



GENETIC ARCHITECHTURE OF FRUIT YIELD AND YIELD ATTRIBUTING TRAITS IN OKRA [*Abelmoschus Esculentus* (L.) MOENCH]

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ABSTRACT

The generations mean analysis was carried out in six crosses of okra to estimate genetic parameters viz., (m), (d), (h), (i), (j) and (l) for fruit yield and other component traits. The estimates of gene effect showed that both additive and non-additive gene effects were found important for the inheritance of yield and its attributes. The fixable gene effects viz., additive(d), and additive x additive (i) were observed in cross VRO-5 x GO-2 for number of nodes per plant and inter nodal length; in cross KS-404 x HRB-108-2 for number of nodes per plant and in cross D-1-87-5 x KS-404 for number of fruits per plant. However, all the three type of gene actions viz., additive (d), dominance (h) and epistatic gene effects [additive x additive (i), additive x dominance (j) and dominance x dominance (l)] were also involved in the inheritance for inter nodal length in cross VRO-5 x GO-2, for number of nodes per plant in cross KS-404 x HRB-108-2 and for fruit length in cross D-1-87-5 x KS-404 indicated that these three type of gene effects were important for these traits in respective crosses. The additive component of genetic variation could be fixed by the simple pedigree selection in the diverse crosses. In case of the characters where both additive and non-additive components are involved, biparental mating coupled with recurrent selection would be highly effective for isolating high yielding lines in okra.

Key words: Generations mean analysis, okra, additive
Okra [*Abelmoschus esculentus* (L.) Moench] is an annual vegetable crop grown in tropical and subtropical regions of the world. It is more remunerative than the leafy vegetables. Fruit yield is the ultimate product of action and interaction of a number of fruit yield components, which are governed by a large number of genes having small effects and greatly influenced by environment. Information on presence of type of epistatic gene effects in the inheritance of various quantitative traits is important for adopting suitable breeding procedures to improve the traits. Generation mean analysis (1) gives a comprehensive picture of gene controlling the trait. It is relatively a simple first degree statistically analyzed technique to know the predominant gene effects that are responsible in effecting the variation of a character. Thus, in the present investigation, genetic parameters viz., additive, dominance and epistatic gene effects were estimated through generation mean analysis for 11 quantitative traits in six crosses of okra.

MATERIALS AND METHODS

Ten parents were selected for making six independent crosses viz., VRO-5 x GO-2(I), VRO-3 x VRO-5(II), KS-404 x HRB-108-5(III), D-1-87-5 x KS-404(IV), Arka Anamika x Parbhani Kranti (V) and HRB-55 x Arka

Abhay(VI) to study the gene effects through generation mean analysis. The experiment with six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) generated in previous two season was grown in a randomized block design with three replications during khrif 2006 at Vegetable Research Station, Junagadh Agricultural University, Junagadh. Each replication was divided into six compact blocks and each block had a single cross of six basic generations. Each block comprised eleven rows consisting of single row each of P_1 , P_2 and F_1 , two rows each of BC_1 and BC_2 and four row of F_2 . Each row was 3.0 m long with a spacing 60 cm x 30 cm. The data were recorded from five plants selected randomly from each P_1 , P_2 and F_1 and 20 plants from F_2 generation in each replication. Observations were recorded for 11 traits viz., days to flowering, days to first picking, plant height (cm), number of branches per plant, number of nodes per plant, inter nodal length (cm), number of fruits per plant, fruit length(cm), fruit girth (cm), average fruit weight (g) and fruit yield (g). The mean values were subjected to generation mean analysis as per the method given by (1,2). The scaling and joint scaling tests for each character were performed as per the method suggested by (3) and (4), respectively. The genetic parameters were estimated according to (1).

Table-1: Estimates of scaling test and gene effects for 11 character in six okra cross

cross	Scale			Genetic Parameter						Epistasis
	A	B	C	m	d	h	j	i	j	
Days to flowering										
I	-1.00 ± 0.59	-0.73 ± 0.93	-0.27 ± 0.93	45.99 ± 0.18**	1.00 ± 0.17**	-2.30 ± 0.35**	-6.00 ± 0.81**	-0.17 ± 0.34	10.73 ± 1.45**	D
II	-2.53 ± 0.55**	-2.20 ± 0.56**	-1.27 ± 0.89	48.03 ± 0.15**	1.13 ± 0.20**	-7.54 ± 0.89**	-5.33 ± 0.07**	1.30 ± 0.32**	9.00 ± 1.37**	D
III	-0.53 ± 0.55	-3.13 ± 0.50**	-1.67 ± 0.93	42.83 ± 0.14**	-0.73 ± 0.25**	-8.57 ± 0.83**	-1.93 ± 0.85*	1.33 ± 0.79	-1.97 ± 0.34**	C
IV	0.07 ± 0.52	3.87 ± 0.57**	-2.47 ± 0.84**	43.92 ± 0.14**	0.97 ± 0.28**	-4.87 ± 0.81**	-4.00 ± 0.75**	0.87 ± 0.32**	6.93 ± 1.33**	D
V	-0.60 ± 0.54	-2.33 ± 0.49**	1.07 ± 0.82	45.96 ± 0.13**	0.47 ± 0.26	-6.76 ± 0.77**	-3.47 ± 0.70**	-1.80 ± 0.30**	1.87 ± 1.26	D
VI	-1.00 ± 0.48*	2.60 ± 0.28**	5.07 ± 0.81**	44.65 ± 0.12**	-4.03 ± 0.25**	-	-	-	-	
Days to first picking										
I	3.53 ± 0.59**	3.13 ± 0.57**	5.13 ± 0.93**	52.22 ± 0.15**	1.00 ± 0.29**	-0.47 ± 0.92	1.53 ± 0.84	0.20 ± 0.35	-8.20 ± 1.05**	D
II	0.27 ± 0.63	0.60 ± 0.61	9.33 ± 0.57**	56.07 ± 0.16**	1.30 ± 0.32**	-9.53 ± 0.98**	-8.47 ± 0.91**	-0.17 ± 0.39	7.60 ± 1.60**	D
III	5.27 ± 0.55**	2.33 ± 0.51**	12.27 ± 0.97**	51.13 ± 0.17**	-0.47 ± 0.25	-8.67 ± 0.91**	-4.67 ± 0.85**	1.47 ± 0.31**	-2.93 ± 1.39*	D
IV	-0.57 ± 0.54	2.13 ± 0.49**	-10.20 ± 0.86**	46.71 ± 0.15**	1.77 ± 0.26**	8.67 ± 0.86**	11.87 ± 0.81**	-1.30 ± 0.31**	-13.5 ± 1.36**	D
V	-2.53 ± 0.47**	-2.93 ± 0.49**	-2.00 ± 0.78*	51.80 ± 0.13**	-0.07 ± 0.24	-3.13 ± 0.78**	-3.47 ± 0.73**	0.20 ± 0.29	8.93 ± 1.26**	D
VI	-0.26 ± 0.55	0.66 ± 0.66	0.33 ± 0.95	50.87 ± 0.18**	-3.03 ± 0.70**	-3.48 ± 0.33**	-	-	-	
Plant height										
I	-13.33 ± 2.71**	-4.00 ± 2.50	-28.00 ± 3.81**	145.83 ± 0.63**	-14.3 ± 1.43**	23.67 ± 4.08**	10.67 ± 3.81**	-4.67 ± 1.64**	6.67 ± 6.88	C
II	19.67 ± 2.56**	2.67 ± 2.83	2.33 ± 4.20**	125.33 ± 0.71**	-4.67 ± 1.55**	6.83 ± 4.22	10.00 ± 3.93*	8.50 ± 1.75*	-32.3 ± 6.85**	D
III	-6.67 ± 2.47**	5.33 ± 2.27*	-3.33 ± 3.71	152.17 ± 0.70**	4.00 ± 1.33**	7.33 ± 4.04	2.00 ± 3.85	-6.00 ± 1.53**	-0.67 ± 6.48	D
IV	8.33 ± 2.16**	-20.00 ± 2.19**	26.33 ± 3.40**	154.25 ± 0.62**	-0.17 ± 1.13	-30.6 ± 3.55**	-38.0 ± 3.75**	14.17 ± 1.44**	49.67 ± 5.67**	D
V	-5.67 ± 2.20**	-19.00 ± 2.39**	-7.67 ± 4.09	142.91 ± 0.67**	-3.76 ± 0.65**	-10.67 ± 3.55**	-17.0 ± 3.48**	6.66 ± 1.35**	41.67 ± 5.92**	D
VI	2.66 ± 2.97	-2.66 ± 2.35	30.33 ± 3.56**	123.58 ± 0.58**	-13.6 ± 1.23**	-36.00 ± 3.60**	-32.33 ± 3.40**	2.66 ± 1.43	32.33 ± 6.10**	D
Number of branches										
I	0.33 ± 0.47	-0.53 ± 0.41	0.60 ± 0.74	2.27 ± 0.12*	0.26 ± 0.12*	0.35 ± 0.25	NS	NS	NS	
II	NS	NS	NS	NS	NS	NS	NS	NS	NS	
III	-0.53 ± 0.37	-0.13 ± 0.34	-0.20 ± 0.53	2.15 ± 0.10**	0.36 ± 0.11**	0.18 ± 0.18	NS	NS	NS	
IV	0.47 ± 0.33	-0.07 ± 0.34	-1.20 ± 0.52	2.14 ± 0.09**	-0.28 ± 0.09**	0.17 ± 0.17	NS	NS	NS	
V	NS	NS	NS	NS	NS	NS	NS	NS	NS	
VI	NS	NS	NS	NS	NS	NS	NS	NS	NS	
Number of nodes per plant										
I	0.06 ± 0.48	3.93 ± 0.50**	-2.00 ± 0.84*	34.93 ± 0.14**	1.07 ± 0.23*	7.00 ± 0.79**	6.00 ± 0.73**	-1.93 ± 0.29**	-10.00 ± 1.25**	D
II	10.73 ± 0.60**	-4.00 ± 0.56**	6.27 ± 0.95**	32.55 ± 0.16**	-0.47 ± 0.29	2.50 ± 0.95**	0.46 ± 0.88	7.37 ± 0.36**	-7.20 ± 1.52**	D
III	-1.33 ± 0.50**	4.80 ± 0.53**	1.33 ± 0.83	40.85 ± 0.14**	0.90 ± 0.27**	7.25 ± 0.83**	-2.13 ± 0.76**	-3.06 ± 0.34**	-5.60 ± 1.53**	D
IV	-5.13 ± 0.47**	-6.93 ± 0.48**	-6.80 ± 0.75**	35.80 ± 0.13**	-3.63 ± 0.26**	-4.80 ± 0.79**	-5.27 ± 0.75**	0.90 ± 0.29**	17.33 ± 1.29**	D
V	2.07 ± 0.48**	2.93 ± 0.48**	6.00 ± 0.89**	32.75 ± 0.15**	1.20 ± 0.21**	1.03 ± 0.81	-1.00 ± 0.75	-0.43 ± 0.27*	-4.00 ± 1.29**	D
VI	-0.53 ± 0.45	0.60 ± 0.51	0.40 ± 0.73	31.65 ± 0.13**	2.89 ± 0.14**	1.67 ± 0.24**	-	-	-	
Inter nodal length										
I	1.70 ± 0.27**	0.73 ± 0.27**	-2.70 ± 0.47**	7.45 ± 0.07**	0.47 ± 0.13**	5.67 ± 0.44**	5.13 ± 0.39**	0.48 ± 0.17**	-7.57 ± 0.69**	D
II	NS	NS	NS	NS	NS	NS	NS	NS	NS	
III	-1.57 ± 0.31**	0.36 ± 0.06**	8.52 ± 0.41**	-0.23 ± 0.17	-2.73 ± 0.45**	-3.00 ± 0.42**	-0.97 ± 0.19**	-	4.20 ± 0.79**	D
IV	-0.43 ± 0.23	-0.47 ± 0.24	-0.60 ± 0.35	7.38 ± 0.07**	-0.33 ± 0.06**	-0.44 ± 0.13**	-	-	-	
V	0.27 ± 0.24	0.07 ± 0.24	-1.40 ± 0.40**	6.97 ± 0.07**	-0.42 ± 0.12**	1.75 ± 0.40**	1.73 ± 0.40**	0.10 ± 0.15	-2.07 ± 0.63**	D
VI	-0.13 ± 0.21	-0.36 ± 0.22	1.20 ± 0.35**	6.85 ± 0.06**	-0.36 ± 0.11**	-1.62 ± 0.36**	-1.70 ± 0.33**	0.11 ± 0.14	2.20 ± 0.58**	D

Table-1: Contd....

cross	Scale			Genetic Parameter						epistasis	
	A	B	C	m	d	h	i	j	l		
Number of fruits per plant											
I	0.93 ± 0.60	3.13 ± 0.59**	1.67 ± 0.84*	26.92 ± 0.14**	0.83 ± 0.33*	8.40 ± 0.93**	5.73 ± 0.88*	1.10 ± 0.38**	-9.80 ± 1.58*	D	
II	0.67 ± 0.56	-2.00 ± 0.52**	-1.00 ± 0.88	21.08 ± 0.14**	-4.07 ± 0.27**	-2.73 ± 0.85**	-0.33 ± 0.77	1.33 ± 0.32**	1.67 ± 1.38	D	
III	1.87 ± 0.58**	5.33 ± 0.61**	7.60 ± 1.01**	30.98 ± 0.14**	0.23 ± 0.27	3.83 ± 0.87**	-0.40 ± 0.76	-1.73 ± 0.33**	-6.80 ± 1.47**	D	
IV	-3.00 ± 0.41**	1.07 ± 0.46*	-9.33 ± 0.70**	24.77 ± 0.12**	-4.30 ± 0.23**	9.60 ± 0.71**	7.40 ± 0.67**	-2.03 ± 0.27**	-5.47 ± 1.15**	D	
V	-3.00 ± 0.45**	-1.48 ± 0.43**	2.47 ± 0.73**	22.70 ± 0.13**	0.20 ± 0.22	-6.97 ± 0.74**	-6.38 ± 0.69**	-0.77 ± 0.27**	11.40 ± 1.17**	D	
VI	-0.26 ± 0.47	1.40 ± 0.65	5.33 ± 0.74**	24.51 ± 0.12**	2.90 ± 0.25**	-4.36 ± 0.75**	-5.60 ± 0.70**	-0.13 ± 0.30	5.87 ± 1.26**	D	
Fruit length											
I	0.20 ± 0.33	-0.03 ± 0.31	0.33 ± 0.48	15.94 ± 0.09**	-0.99 ± 0.09**	0.15 ± 0.18	0.15 ± 0.18	0.15 ± 0.18	0.15 ± 0.18		
II	0.20 ± 0.30	0.17 ± 0.26	0.47 ± 0.46	13.32 ± 0.08**	-1.72 ± 0.09**	-0.67 ± 0.17**	-0.67 ± 0.17**	-0.71 ± 0.17**	-3.57 ± 0.73**	D	
III	2.10 ± 0.28**	0.66 ± 0.29*	1.97 ± 0.44**	16.00 ± 0.08**	1.50 ± 0.15**	2.65 ± 0.44**	0.80 ± 0.40*	0.62 ± 0.16**	-7.80 ± 0.74**	D	
IV	2.93 ± 0.27**	1.70 ± 0.29*	1.46 ± 0.46**	14.23 ± 0.08**	-0.38 ± 0.14**	3.10 ± 0.45**	3.17 ± 0.41**	0.60 ± 0.35	0.67 ± 0.15**	D	
V	1.83 ± 0.20**	0.50 ± 0.26	1.73 ± 0.36**	13.80 ± 0.06**	1.08 ± 0.12**	0.65 ± 0.38	0.60 ± 0.35	0.67 ± 0.15**	-2.93 ± 0.61**	D	
VI	2.70 ± 0.22**	0.76 ± 0.24**	3.37 ± 0.37**	14.31 ± 0.07**	0.77 ± 0.12**	0.23 ± 0.38	0.10 ± 0.35	0.97 ± 0.15**	-3.57 ± 0.61**	D	
Fruit girth											
I	NS	NS	NS	NS	NS	NS	NS	NS	NS		
II	0.33 ± 0.26	0.67 ± 0.29*	2.03 ± 0.44**	5.93 ± 0.08**	-0.68 ± 0.14**	-1.35 ± 0.45**	-1.03 ± 0.43*	-0.17 ± 0.17	0.03 ± 0.72	D	
III	-0.10 ± 0.30	-0.63 ± 0.26*	-0.76 ± 0.42	5.98 ± 0.07**	0.80 ± 0.15**	0.45 ± 0.43	-0.07 ± 0.41	0.22 ± 0.10*	0.90 ± 0.74	C	
IV	-0.37 ± 0.19	-0.63 ± 0.21**	-0.87 ± 0.31**	5.30 ± 0.05**	-0.23 ± 0.10*	-0.23 ± 0.32	-0.13 ± 0.30	0.13 ± 0.12	1.13 ± 0.52*	D	
V	NS	NS	NS	NS	NS	NS	NS	NS	NS		
VI	-0.13 ± 0.23	-0.10 ± 0.22	0.56 ± 0.36	5.78 ± 0.06**	0.27 ± 0.07**	-0.16 ± 0.13	-0.16 ± 0.13	-0.16 ± 0.13	-0.16 ± 0.13		
Average fruit weight											
I	-1.00 ± 1.70	-1.93 ± 3.28**	2.40 ± 0.98*	18.93 ± 0.16**	0.93 ± 0.29**	-3.87 ± 0.96**	-5.33 ± 0.89*	0.47 ± 0.35	8.27 ± 1.55**	D	
II	1.13 ± 0.54*	1.93 ± 0.51**	-0.67 ± 0.83	16.10 ± 0.14**	-1.86 ± 0.27**	3.20 ± 0.83**	3.73 ± 0.77**	-0.40 ± 0.33	-6.80 ± 1.35**	D	
III	0.67 ± 0.50	0.67 ± 0.54	0.93 ± 0.85	17.61 ± 0.16**	0.56 ± 0.15**	2.62 ± 0.31**	0.32 ± 0.25	0.32 ± 0.25	0.32 ± 0.25		
IV	-0.07 ± 0.44	0.40 ± 0.44	0.13 ± 0.80	16.75 ± 0.12**	-0.66 ± 0.11**	-0.33 ± 0.70	-0.27 ± 0.65	0.60 ± 0.27*	-2.00 ± 1.12	C	
V	1.73 ± 0.46**	0.53 ± 0.40	2.53 ± 0.71**	16.66 ± 0.13**	-0.26 ± 0.22	0.83 ± 0.23**	2.10 ± 0.75**	1.73 ± 0.71*	0.40 ± 0.28	-3.20 ± 1.20**	D
Fruit yield											
I	-12.13 ± 22.45	-1.73 ± 22.05	25.60 ± 33.62	459.60 ± 5.90	44.45 ± 5.64	90.50 ± 12.03	13.60 ± 10.99	13.60 ± 10.99	113.4 ± 44.21*	D	
II	29.80 ± 14.61*	2.60 ± 18.72	-48.67 ± 24.45*	339.80 ± 4.21**	-108.5 ± 8.66**	22.60 ± 26.48	81.07 ± 24.16*	81.07 ± 24.16*	-27.87 ± 12.41*	D	
III	52.87 ± 21.52*	108.60 ± 22.93**	157.13 ± 38.16**	586.90 ± 5.50**	-20.77 ± 9.85*	154.30 ± 33.60**	4.33 ± 29.78	4.33 ± 29.78	-165.8 ± 55.2**	D	
IV	-54.27 ± 15.53**	29.80 ± 17.11*	-158.00 ± 28.68**	418.80 ± 4.39**	-55.30 ± 7.58**	176.93 ± 25.82**	133.53 ± 23.50**	133.53 ± 23.50**	-42.03 ± 8.99*	D	
V	-9.66 ± 12.92	-12.46 ± 11.87	18.26 ± 21.37**	378.72 ± 4.15**	-3.70 ± 6.31	-124.10 ± 21.92**	122.40 ± 20.85**	122.40 ± 20.85**	1.40 ± 8.29	D	
VI	23.20 ± 15.23	5.86 ± 14.35	78.40 ± 22.88**	405.75 ± 3.87**	68.37 ± 7.75**	-21.77 ± 23.30	-49.33 ± 21.66*	8.86 ± 9.23	20.27 ± 38.53	D	

* , ** Significant at P=0.05 and 0.01, respectively
 I = VRO-5 x GO-2, II = VRO-3 x VRO-5, III = KS-404 x HRB-108-5, IV = D-187-5 x KS-404, V = Arka Anamika x Parbhani Kanti
 VI = HRB-55 x Arka Abhay

RESULTS AND DISCUSSION

Estimates of scaling test and gene effects viz., m, d, h, i, j and l parameters are presented in Table-1. A simple additive-dominance model was adequate to detect the genetic differences in cross I for days to flowering and fruit yield per plant, in cross V for number of nodes per plant and fruit girth, in crosses I and IV for number of branches plant per plant, in crosses I and II for fruit length and in crosses III and IV for fruit girth, while for other characters in all the six crosses the presence of digenic interaction played an important role for governing these traits. Similar results were also obtained by (5).

Additive effect was significant for fruit yield per plant in crosses II, III, IV and VI. These crosses also showed significant additive effect for average fruit weight, number of fruits per plant, number of nodes per plant, plant height, days to flowering and days to first picking. Dominance effect was found to be important for all the characters in all the six crosses except number of branches per plant and fruit girth. The present findings are in agreement with the results obtained by (6).

Both additive and dominance effect were significant for days to flowering and number of fruits per plant in crosses I, II, III, IV and V, for days to first picking in crosses II, IV and VI, for number of nodes in crosses II, III and VI, for fruit length in crosses I, II and IV, for average fruit weight in crosses I, II, III and VI and in crosses III and IV for fruit yield per plant. These findings are in accordance with the result of (6).

Among the interaction components, the fixable (additive x additive) interaction effect was significant for days to flowering in crosses II, III, V and VI, for days to first picking in crosses II, III, IV and V, for number of branches per plant in crosses I, II, IV, V and VI, for number of nodes per plant in cross VI, for fruit length in crosses III and IV, for fruit girth in crosses IV, V and VI, for average fruit weight in crosses II, IV, V and VI and for fruit yield in crosses II, IV, V and VI, while non fixable (dominance x dominance) interaction was significant in crosses III, IV and V for days to flowering and fruit length, in crosses III and IV for days to first picking and average fruit weight and in crosses I, II, III, IV and V for plant height and number of fruits per plant. Additive x dominance (non-fixable) interaction was

observed for almost all the characters except number of branches per plant and fruit girth.

Duplicate type of epistasis was predominant in the most of characters except number of nodes per plant. Duplicate type of epistasis for fruit yield and its component were earlier reported by (7). Inheritance of these traits might pose problems in their genetic improvement but one can expect some progress in the selection programme due to presence of substantial amount of non-allelic gene interaction (8). Complementary epistasis was observed in cross IV for days to flowering, in cross III for fruit girth and in cross V for average fruit weight and selection for these traits could be effective at advance generation.

The present study revealed that different type of genes effect were responsible for the inheritance of same traits in different crosses and different traits in same cross. Most of the quantitative traits were governed by both fixable and non fixable gene effects. The characters in which additive gene effect is predominance, simple selection method can be used efficiently. However, the traits for which additive x additive gene effect is also important, it is possible to get transgressive segregants in advanced generation for fixing that particular trait. The presence of dominance gene action and duplicate type of epistasis would slow down the progress of selection. In such situation to exploit additive, dominance and epistasis gene effect simultaneously and to break down undesirable linkage, biparental mating as well as mating of selected plant in early segregating generations would be advantageous in developing okra population.

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