Research Article

Genetic analysis of yield and its biometric traits in castor (*Ricinus communis* L.)

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Abstract
The genetics of seed yield and its components was studied in castor (*Ricinus communis* L.) utilizing three crosses *viz.,* AKC-1 x RG1636 (Cross - I); Aruna x RG1636 (Cross-II) and AKD-1 x RG1636 (Cross-III) through generation mean analysis. The additive-dominance model was found to be adequate for days to maturity of primary spikes in cross II (Aruna x RG1636) indicating the absence on non- allelic interactions. Additive (d) gene actions along with epistatic gene interactions were found to be significant for effective length of secondary spikes, oil content in the cross I (AKC-1 x RG1636); total number of capsules, 100 seed weight in the cross III (AKD-1 x RG1636), while rest of the characters were found to be governed by non additive gene actions. The classification of gene actions showed the 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 resorted to get transgressive segregants.

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), 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 yield. For increasing 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.

Materials and methods

The P_1, P_2, F_1, F_2, BC_1 and BC_2 generations of three crosses *viz.*, AKC-1 x RG1636 (Cross-I); Aruna x RG1636 (Cross-II) and AKD-1 x RG1636 (Cross-III) 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 2013*-14.

The experimental material was grown with 90cm and 45cm 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 test and gene effects was tested by using the t-test (Singh and Chaudhary, 2004). The type of epistasis was determined only when both 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 revealed that the mean squares due to families (generations) were significant for all the characters except number of tertiary spikes in the cross I (AKC-1 x RG 1636); number of tertiary spikes and total number of spikes in the cross II (Aruna x RG1636) and days to maturity of primary spikes and oil content in the cross III (AKD-1 x RG1636).

The additive-dominance model was found to be adequate for days to maturity of primary spikes in cross II (Aruna x RG1636) indicating the absence on non- allelic interactions in the control of this character and also showed the higher magnitude of additive gene effect than dominance gene effect. This predominant fixable genetic component can be exploited through simple selection procedure for improvement of this character. However, in the remaining crosses, the additive-dominance model was found to be inadequate, therefore, six parameter model (Hayman,1958) was used to estimate 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 epistatic gene interactions were found to be highly significant for the characters days to 50 per cent flowering of primary spikes, effective length of tertiary spikes, number of capsules on primary, secondary and tertiary spikes and seed yield in all the crosses; number of nodes up to primary spikes and plant height in the cross II (Aruna x RG1636) and III (AKD-1 x RG1636); effective length of primary spikes, effective length of secondary spikes and oil content in the cross II (Aruna x RG1636) only; number of secondary spikes and total number of spikes in the cross I (AKC-1 x RG1636) and the cross III (AKD-1 x RG1636); days to maturity of primary spikes, total number of capsules in cross I (AKC-1 x RG 1636); and cross

II (Aruna x RG1636) and 100 seed weight in the cross I (AKC-1 x RG 1636); whereas the characters, number of nodes upto primary spikes, plant height, effective length of primary spikes and 100 seed weight in the cross I (AKC-1 x RG 1636); number of tertiary spikes and effective length of secondary spikes in the cross III (AKD-1 x RG1636); number of secondary spikes in the cross II (Aruna x RG1636) depicted significant dominance gene effects along with epistatic interactions. Presence of non-additive gene action for these character indicated that conventional selection procedure may not be effective enough for improvement these characters. Therefore, postponement of selection in later generations or inter- mating 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 effects along with epistatic gene interactions were observed to be significant for effective length of secondary spikes, oil content in the cross I (AKC-1 x RG 1636); total number of capsules, 100 seed weight in the cross III (AKD-1 x RG1636) indicating the role additive gene action in the control of these characters. These characters can be improved through simple selection.

Looking to the interaction components, any one or any two or all the three interaction parameters were found to be significant for most of the traits in all the crosses indicating that the interaction parameters also played an important role in the inheritance of majority of the characters. The classification of gene action showed the importance of duplicate type of gene action for most of the characters in all the crosses except total number of capsules in cross I (AKC-1 x RG 1636); number of capsules on secondary spikes in the cross II (Aruna x RG1636) where complimentary type of gene action was found. 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.

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 through generation mean analysis for three crosses in six generations, Gondaliya *et al.* (2001) also reported that additive

and non-additive gene effects for seed yield and majority of the traits were significant. Similarly, Solanki *et al.* (2003) estimated the gene effects based on analysis of generation mean for eight characters in five crosses of castor and also 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) also found the presence of additive, dominance and epistatic 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.

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Table 1. Estimates of scaling tests and gene effects for different traits in castor

Cross	A	B	C	D	m	[d]	[h]	[l]	[j]	[i]	Type of Epistasis
Days to 50% flowering of primary spikes											
Cross I	*	*	-	-	64.00**±0.23	6.67**±0.42	24.17**±1.30	-31.00**±2.06	24.00**±1.24	0.50±0.46	D
Cross II	*	-	*	-	68.00**±0.15	6.67**±0.1	13.33**±0.87	-9.33**±1.39	8.00**±0.70	1.67**±0.30	D
Cross III	*	*	*	-	69.33**±0.10	-3.00**±0.64	22.50**±1.54	-34.33**±2.99	12.00**±1.48	0.50**±0.73	D
Days to maturity of primary spikes											
Cross I	*	-	-	-	117.67**±0.22	6.33**±0.55	10.17**±1.46	-8.33**±2.50	10.00**±1.40	4.50**±0.64	D
Cross II	-	-	-	-	117.67**±2.41	2.33**±0.24	-0.67*±5.98	-	-	-	
Cross III	-	-	-	-	-	-	-	-	-	-	-
Number of nodes up to primary spikes											
Cross I	*	*	*	-	20.33**.08	0.42±0.24	10.53**±0.59	-27.73**±1.05	10.83**±0.57	0.78**±0.25	D
Cross II	-	*	-	-	17.74**±0.06	-0.67**±0.18	12.32**±0.47	-11.59**±0.88	10.12**±0.43	-0.13±0.19	D
Cross III	*	*	*	*	20.93**±0.02	-2.33**±0.26	2.37**±0.53	-7.13**±1.05	-2.80**±0.52	1.83**±0.26	D
Plant height up to primary spikes (cm)											
Cross I	*	*	-	-	111.61**±0.04	1.25±1.69	141.76**±3.41	-255.96**±6.81	156.06**±3.39	-11.22**±1.73	D
Cross II	*	*	-	-	129.99**±0.40	6.27**±0.42	91.34**±1.87	-126**.11±2.50	78.44**±1.82	-4.63**±0.57	D
Cross III	*	-	*	*	108.71**±2.15	-19.00**±3.58	83.33**±11.22	-70.56**±16.77	40.49**±11.21	11.43**±3.62	D
Effective length of primary spikes (cm)											
Cross I	*	*	*	*	38.40**±0.04	1.25±1.69	56.76**±3.41	-235.96**±6.81	146.06**±3.39	-11.32**±1.73	D
Cross II	*	*	*	-	27.22**±0.40	5.27**±0.42	91.34**±1.87	-126**.11±2.50	78.44**±1.82	-4.63**±0.57	D
Cross III	-	*	*	*	27.1**±2.15	-18.04±3.48	54.33**±11.12	-70.56**±16.77	40.49**±11.21	11.43**±3.62	D
Effective length of secondary spikes(cm)											
Cross I	-	-	*	*	15.53**±0.01	4.50**±0.34	-21.44±0.71	23.42**±1.42	-16.80**±0.68	4.28**±0.37	-
Cross II	-	-	-	*	13.71**±0.07	3.80**±0.20	-13.22**±0.62	31.59**±1.14	-10.44**±0.49	1.11**±0.21	D
Cross III	-	-	*	*	21.67**±0.13	-0.47±0.26	-39.31**±1.02	61.82**±1.85	-41.20**±0.73	-0.96**±0.30	D

*, ** Significant at 5 and 1 per cent levels, respectively

Cross I - *AKC-1 x RG1636*; Cross II - *Aruna x RG1636;* Cross III - *AKD-1 x RG1636*

m = mean of all generations; [d] =additive; [h] =dominance; [i] = additive x additive; [j] = additive x dominance; [i] = dominance x dominance. D=Duplicate ; C=Complementary epistatic interaction

Table 1. Contd.,

Cross	A	B	C	D	m	[d]	[h]	[l]	[j]	[i]	Type of Epistasis
Effective length of tertiary spikes(cm)											
Cross I	*	-	*	*	6.71**±0.02	1.42**±0.16	-3.13**±0.33	6.07**±0.66	-3.69**±0.32	2.06**±0.17	D
Cross II	*	-	*	*	9.51**±0.06	2.93**±0.29	-1.93**±0.63	1.80±1.20	-2.85**±0.62	1.61**±0.31	-
Cross III	-	-	*	*	10.76**±0.06	5.13**±0.19	-11.20**±0.77	8.71**±1.49	-12.23**±0.44	5.58**±0.21	D
Number of secondary spikes											
Cross I	-	*	*	*	3.47**±0.05	-0.42**±0.08	-6.78**±0.26	5.03**±0.40	-5.70**±0.26	-0.33**±0.09	D
Cross II	-	-	-	*	2.39**±0.03	0.13±0.12	1.70**±0.30	-0.15±0.55	0.59±0.27	0.55**±0.12	D
Cross III	-	*	*	*	4.08**±0.08	-2.47**±0.10	-4.27**±0.37	2.89**±0.53	-4.45**±0.36	-2.45**±0.11	D
Number of tertiary spikes											
Cross I	-	-	-	-	-	-	-	-	-	-	-
Cross II	-	-	-	-	-	-	-	-	-	-	-
Cross III	-	-	*	*	2.81**±0.03	0.07±0.08	-6.20**±0.23	9.42**±0.42	-6.04**±0.20	-0.24**±0.12	D
Total number of spikes											
Cross I	-	*	-	*	7.29**±0.03	-11.67**±0.38	-11.67**±5.23	12.18**±0.73	-10.83**±0.29	0.08±0.17	D
Cross II	-	-	-	-	-	-	-	-	-	-	-
Cross III	-	*	*	*	7.87**±0.10	-2.27**±0.15	-10.71**±0.52	12.62**±0.77	-10.67**±0.50	-2.56**±0.19	D
Number of capsules on primary spikes											
Cross I	*	-	-	-	40.77**±0.11	9.67**±1.20	37.55**±0.75	-32.17**±1.30	24.27**±0.59	7.62**±0.49	D
Cross II	*	*	*	-	46.90**±0.20	20.60**±0.80	26.90**±1.90	-74.70**±3.50	20.80**±1.8	21.20**±0.90	D
Cross III	-	-	*	*	59.16**±0.36	-1.07**±0.26	-60.41**±1.78	93.26**±2.52	-65.16**±1.54	-12.42**±0.66	D
Number of capsules on secondary spikes											
Cross I	-	-	*	*	15.71**±0.02	4.50**±0.34	-17.66**±0.75	33.14**±1.49	-17.52**±0.68	4.28**±0.37	D
Cross II	*	--	-	*	14.38**±0.04	13.13**±0.32	2.61**±0.69	6.07**±1.35	-0.85±0.66	14.48**±0.34	C
Cross III	-	-	*	*	20.44**±0.05	2.53**±0.22	-52.12**±0.52	70.19**±0.99	-50.57**±0.48	4.14**±0.25	D

*, ** Significant at 5 and 1 per cent levels, respectively

Cross I - *AKC-1 x RG1636*; Cross II - *Aruna x RG1636;* Cross III - *AKD-1 x RG1636*

m = mean of all generations; [d] =additive; [h] =dominance; [i] = additive x additive; [j] = additive x dominance; [i] = dominance x dominance. D=Duplicate ; C=Complementary epistatic interaction

Table 1. Contd.,

Cross	A	B	C	D	m	[d]	[h]	[l]	[j]	[i]	Type of Epistasis
Number of capsules on tertiary spikes											
Cross I	-		*	*	10.70**±0.06	1.75**±0.62	-6.08**±1.30	14.68**±2.56	-8.97**±1.27	0.73±0.64	D
Cross II	*	-	*	-	10.77**±0.10	7.00**±0.38	8.79**±0.91	-11.32**±1.71	3.73**±0.85	7.14**±0.41	D
Cross III	*	-	*	*	13.51**±0.20	5.07**±0.35	-14.50**±1.09	10.14**±1.66	-16.45**±1.06	5.64**±0.41	D
Total number of capsules											
Cross I	*	-	-	-	67.18**±0.11	15.92**±0.99	13.83**±2.10	15.64**±4.14	-2.21±2.02	12.62**±1.12	C
Cross II	*	-	-	-	72.06**±0.35	40.73**±1.32	38.27**±3.06	-79.97**±5.63	23.64**±2.97	42.83**±1.47	D
Cross III	-	-	*	*	93.11**±0.56	6.53**±0.63	-127.02±2.75	173.59**±3.92	-132.19**±2.55	-2.63**±0.83	-
100-Seed weight (g)											
Cross I	-	*	-	-	21.49**±0.02	-3.53±0.60	7.67**±1.20	-19.04±2.40	11.37**±1.20	-6.05±0.60	-
Cross II	*	*	-	-	23.64**±0.01	-2.09**±0.27	14.17**±0.59	-17.12**±1.18	9.31**±0.54	-1.93**±0.33	D
Cross III	-	-		*	23.74**±0.04	3.66**±0.37	-0.18±2.83	1.50±5.64	4.96**±0.75	-3.76±2.75	-
Oil content (%)											
Cross I	-	*	-	*	47.29**±0.02	-8.85**±0.56	-0.10±1.12	12.22**±2.24	-3.83**±1.12	-8.84**±0.56	-
Cross II	*	*	*	*	49.64**±0.00	-0.89**±0.01	-4.04**±0.05	-1.09±0.21	-4.95**±0.03	-0.76**±0.02	-
Cross III	*	-	-	-	-	-	-	-	-	-	-
Seed yield per plant(g)											
Cross I	*	*	*	*	58.45**±0.12	2.71**±0.64	-26.64**±1.44	21.78**±2.75	-40.05**±1.38	5.74**±0.68	D
Cross II	-	*	-	-	47.37**±0.06	-3.41**±0.87	9.80**±2.28	-7.57±4.53	2.97±1.75	-6.76**±0.89	-
Cross III	-	-	*	*	143.85**±4.49	1.98**±0.76	-409.33**±18.03	457.44**±18.23	-427.32**18.03	6.62**±0.76	D

*, ** Significant at 5 and 1 per cent levels, respectively

Cross I - *AKC-1 x RG1636*; Cross II - *Aruna x RG1636;* Cross III - *AKD-1 x RG1636*

m = mean of all generations; [d] =additive; [h] =dominance; [i] = additive x additive; [j] = additive x dominance; [i] = dominance x dominance. D=Duplicate ; C=Complementary epistatic interaction