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Research Article

Genetic analysis for fruit yield and yield attributes in okra (*Abelmoschus esculentus* L. Moench)

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Abstract

The components of gene effects for yield and its components in okra were studied using generation mean analysis from six generations (P_1, P_2, F_1, F_2, BC_1, and BC2) derived from six different genotypes. Joint scaling test was applied to detect the presence of epistasis. Epistasis was detected in both the cases. Prevalence of duplicate type of epistasis was observed in all the cases except number of fruits/ plant, fruit length in C_1 (IC 3307 x IC 433645), fruit diameter, inter node length in C_2 (IC-43736 x Parbhani Kranti), fruit length, fruit diameter and fruit weight in C_3 (IC-342075 X IC-332453). Additive, dominance and epistatic gene effects contribute significantly to the inheritance of various yield characters studied. The joint scaling test confirmed the inadequacy of the additive dominance model in most of the crosses for majority of the characters and indicated the presence of epistasis. Low narrow sense heritability values for most of the characters indicating that these characters are more influenced by the environment and they cannot be improved by simple selection.

Key words
Okra, generation mean analysis, gene action, yield

Introduction

Okra (*Abelmoschus esculentus* L. Moench), popularly known as bhendi or lady’s finger, is primarily a warm season, annual vegetable crop grown mainly for its tender green fruits. The realisable yield potential in this crop as revealed by available literature is much higher than that has been achieved so far in India. Therefore, a suitable crop improvement programme to increase yield in this crop is inevitable. In a crop improvement programme, understanding of the genetics of yield contributing characters facilitate tailoring of suitable breeding strategies. In this respect, generation mean analysis is relatively simple and statistically reliable tool suitable for preliminary estimation of various genetic effects (Mather *et.al.* 1971). Estimation and interpretation of non-allelic interactions are more progressive with generation mean analysis as it utilises the first order statistics which are less compounded with each other when compared with variance estimates. Moreover, the populations evaluated in these studies can be utilised in actual breeding programme.

In the present study, generation mean analysis for fruit yield and yield attributes involving genetically divergent parents and their crosses in okra was taken up to understand the genetic basis of such characters in each of the populations.

Material and Methods

Data on the crop comprising six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) all grown in a year for each of the following three cross combinations, were collected and computed in this study. The cross combinations were C_1: IC 3307 x IC 433645; C_2: IC- 43736 x Parbhani Kranti ; and C_3: IC-342075 x IC-332453. Seeds of the parents used in the present study were collected from NBPGR, Regional Station Akola, Maharashtra. The initial crosses were made at the Experimental Farm, C Block; B.C.K.V. Kalyani, Nadia (W.B.) during the Kharif season of 2012 and subsequent generations (F_2, BC_1 and $BC_{2\ for}$ each of the crosses) were developed during Rabi season of 2012. Seed of all the six generations were gown in a randomised block design with three replications during Kharif 2013. There were three rows of 3m length grown at a spacing of 60 cm between rows and 40 cm between plants for each of the parents and crosses. Recommended package of practices were adopted to raise the crop. Five competitive plants were selected randomly and tagged from the middle row of each of (P_1, P_2, F_1 and BC_1 and BC_2 10 plants and F_2 20 plants) in each replication for recording observation on eleven plant characters viz, days to first flowering, days to 50% flowering, number of fruits/plant, fruit length (cm), fruit diameter (cm), weight/ fruit (g), plant height (cm), number of primary branches/plant, number of nodes on main stem, inter nodal distance and fruit yield/ plant (g). The analysis of variance for randomised block design was performed cross-wise for all the characters as per standard procedure (Panse *et. al.*, 1969). The mean values of various generations were subjected to simple scaling test A, B, C and D (Hayman *et. al.*, 1955) to justify the adequacy of additive dominance model. In case of significance of any of the scaling tests, data were then subjected to the estimation of various genetic components with six parameter model m, d, h, i, j and l (Hayman, 1958). More precise estimate of various parameters was then obtained by applying weighed joint scaling test (Cavalli, 1952). In the event of non significant estimates of simple scaling test ad joint scaling test, i.e. adequacy of additive dominance model, the three parameter model (Cavalli, 1952), which is based on least square estimates (weighed analysis) was used to determine main effects, m, d and h. The statistical analysis of present study was carried out by using INDOSTAT software.

Results and Discussion

The analysis of variance for all the characters under study is presented in Table 1. The mean squares due to the six generations P_1, P_2, F_1, F_2, BC_1 and BC_2 were highly significant for all the characters in the three crosses. The magnitude of the mean squares was very high for fruit yield per plant and plant height in all the three crosses. This necessitated further scaling test to detect the presence or absence of epistasis and the estimation of the genetic components.

Accordingly, the estimates of the scales A, B, C and D as proposed by Mather (1949) and six genetic parameters m (mean), d (additive), h (dominance), i (additive x additive), j (additive x dominance) and l (dominance x dominance) as proposed by Jinks and Jones (1958) were worked out and presented in Table 2. The results of scaling tests revealed that simple additive - dominance model was inadequate to explain the nature of gene action for most of the characters in all the crosses studied except number of fruits per plant and inter node length in C_1 and fruit length, fruit diameter and number of nodes on main stem in C_3. Therefore, the importance of non allelic interactions (epistasis) in most of the cases has been manifested. Similar observations for the morphological characters had earlier been reported by Tripathi *et al.* (2002), Kumar *et al.* (2005) in okra and Patel *et al.* (2006) in chilli. The mean effects ‘m’ were highly significant in all the characters of different crosses. Significant additive gene action (d) in all the characters except fruit diameter in C_1 and fruit length in C_2 revealed importance of additive gene action. Similar opinion was put forth by Biju *et al.* (2007) and Tripathi *et al.* (2002) in okra.

The dominance component (h) also was predominantly significant for most of the characters in all the crosses except for number of nodes on main stem per plant in C_2 and fruit weight and fruit yield in C_3 thus suggesting the importance of dominance gene effects in the expression of all such characters. The above results thus indicated both additive and dominance gene effects to be equally important for the inheritance of the characters conforming observations of Biju *et al.* (2007), Tripathi *et al.* (2002) and Patel *et al.* (2006). Since the dominance component was generally higher in magnitude than additive component, they were in the negative direction in most of the crosses for majority of the characters. Therefore, decreased expression of characters due to dominance gene effect might have been manifested and consequently, selection would be effective in the latter generations only. Panda *et al.* (2001) also were of similar opinion in okra. Considering epistatic gene effects, additive × additive (i) type was significant and important in all the characters under study in the three crosses except for number of fruits per plant and plant height in C_1 and fruit lengthin C_3. As observed by Tripathi *et al.* (2002) and Kumar *et al.* (2005) values of genetic component (i) in many of these crosses were in the negative direction indicating little scope of improvement through simple line selection. Additive × dominance (j) type interaction was found to be operative in C_2 for number of primary branches per plant and for fruit yield per plant in C_3. Interestingly, dominance × dominance (l) type of gene interaction was significant for all the three crosses for all the characters studied. The above findings thus indicated that besides additive and dominance gene effects, the epistatic effects are also important in the expression of the characters studied. Ahmad *et al.* (2004) and Deo *et al.* (2004) advocated the significance of additive gene effects for the control of marketable yield per plant in okra.

Perusal of Table 2 further reveals that duplicate type of epistasis was prevalent for all the characters studied in the three cross combinations except for number of fruits per plant in C_1, fruit length in C_1 and C_3, fruit diameter in C_2 and C_3, fruit weight in C_3, inter node length in C_2 and fruit yield per plant in C_1 where complementary type of epistasis was evident. Similar type of duplicate and complimentary epistasis gene action has earlier been recorded by Biju *et al.* (2007).

Duplicate epistasis as observed in the crosses for majority of the characters may result in decreased variation in F_2 and subsequent generations and consequently reduce heterosis and also might hinder the pace of crop improvement through selection alone. However, such characters including yield indicated that they might be improved through recurrent selection practiced in the progenies obtained through biparental mating system that in turn would help in exploiting the duplicate type of non-allelic interaction and allow recombination and concentration of genes resulting cumulative effects in population since this method is helpful in breaking up undesirable linkages as suggested by Panda and Singh (1998) and Tripathi (2002). Complementary epistasis as evident from the crosses of some characters may lead to a situation in which selection would be effective in advanced generations to pick up superior segregants. Chandra Deo *et al.* (1997) opined similar type of gene action from their studies in okra. The present study indicated that additive, dominance and epistatic gene effects contribute significantly to the inheritance of yield and its attributes. Therefore, few cycles of recurrent selection followed by pedigree method would be effective and useful to utilize all the three types of gene effects. It might lead to increased variability in later generations for effective selection by obtaining considerable heterogeneity and heterozygosity through mating of selected plants in early segregating generation.

The χ^2 values obtained from the joint scaling test following Cavalli (1952) along with the elucidation about the epistasis (Table 3) revealed that four characters, *viz.* number of fruits per plant, fruit length, fruit weight and inter node length in $C_{1;}$ inter node length in C_2 and three characters *viz*; fruit length, fruit diameter and number of nodes on main stem per plant in C_3 showed absence of epistasis due to non significant χ^2 values and all the remaining characters in the three crosses showed presence of epistasis. The χ^2 values revealed that seven characters had presence of epistasis in all the three crosses.

The joint scaling tests (Table 4) combined the whole set of scaling tests into one and thus offered a more informative approach. The significance of the χ^2 tests in all the three crosses for all the characters studied except the characters that revealed absence of epistasis corroborated the findings of the scaling test proposed by Mather (1949). Therefore, the joint scaling test confirmed the inadequacy of the additive-dominance model in most of the crosses for majority of the characters and indicated the presence of epistasis.

The estimates of gene effects, variance components and allied statistics in the absence of epistasis are presented in Table 4. The characters indentified on the basis of χ^2 test *viz.*, number of fruits/plant, fruit length, fruit weight and inter node length in $C_{1,}$ inter node length in C_2 and fruit length, fruit diameter, number of nodes on main stem per plant in C_3 showed degree of dominance to be greater than one. All the characters showed low heritability (narrow sense). In the absence of epistasis, the main effects i.e., additive and dominance gene effects accounted for the total phenotypic mean performance of the crosses (Table 4). The table further reveals that among main effects additive component (d) was significantly positive for inter node length and significantly negative for number of fruits per plant, fruit length and fruit weight in $C_{1;}$ in case of C_2 however, it was significantly positive for inter node length and in case of C_3 it was significantly negative for fruit length and fruit diameter and positively significant for number of nodes on main stem per plant.

It may, therefore, be concluded that there was preponderance of additive gene effects for these characters. However, considering dominance component (h), all the above characters under respective crosses had significant values thereby indicating the predominance of non-additive gene effects. The degree of dominance was greater than unity for many of the characters distributed in the three crosses. Therefore, over dominance might be the cause of heterosis for them. Narrow sense heritability values were low for most of the characters indicating that these characters are more influenced by the environment and selection would not be successful in improving them and environment played an important role in their expression and they cannot be improved by simple selection.

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Table 1. Analysis of variance of the six generations for the three crosses

Characters	Treatment df	Error df	Mean square(MS)		
			C_1(IC 3307 x IC 433645)	C_2 (IC- 43736 x Parbhani Kranti.)	C_3(IC-342075 X IC-332453)
Days to 1st flowering	5	10	11.66***	24.48***	18.5***
Days to 50% flowering	5	10	9.15**	28.35***	26.53***
Number of fruits / plants	5	10	7.72**	13.64***	17.52***
Fruit length (cm)	5	10	3.47**	3.01***	1.96***
Fruit diameter (mm)	5	10	0.37	0.03***	3.83***
Fruit weight (g)	5	10	5.38***	4.31***	7.89***
Plant height (cm)	5	10	142.0***	239.2***	102.1***
Number of primary branches / plant	5	10	0.43**	0.72***	0.30***
Number of nodes on main stem / plant	5	10	13.88***	18.77***	19.45***
Inter node length (cm)	5	10	0.76*	0.37***	0.32**
ruit yield / plant (g)	5	10	4441.9***	7195.4***	12112.1***

*; **: *** Significant at 5%, 1% and 0.1% level of probability. C_1=Cross number 1, C_2=Cross number 2 & C_3=Cross number 3

Table 2. Scaling test and gene effects of yield and its attributing characters in okra crosses, following six parameter model following Jinks and Jones (1958)

Cross	**Scale**				**Genetic component**						Epistasis
	A	B	C	D	**m**	**(d)**	**(h)**	**(i)**	**(j)**	**(l)**	
Days to 1st flowering											
C1	-5.33***	5.00***	9.67***	5.00***	36.0***	-3.00***	-11.16***	-10.0***	-5.16	10.0***	D
C2	5.33***	9.66***	5.66***	-4.66***	34.0***	0.67***	4.83***	9.33***	-2.16	-24.3***	D
C3	6.00***	5.00***	5.00***	-3.00***	34.0***	3.00***	2.50***	6.00***	0.50	-17.0***	D
Days to 50% flowering											
C1	-3.67***	3.00***	8.00***	4.33***	37.7***	-3.00**	-12.0**	-8.66***	-3.33	9.33***	D
C2	4.66***	11.0***	7.66***	-4.00***	36.3***	3.16***	3.16***	8.00***	-3.16	-23.67***	D
C3	5.33***	4.00***	7.33**	-1.00***	37.3***	3.66***	-3.00***	2.00***	0.66	-11.33***	D
Number of fruits / plant											
C1	-2.70***	1.26***	-1.50***	0.03	18.3***	-1.10***	4.05***	0.06	-1.98	1.36*	C
C2	-7.8***	-8.30***	-9.30***	3.40***	16.4***	-0.13*	-3.31***	-6.80***	0.25	22.9***	D
C3	-9.20***	-8.00***	-10.9***	3.13***	19.6***	0.46***	-2.26***	-6.27***	-0.60	23.46***	D
Fruit length (cm)											
C1	-2.40***	-3.01***	-7.47***	-1.03**	13.3***	-0.05***	3.67***	2.05***	0.30	3.67***	C
C2	-3.43***	-4.00***	-4.83***	1.30***	11.56***	0.07	-0.97***	-2.60***	0.28	10.03***	D
C3	-3.16***	-2.26***	-5.50***	-0.03	11.2***	-0.70***	1.18***	0.06	-0.45	5.36***	C
Fruit diameter (mm)											
C1	-0.76***	-1.22***	-0.71*	0.64***	11.07***	-0.14	-0.87***	-1.28***	0.23	3.26***	D
C2	3.56***	3.24***	7.72***	0.45***	11.76***	-0.33***	-1.61***	-0.91***	0.15	-5.89***	C
C3	-5.05***	-03.19	-7.30***	0.47***	10.9***	-0.99***	0.42***	-0.94***	-0.93	9.18***	C
Fruit weight (g)											
C1	-4.54***	-4.38***	-5.85***	1.53***	13.74***	-1.05***	-1.46***	-3.07***	0.08	12.00***	D
C2	-5.59***	-2.80***	-1.58***	3.41***	14.32***	-0.89***	-5.06***	-6.81***	-1.39	15.21***	D
C3	-7.10***	-4.94***	-10.04***	1.00***	11.10***	-0.93***	0.24	-2.00***	-1.08	14.04***	C
Plant height (cm)											
C1	-18.53***	-10.93***	-17.86***	5.80***	131.5***	5.13***	-8.60***	-11.60	-3.80	41.06***	D
C2	-19.06***	-26.83***	10.56***	28.23***	137.5***	8.10***	-40.38***	-56.5***	3.88	102.3***	D
C3	-26.2***	-20.0***	-23.6***	11.3***	126.4***	-1.03***	-15.8***	-22.6***	-3.08	68.8***	D
Number of primary branches / plant											
C1	-0.25***	-0.38***	1.90***	1.27***	2.36***	0.20***	-1.81***	-2.53***	0.06	3.16***	D
C2	-1.61***	-1.92***	-1.38***	1.07***	2.4***	0.32***	-1.37***	-2.14***	0.15***	5.68***	D
C3	-1.23***	-0.93***	-0.56***	0.80***	2.8***	-0.20***	-1.01***	-1.60***	-0.15	3.76***	D

Table 2. Contd.

Cross	**Scale**				**Genetic component**						Epistasis
	A	B	C	D	**m**	**(d)**	**(h)**	**(i)**	**(j)**	**(l)**	
Number of nodes on main stem / plant											
C1	-9.70***	-5.53***	-6.76***	4.23***	19.5***	-0.56***	-5.78***	-8.46***	-2.08	23.7***	D
C2	-8.26***	-9.46***	-14.76***	1.48***	18.6***	-0.88***	-0.08	-2.96***	0.60	20.7***	D
C3	-9.86	-9.83***	-10.1***	4.8***	23.4***	0.80***	-6.11***	-9.60***	-0.02	29.3***	D
Inter node length (cm)											
C1	-0.10	-0.90***	-2.73***	-0.86***	5.63***	0.33***	0.76***	1.73***	0.40	-0.73***	D
C2	1.33***	0.90***	2.1***	-0.06*	5.96***	0.40***	-0.35***	0.13*	0.21	-2.36***	C
C3	1.03***	1.40***	1.16***	-0.63***	5.43***	-0.30***	0.85***	1.26***	-0.18	-3.70***	D
Fruit yield / plant (g)											
C1	-124.5***	-63.8***	-134.9***	26.7***	250.6***	-33.7***	37.9***	-53.39***	-30.33	241.8***	C
C2	-200.5***	-164.2***	-168.1***	98.2***	234.5***	-14.9***	-112.5***	-196.5***	-18.17	561.3***	D
C3	-258.0***	-202.2***	-354.6***	52.8***	217.7***	-11.77***	-0.99	164.3***	-105.5***	565.1***	D

Table 3. χ^2 test between observed and expected means of different generations for yield and its attributing characters as per "Joint Scaling Test" proposed by Cavalli (1952)

Character	C_1 (IC- 3307 x IC -433645)		C_2 (IC- 43736 x Parbhani Kranti.)		C_3 (IC-342075 X IC-332453)	
	χ^2 value	Epistasis	χ^2 value	Epistasis	χ^2 value	Epistasis
Days to 1st flowering	246.1**	Present	531.9**	Present	9.44*	Present
Days to 50% flowering	14.49**	Present	792.2**	Present	12.18**	Present
Number of fruits / plant	0.31	Absent	5.16*	Present	23.38**	Present
Fruit length (cm)	0.27	Absent	14.5**	Present	0.19	Absent
Fruit diameter (mm)	7.75**	Present	4.07*	Present	2.68	Absent
Fruit weight (g)	0.63	Absent	54.01**	Present	3.82*	Present
Plant height (cm)	297.2**	Present	425.6**	Present	115.04**	Present
Number of primary branches / plant	3.82*	Present	16.08**	Present	3.95*	Present
Number of nodes on main stem / plant	196.6**	Present	13.87**	Present	0.01	Absent
Inter node length (cm)	3.04	Absent	3.86	Absent	38.74**	Present
Fruit yield / plant (g)	15.61**	Present	50.21**	Present	197.7**	Present

*, ** Significant at 5% and 1% levels of probability, respectively

Table 4. Estimates of gene effects (Jinks and Jones, 1958), variance components and allied statistics (Mather, 1949), when epistasis is absent for five yield related characters in okra

Cross	Gene effects			Variance components				Allied Statistics	
	m	(d)	(h)	D	H	E	V_P	$[H/D]^{0.5}$	h^2_{NS} (%)
Number of fruits / plant									
C1	18.26***	-1.10***	4.05***	0.72	-0.29	0.47	0.90	-0.40	1.62
Fruit length (cm)									
C1	13.3***	-0.52***	3.67***	0.34	-0.012	0.042	0.37	-0.035	0.71
Fruit weight (g)									
C1	13.74***	-1.05***	-1.46***	0.09	-0.16	0.31	0.24	-1.77	0.33
Inter node length (cm)									
C1	5.6***	0.33***	0.76***	-0.08	0.14	0.07	0.13	-1.75	0.05
Inter node length (cm)									
C2	5.96***	0.40***	-0.35***	0.02	-0.03	0.039	0.029	-1.5	0.05
Fruit length (cm)									
C3	11.23***	-0.7***	1.18***	0.003	0.027	0.08	0.11	9.00	0.12
Fruit diameter (mm)									
C3	10.9***	-0.99***	0.41*	0.019	-0.093	0.12	0.05	-4.89	0.07
Number of nodes on main stem / plant									
C3	23.4***	0.80***	-6.1***	0.33	-0.23	0.59	0.69	-0.69	1.03

*,significant at 5% level; ** Significant at 1% level;

C_1=(IC- 3307 x IC -433645); C_2 = IC- 43736 x Parbhani Kranti; C_3 = (IC-342075 X IC-332453);

D = Additive variance; H = Dominance variance, E = Environmental variance; V_P = Total F_2 variance (D+H+E); $[H/D]^{0.5}$ = Degree of dominance; h^2_{NS} = Narrow sense heritability.