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Research Article

Genetic architecture studies of yield and its components in castor

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Abstract
Generation mean analysis implies to study genetics of seed yield and its components in castor (*Ricinus communis* L.) through generation mean analysis. The additive-dominance model was found adequate for days to maturity of primary spikes in cross I (AKC-1 x RG550), effective length of primary spikes in cross II (48-1 x RG550) and effective length of secondary spikes and number of secondary spikes in cross III (Aruna x RG550). Either dominance gene action or both additive and dominance gene actions were observed to be significant indicating the role of non additive component in the inheritance of most of the characters studied while only additive gene action along with epistatic interaction components were noted for effective length of secondary spikes in the cross I (AKC-1 x RG550) and number of capsules on primary spikes in the cross III (Aruna x RG550).

Key words
Castor, generation mean analysis; scaling tests, additive, dominance, epistatic gene interactions

Introduction

Castor (*Riccinus communis* L., 2n=20, Family: Euphorbiaceae) is a non-edible oilseed crop cultivated around the world because of commercial importance of its oil. The oil is mainly used as lubricant because of its property to remain liquid at very low temperatures (-32°C) and high density and viscosity (18 times higher than that of any other vegetable oil). Castor oil and its derivatives have wide range of uses in the manufacture of lubricants, plastics, adhesives, waxes, polishes, coating applications, inks, paints etc.

Besides India, Brazil and China are the most important castor growing countries in the world. India contributes more than one third of the world production of castor oil and meets about 80 per cent world castor oil demands. Hence, castor plays an important role in Indian economy by earning valuable foreign exchange.

Seed yield of a crop 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 the yield. In breeding to increase the inherent yielding potential of a crop plant, the selection criterion may be yield or some of the 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. The variance components estimated from generation mean analysis 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 four crosses in castor.

Materials and Methods

P_1, P_2, F_1, F_2, BC_1 and BC_2 generations of four crosses viz., AKC-1 x RG550 (Cross I); 48-1 x RG550 (Cross II); Aruna x RG550 (Cross III) and AKD-1 x RG550 (Cross IV) were used as experimental material in the present study. The experiment was laid out in Randomized Block Design with three replications at the farm of AICRP for Dryland Agriculture, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra during *kharif* 2014-15.

The experimental material was grown with 90 cm and 45 cm inter and intra row spacing respectively. All the recommended cultural and plant protection practices were followed to raise healthy crop. Observations were recorded on seed yield and other component traits *viz.,* days to 50 per cent flowering of primary spikes, days to maturity of primary spikes, number of nodes up to primary spikes, plant height, effective length of primary spikes, effective length of secondary spikes, effective length of tertiary spikes, number of secondary spikes, number of tertiary spikes, total number of spikes, number of capsules on primary spikes, number of capsules on secondary spikes, number of capsules on tertiary spikes, total number of capsules per plant, 100 seed weight and oil content.

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 gene effects were estimated using the models suggested by Jinks and Jones (1958) and Hayman (1958). The significance of the scaling tests 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) gene effects were significant; when these effects had the same sign the effects were complementary, while different signs indicated the duplicate epistasis.

Results and Discussion

The analysis of variance revealed that the mean squares due to families (generations) were significant for all the characters except for number of secondary spikes and total number of spikes in the cross I (AKC-1 X RG550); days to maturity of primary spikes, 100 seed weight and seed yield per plant in the cross II (48-1 X RG 550); days to maturity of primary spikes, number of tertiary spikes and total number of spikes in the cross III (Aruna x RG 550); days to maturity of primary spikes and number of tertiary spikes in cross IV (AKD-1 X RG 550). Hence further, statistical analysis was not carried out in respect of these non-significant characters in these crosses.

Perusal to Table 1, the scaling tests showed the adequacy of additive-dominance model in respect of days to maturity of primary spikes in cross I (AKC-1 X RG550); effective length of primary spikes in cross II (48-1 X RG 550) and effective length of secondary spikes and number of secondary spikes in the cross III (Aruna x RG 550) indicating the absence on non-allelic interactions in the control of these characters. Hence three parameter model (Jinks and Jones, 1958) was used to estimate the additive and dominance gene effects for these characters. However, the magnitudes of dominance gene effects were found to be higher than the additive gene effects for these characters in these crosses.

For others, the additive-dominance model was found to be inadequate, therefore six parameter model (Hayman,1958) was used to estimate the non- allelic interactions along with additive and dominance gene effects. On the basis of perfect fit solution of six parameter model, both additive (d) and dominance (h) as well as epistasis gene interactions were found to be highly significant for the characters under study.

Both additive and dominance gene effects along with epistatic interactions were found to be significant for days to 50 % flowering of primary spikes, effective length of secondary spikes, number of secondary spikes and total number of spikes in the crosses II (48-1 X RG 550) and IV (AKD-1 X RG 550); plant height and oil content in all the crosses; effective length of primary spikes and number of capsules on secondary spikes in the crosses I (AKC-1 X RG550), III (Aruna x RG 550) and IV(AKD-1 X RG 550); effective length of tertiary spikes in the crosses II (48-1 X RG 550) and III (Aruna x RG 550); number of nodes up to primary spikes and number of tertiary spikes in the cross II (48-1 X RG 550); number of capsules on primary spikes in the crosses I (AKC-1 X RG550), II (48-1 X RG 550) and IV (AKD-1 X RG 550); number of capsules on tertiary spikes and total number of capsules in the crosses I (AKC-1 X RG550), II (48-1 X RG 550) and III (Aruna x RG 550); 100 seed weight in the cross III (Aruna x RG 550) and IV (AKD-1 X RG 550) and seed yield per plant in the crosses I (AKC-1 X RG550) and IV(AKD-1 X RG 550).

Significant dominance gene effects only were noted for days to 50% flowering of primary spikes, number of tertiary spikes and 100 seed weight in the cross I (AKC-1 X RG550); number of nodes up to primary spikes in the crosses I (AKC-1 X RG550) and III (Aruna x RG 550); effective length of tertiary spikes in the cross IV (AKD-1 X RG 550); number of capsules on secondary spikes in the cross II (48-1 X RG 550); number of capsules on tertiary spikes and total number of capsules in the cross IV (AKD-1 X RG 550) and seed yield per plant in the cross III (Aruna x RG 550)along with epistatic interactions (Table1). Presence of non-additive gene for these character indicate that conventional selection procedure may not be effective enough for improvement these characters. Therefore postponement of selection to later generations or intermating among the selected segregants followed by one or two generations of selfing could be

suggested to break the undesirable linkage and allow the accumulation of favorable alleles for the improvement of this trait.

Only additive gene action along with dominance x dominance (I) and additive x additive (i) epistatic interaction with high magnitude of dominance x dominance (i) component was observed for effective length of secondary spikes in the cross I (AKC-1 X RG550) and number of capsules on primary spikes in the cross III (Aruna x RG 550). The additive gene effects can be exploited effectively by selection for the improvement these characters.

Only three types of epistatic gene interactions were found to be significant for days to 50% flowering of primary spikes in cross III (Aruna x RG 550); only additive x additive (i) interaction for number of nodes up to primary spike in cross IV (AKD-1 X RG 550) and dominance x dominance (l) The interaction effect for effective length of tertiary spikes in the cross I (AKC-1 X RG550) indicating interaction effects also played an important role in the inheritance of the characters in all the four crosses.

Similar findings are 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. Gondaliya *et al*. (2001) also reported that additive and non-additive gene effects for seed yield and majority of the traits were significant. Similarly, Sakhare *et al.* (2017), Solanki *et al.* (2003) and Punewar (2017), also observed the presence of additive, dominance and epistatic gene effects. Golakia *et al.* (2004) also found the 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 .

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 nodes up to primary spikes, number of capsules on secondary spikes in the cross I (AKC-1 X RG550); plant height and effective length of primary spikes and oil content in the cross III 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.

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Table1. Estimates of scaling tests and gene effects and type of gene interactions for different characters in castor.

Cross	A	B	C	D	m	[d]	[h]	[l]	[j]	[i]	Type of Epistasis
1.Days to 50% flowering of primary spikes											
Cross I	-	*	-	-	66.00**±0.09	-1.67±0.68	24.33**±1.67	-26.00**±3.28	22.00**±1.40	-6.67**±0.71	d
Cross II	-	*	-	-	67.00**±0.15	-4.67**±0.36	18.33**±0.95	-11.33**±1.59	16.00**±0.93	-11.33**±0.38	d
Cross III	-	*	*	*	72.67**±0.13	-1.00±0.64	-1.83±1.42	7.67**±2.68	-7.33**±1.39	-4.83**±0.69	-
Cross IV	*	*	-	-	64.33**±0.18	-1.67**±0.50	32.33**±1.27	-30.00**±2.21	22.00**±1.24	0.00±0.53	d
2.Days to maturity of primary spikes											
Cross I	-	-	-	-	109.33**±1.86	1.67**±0.33	27.00**±4.96	-	-	-	
Cross II	-	-	-	-	-	-	-	-	-	-	
Cross III	-	-	-	-	-	-	-	-	-	-	
Cross IV	-	-	-	-	-	-	-	-	-	-	
3.Number of nodes up to primary spikes											
Cross I	-	*	-	-	18.63**±0.11	-3.40±0.11	1.30*±0.58	3.93**±0.84	-0.80*±0.51	-3.83±0.13	c
Cross II	*	*	*	-	21.57**±0.02	2.33**±0.13	3.63**±0.26	-13.00±0.52	3.20**±0.26	0.37**±0.13	-
Cross III	-	*	-	-	17.17**±0.01	-1.67±0.13	17.60**±0.28	-15.87±0.55	13.60**±0.27	-1.93±0.15	-
Cross IV	*	*	*	*	21.84**±0.04	0.13±0.20	-0.47±0.43	-5.63±0.83	-6.31±0.43	3.50**±0.21	-
4.Plant height up to primary spikes (cm)											
Cross I	-	-	*	*	138.59**±0.09	5.07**±0.17	-72.13**±0.68	78.96**±1.20	-59.16**±0.50	-4.97**±0.21	d
Cross II	-	*	-	-	106.99**±0.05	-29.60**±0.55	112.29**±1.26	-126.39**±2.50	116.32**±1.12	-39.97**±0.06	d
Cross III	-	*	-	-	111.69**±0.50	-50.33**±0.86	48.84**±2.65	17.96**±4.00	41.91**±2.64	-58.80**±0.88	c
Cross IV	-	*	*	-	107.81**±2.09	-35.80**±6.48	29.55**±15.49	-7.41**±27.38	1.15**±15.41	-2.93**±6.49	d
5.Effective length of primary spikes (cm)											
Cross I	-	-	*	*	38.40**±0.16	-7.40**±0.27	-89.13**±0.99	129.73**±1.61	-73.73**±0.85	-7.73**±0.39	d
Cross II	-	-	-	-	30.53**±2.21	-0.23**±0.18	-3.22**±6.63	-	-	-	-
Cross III	-	*	-	-	27.11**±0.11	-17.80**±0.10	27.03**±0.54	3.64**±0.77	27.16**±0.49	-18.13**±0.21	c
Cross IV	-	*	-	-	27.71**±0.08	-17.67**±0.13	0.93**±0.47	-53.76**±0.77	27.43**±0.40	-17.57**±0.26	d
6.Effective length of secondary spikes(cm)											
Cross I	-	-	*	*	14.37**±0.17	4.33**±0.26	-26.63±0.90	35.53**±1.35	-21.07±0.87	4.30**±0.31	
Cross II	-	*	-	-	7.40**±0.02	-8.33**±1.07	16.27**±2.28	-29.07**±4.56	22.80**±2.14	-7.67**±1.12	d
Cross III	-	-	-	-	1.07**±0.91	2.50**±0.09	8.69**±2.74	-	-	-	-

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Cross IV	-	*	*	*	15.11**±0.08	-6.53**±0.13	-20.62**±0.45	26.12**±0.72	-16.19**±0.41	-6.83**±0.21	d
7.Effective length of tertiary spikes(cm)											
Cross I	-	-	*	*	8.75**±0.07	-1.67±0.17	-2.28±0.46	9.28**±0.77	-6.08±0.44	-1±0.19	-
Cross II	-	-	-	*	7.66**±0.05	-0.33**±0.08	-1.13**±0.29	9.76**±0.46	-3.03**±0.26	-1.17**±0.13	d
Cross III	-	*	-	-	7.44**±0.05	-1.53**±0.08	2.79**±0.29	-4.43**±0.46	3.16**±0.26	-2.83**±0.15	d
Cross IV	-	-	*	*	9.59**±0.03	-0.13±0.09	-15.83**±0.27	21.29**±0.50	-16.49±0.22	0.33**±0.14	d
8.Number of secondary spikes											
Cross I	-	-	-	-	-	-	-	-	-	-	-
Cross II	-	*	-	-	2.34**±0.03	-1.53**±0.09	-0.61**±0.23	1.17**±0.41	-0.17±0.22	-1.50**±0.11	d
Cross III	-	-	-	-	1.17**±0.19	-0.57±0.04	2.30**±0.43	-	-	-	-
Cross IV	*	*	-	-	1.87**±0.03	-0.27**±0.10	1.70**±0.23	-4.20±0.43	2.67**±0.23	-0.10±0.11	d
9. Number of tertiary spikes											
Cross I	-	*	*	*	2.27**±0.02	-0.13±0.11	-1.01**±0.27	0.41±0.51	-1.08**±0.24	-0.27**±0.15	-
Cross II	-	-	*	*	2.57**±0.02	0.47**±0.08	-1.67**±0.21	3.20**±0.39	-2.13**±0.18	0.07**±0.12	d
Cross III	-	-	*	*	-	-	-	-	-	-	-
Cross IV	-	-	-	-	-	-	-	-	-	-	-
10. Total number of spikes											
Cross I	-	-	-	-	-	-	-	-	-	-	-
Cross II	-	*	-	*	5.88**±0.03	-1.07**±0.11	-2.21**±0.28	4.37**±0.50	-2.17**±0.26	-1.50**±0.13	d
Cross III	-	-	-	-	-	-	-	-	-	-	-
Cross IV	*	*	-	-	4.92**±0.04	-0.93**±0.22	3.11**±0.48	-8.84**±0.93	4.57**±0.47	-1.20**±0.23	d
11. Number of capsules on primary spikes											
Cross I	-	-	*	*	46.67**±0.26	8.47**±0.48	-67.87**±1.47	78.93**±0.32	-59.07**±1.41	9.47**±0.57	d
Cross II	*	-	-	-	33.67**±0.09	27.00**±0.35	14.23**±0.83	2.73±1.54	19.60**±0.79	22.43**±0.40	-
Cross III	-	-	-	*	37.56**±0.24	4.60**±0.52	-0.23±1.47	17.43**±2.46	-3.43±1.40	8.27**±0.65	-
Cross IV	-	-	*	*	62.67**±0.03	4.40**±0.61	-120.50**±1.33	117.00**±2.65	-101.60**±1.22	-3.90**±0.79	d
12. Number of capsules on secondary spikes											
Cross I	*	*	*	*	14.29**±0.06	1.67**±0.24	-6.45**±0.59	-6.12**±1.11	-2.08**±0.55	0.03±0.30	c
Cross II	-	*	*	*	14.11**±0.05	-0.13±0.34	-15.99**±0.77	6.99**±1.50	-7.39**±0.71	-4.33**±0.41	d
Cross III	-	-	-	*	11.31**±0.03	-1.27**±0.22	-15.84**±0.49	32.31**±0.96	-14.97**±0.45	-1.33**±0.27	d
Cross IV	-	*	*	*	11.88**±0.15	-4.67**±0.22	-9.12**0.83	11.52**±1.25	-7.25**±0.78	-4.47**±0.28	d
13. Number of capsules on tertiary spikes											
Cross I	-	*	*	*	11.41**±0.03	-0.47**±0.09	-9.09**±0.55	10.92**±1.08	-10.85**±0.22	-2.10**±0.13	d

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Cross II	-	*	*	*	11.87**±0.02	-0.67**±0.15	-2.21**±0.38	6.55**±0.75	-7.21**±0.30	-1.87**±0.18	d	
Cross III	-	-	*	*	10.40**±0.15	-1.20**±0.09	-8.53**±0.64	19.20**±0.73	-12.80**±0.64	-1.67**±0.12	d	
Cross IV	-	-	*	*	9.43**±0.16	0.47±0.41	-11.50**±1.04	15.40**±1.79	-12.80**±1.02	0.43±0.44	d	
14. Total number of capsules												
Cross I	-	-	*	*	72.37**±0.20	9.67**±0.69	-83.40**±1.66	83.73**±3.03	-72.00**±1.59	7.40**±0.81	d	
Cross II	*	-	-	-	59.64**±0.15	26.20**±0.50	-3.94**±1.36	16.24**±2.50	5.03**±1.16	16.23**±0.63	d	
Cross III	-	-	-	*	59.26**±0.41	2.13**±0.73	-24.59**±2.28	68.92**±3.58	-31.19**±2.19	5.27**±0.91	d	
Cross IV	-	-	*	*	83.98**±0.33	0.20±1.01	-141.11**±2.46	143.91**±4.36	-121.64**±2.41	-7.93**±1.09	d	
15.100-Seed weight (g)												
Cross I	-	*	*	*	30.89**±0.23	-0.39±0.13	-26.84**±4.31	19.51**±6.01	-24.00**±4.25	-1.98**±0.14	d	
Cross II	-	-	-	-	-	-	-	-	-	-		-
Cross III	-	*	*	*	26.73**±0.03	-3.05**±0.20	-5.75**±0.49	7.21**±0.97	-8.91**±0.47	-1.96**±0.29	d	
Cross IV	-	*	-	*	26.48**±0.00	-2.19**±0.09	-7.94**±2.74	5.84±5.47	-1.83**±0.19	-8.69**±2.73	d	
16. Oil content (%)												
Cross I	*	-	-	*	47.79**±0.01	7.60**±0.28	-3.77**±0.60	13.20**±1.20	-6.33**±0.55	7.71**±0. 32	d	
Cross II	-	*	-	-	38.24**±0.02	-10.63**±0.26	9.21**±0.60	-8.96**±1.19	14.41**±0.52	-9.68**±0.37	d	
Cross III	-	*	-	-	41.27**±0.01	2.93**±0.42	3.01**±0.86	15.28**±1.73	2.95**±0.84	3.14**±0.46	c	
Cross IV	*	-	-	-	46.16**±0.04	3.25**±0.36	11.35**±0.76	-6.91**±1.49	8.53**±0.73	2.72**±0.40	d	
17. Seed yield per plant(g)												
Cross I	*	-	-	-	53.71**±0.05	1.45**±0.44	-38.00**±1.02	116.23**±2.00	-63.47**±0.90	5.63**±0.59	d	
Cross II	-	-	-	-	-	-	-	-	-	-	d	
Cross III	-	-	*	*	49.77**±0.16	0.82±0.50	-16.32**±1.24	5.83**±2.21	-14.69**±1.19	-1.39**±0.60	d	
Cross IV	*	*	*	*	51.60**±0.29	-1.56**±0.49	-10.95**±1.65	-59.51**±2.60	-5.50**±1.54	4.22**±0.57	d	

*, ** Significant at 5% and 1% levels, respectively.
Cross I - AKC-1 x RG550, Cross II -48-1 x RG550, Cross III - Aruna x RG550 and Cross IV- AKD-1 x RG550
m=mean of all generations; [d] = additive effects; [h]=dominance effects; [i]=additive x additive type of gene interaction .
[j]=additive x dominance type of gene interaction;
[i]=dominance x dominance type of gene interaction.
A, B, C, D = scaling tests
d=Duplicate; c=Complementary epistatic interaction