greater role than complementary epistasis in most of the crosses for most of the traits.

REFERENCES

- Azizi, F., Rezai, A. M. and Saeidi, G. (2006). Generation Mean Analysis to Estimate Genetic Parameters for Different Traits in Two Crosses of Corn Inbred Line at Three Planting Densities. *J. Agr. Sci. Tech.*, **8**(2): 153-169.
- Giriraj, K., Mensinkai, S. W. and Sindagi, S. S. (1973). Heterosis in castor (*Ricinus communis* L.). *Mysore J. Agric. Sci.*, **7**(3): 389-393.
- Golakiya, P. R., Madaria, R. B., Kavani, R. H. and Mehta, D. R. (2004). Gene effects, heterosis and inbreeding depression in castor. *J. Oilseeds Res.*, **21**(2): 270-273.
- Gondaliya, A. B., Dangaria, C. J., Kavani, R. H. and Golakia, P. R. (2001). Genetic architecture for yield and its components in castor. *J. Oilseeds Res.*, **18**(2): 150-153.
- Gopani, D. D., Kabaria, M. M. and Patel, R. H. (1968). Study of hybrid vigour in castor. *Indian J. Agric. Sci.* **38**: 520-527.
- Jinks, J. L. and Jonse, R. M. (1958). Estimation of the components of heterosis. *Genet.*, **43**: 223-234.
- Kearsey, M. J. and Pooni, H. S. (1996). The Genetical Analysis of Quantitative Traits. 1st Edition, Chapman and Hall, London, PP. 381.
- Mather, K. (1949). Biometrical Genetics. Methuen and Co. Ltd., London.
- Mather, K. and Jinks, J. L. (1982). Biometrical Genetics: The Study of Continuous

-
- Variation. Chapman and Hall, London.
- Pathak, H. C., Dixit, S. K. and Patel, P. G. (1988). Gene effects and heterosis in castor (*Ricinus communis* L.). *Indian J. Agric. Sci.*, **58**(6): 476-478.
- Singh, R. K. and Chaudhary, B. D. (2004). Biometrical Method in Quantitative Genetics Analysis. Kalyani Publisers, Ludhiana.
- Solanki, S. S., Joshi, P., Gupta, Deepak and Deora, V. S. (2003). Gene effects for seed yield contributing characters in castor (*Ricinus communis* L.) by generation mean analysis. *J. Oilseeds Res.*, **20**: 217-219.

Table 1: Estimates scaling test and gene effects for different traits in castor.

Cross	A	B	C	m	[d]	[h]	[i]	[j]	[l]	Type of Epistasis
Days to Flowering of Main Raceme										
C ₁	-	-	-	-	-	-	-	-	-	-
C ₂	**	-	**	57.10**±2.74	0.80±0.45	-1.16±7.03	3.16±2.70	-2.25*±1.04	6.20±4.70	D
C ₃	**	*	**	47.76**±3.40	3.46**±0.24	19.83**±7.86	10.10**±3.40	-5.31**±0.89	-4.86±4.61	D
Days to Maturity of Main Raceme										
C ₁	**	**	**	183.70**±4.43	1.83**±0.38	-120.06**±11.52	-31.93**±4.41	-1.15±1.66	86.03**±7.45	D
C ₂	**	**	**	149.86**±4.65	-156**±0.19	-48.00**±11.91	1.96±4.65	-0.65±1.66	38.66±7.52	D
C ₃	**	**	**	145.50**±5.18	-2.90±0.49	-46.36±13.31	4.26±5.15	0.80±1.91	55.06**±8.36	D
Plant Height up to Main Raceme (cm)										
C ₁	**	*	**	117.33**±14.64	-2.83**±0.57	-69.50*±35.19	-51.83**±14.62	-0.83±4.38	20.16±21.14	D
C ₂	**	**	-	49.50*±24.29	-12.33**±0.46	106.83*±53.16	25.83±24.28	-1.51±4.84	-94.66*±29.51	D
C ₃	*	*	**	90.990**±20.04	-31.16**±3.26	18.36±51.01	-16.40±19.77	-3.66±7.58	-37.60±31.89	D
Number of Nodes up to Main Raceme										
C ₁	-	-	-	-	-	-	-	-	-	-
C ₂	**	-	-	16.00**±1.20	0.60±0.40	-4.86±3.18	-0.20±1.13	-1.73**±0.57	2.06±2.12	D
C ₃	**	*	**	14.56**±1.71	-4.00**±0.24	3.83±4.43	-0.03±1.69	0.65±0.63	-6.26*±3.15	D
Length of Main Raceme (cm)										
C ₁	**	-	**	18.33**±6.69	-4.50*±1.88	91.66**±17.02	37.83**±6.42	12.58**±2.84	-51.33**±0.79	D
C ₂	**	**	**	47.50**±7.41	2.00±1.68	52.66**±18.90	-1.16±7.21	5.66±2.99	-61.83**± 11.8	D
C ₃	*	-	-	61.36**±5.74	-5.66**±0.93	-36.93*±15.20	-15.03**±5.67	-3.23±2.33	26.23**±10.18	D
Effective Length of Main Raceme (cm)										
C ₁	**	-	**	19.66**± 6.48	-4.50*±1.82	86.16**±16.33	36.50**±6.18	12.66**±2.71	-47.16**±10.37	D
C ₂	**	**	**	45.66**±7.04	2.00±1.68	54.66**± 18.06	0.66±6.84	5.50±2.90	-62.33**±11.41	D
C ₃	**	-	-	60.53**±5.59	-5.66**± 0.93	-36.93*±14.78	-14.20*±5.51	-3.06±2.27	27.06**±9.93	D
Number of Effective Branches Per Plant										
C ₁	-	-	-	-	-	-	-	-	-	-
C ₂	-	-	-	-	-	-	-	-	-	-
C ₃	*	-	-	1.93*±0.79	-0.33±0.23	0.61± 0.36	2.60**±0.76	0.61±0.36	-3.76**±1.37	D

Number of Capsules on Main Raceme										
C ₁	-	**	**	36.36**±9.91	-5.66*±2.69	31.40±26.06	21.70*±9.54	9.13*±4.41	1.10±16.89	C
C ₂	**	**	**	32.80**±8.36	-1.76±2.21	73.96**± 22.05	14.56±8.06	5.23±3.71	59.50**±14.43	D
C ₃	-	**	-	81.70**±9.82	-14.90**±2.04	-76.00**±25.07	-21.20*±9.61	5.31±3.84	54.16**±16.65	D
Shelling Out Turn (%)										
C ₁	**	-	**	58.06**±2.49	3.33**±0.13	12.10*±6.15	4.86*±2.44	-0.28±0.81	-0.83±3.75	D
C ₂	*	**	**	73.90**±1.84	1.30**±0.08	-26.20**±4.94	-8.93**±1.84	-0.91±0.73	13.70**±3.15	D
C ₃	-	-	-	-	-	-	-	-	-	-
100-Seed Weight (g)										
C ₁	**	-	**	23.48**±2.17	4.42**±0.05	17.09**±5.25	6.79**±2.17	-0.54±0.65	-5.05± 3.16	D
C ₂	-	**	**	27.21**±1.68	3.02**±0.09	11.70**±4.07	4.55**±1.68	-1.28*±0.51	-4.92*±2.45	D
C ₃	**	-	-	22.05**±1.06	1.85**±0.15	3.35±2.61	0.89±1.05	-0.85**±0.36	-0.63±1.58	D
Oil Content (%)										
C ₁	**	-	*	52.80**± 1.42	2.33**±0.20	-0.53±3.18	1.58± 1.41	-0.80*±0.36	0.28±1.79	D
C ₂	**	**	**	54.85**±1.40	0.99**±0.04	-6.02±4.03	0.44±1.39	-1.15±0.65	7.41**±2.64	D
C ₃	-	**	-	42.66**±1.94	2.52**±0.04	7.69±4.92	3.18±1.94	-1.32*±0.65	-3.96±3.04	D
Seed Yield Per Plant (g)										
C ₁	**	**	**	164.50**±19.18	1.80±3.56	-375.66**±46.79	-29.36±18.85	-15.46*±6.62	383.56**±30.04	D
C ₂	**	-	**	146.30**± 23.38	36.46**± 3.70	-224.30**±52.41	-39.96±23.07	-41.41**± 6.1	149.20**±30.72	D
C ₃	**	**	**	79.50**±17.96	-10.90**±2.80	-73.53±44.32	-24.20±17.74	9.21±6.26	117.50**±27.45	D

C₁= JP 96 x JI 368; C₂=JP 96 x JI 372; C₃=JP 101 x SKI 215;

m = mean of all generation; [d] = additive; [h] = dominance; [i] = additive x additive; [j] = additive x dominance;

[i] = dominance x dominance.

An asterisk (*) indicated that the value was significant by the t-test at the 5 per cent probability level.

D = Duplicate; C = Complementary.

[MS received: April 07, 2013]

[MS accepted: May 13,2013]