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Generation Mean Analysis of Some Economic Traits in Okra (*Abelmoschus esculentus* L. Moench)

[1]Soher E.A. El-Gendy and [2]M.H. Abd El-Aziz
[1]Department of Vegetable Research, Institute of Horticultural Research, Agricultural Research Center, Egypt
[2]Department of Genetics, Faculty of Agriculture, Mansoura University, Mansoura, Egypt

Abstract: In order to determine the mode of gene action involved in some okra economic traits, three different crosses as started genetic materials were used for this purpose applying generation mean analysis. Significant differences for all studied traits for six populations P_1, P_2, F_1, F_2, BC_1 and BC_2 within each cross were found indicating the existence of genetic variation and possibility of selection for these traits. Insignificant negative or positive heterosis and inbreeding depression were registered in most crosses for all studied traits except in plant height. Additive-dominance model was adequate to demonstrate the genetic variation and it is important in the inheritance for weight of 100 seeds, fruit diameter, fruit length and total yield per plant traits. While, non-allelic interactions were found in the other traits for most crosses. The dominance×dominance effects were greater than additive×additive and additive×dominance, when non-additive portion is larger than additive in most cases which recorded non-allelic interaction. Phenotypic Coefficients of Variation (PCV) was higher than Genotypic Coefficients of Variation (GCV) for all traits indicating sensitivity of studied traits to the environmental conditions. GCV, PCV, heritability and expected Genetic advance GA% of mean in most crosses were found high or moderately high. As most studied traits are influenced by additive model and others showed non-allelic gene interaction, it is suggested that pedigree phenotypic selection method is a useful breeding program for improving these traits.

Key words: Okra, generation mean analysis, heterosis, inbreeding depression, additive-dominance model, non-allelic interactions, heritability, phenotypic and genotypic coefficient of variation genetic advance

INTRODUCTION

Okra (*Abelmoschus esculentus* L.) is considered one of the most important vegetable crops in Egypt having prominent position among short duration ones. As a good source of protein, carbohydrate, vitamins and minerals in the diet, the mucilaginous property of crop makes easy the consumption of bulky food (Adeniji and Kehinde, 2012). It is grown throughout the tropical and sub-tropical regions as well as in the warmer parts of the temperate regions. In order to increase the yielding potential, it is important to utilize the available genetic potential efficiently. The nature and magnitude of genetic variation present in population is elucidated by genetic analysis of quantitative traits. Estimating the type of gene effects in plant population is essential to decide the type of breeding procedure to be followed (Arora *et al*., 2010). Applying the generation mean analysis as the most common tool helps directly in the estimation of gene effects and components of genetic variance (Hayman and Mather, 1955; Hayman and Mather, 1955). Generation mean analysis can be used to evaluate the mode of gene action for quantitative traits especially its yield components. Thus, knowing the genetic diversity and relationships among breeding materials is essential to the plant breeders for improving this crop.

Several models for analysis of generation mean as was described by Anderson and Kempthorne (1954), Hayman (1958) and Gamble (1962) have been developed. Parents (P_1 and P_2), F_1, F_2 and first and second backcrosses (BC_1 and BC_2) as six basic generations were used to propose estimating mean and variance of quantitative traits. Estimating additive, dominance and epistatic effects could be done using generation mean analysis as a quantitative genetic method (Mather and Jinks, 1982). Also, heterosis breeding as an important genetic tool can be used to enrich many desirable quantitative and qualitative traits as well as facilitating yield enhancement. The presence or absence of epistasis can be detected by the analysis of generation mean using scaling test which measures epistasis accurately whether it is complementary (additive×additive) or duplicate

Corresponding Author: Soher E.A. El-Gendy, Department of Vegetable Research, Institute of Horticultural Research, Agricultural Research Center, Egypt

(additive×dominance) and (dominance×dominance) at the dysgenic level (Farshadfar *et al*., 2008). The analysis of generation mean through scaling test detects the presence or absence of epistasis as well as measuring them appropriately. It also determines the components of heterosis in terms of gene-effects (Rebetzke *et al*., 2006; Farshadfar *et al*., 2008), considering the improvement of pod yield and its components as the most frequent gool of okra breeding programs (Alake *et al*., 2012).

The present research aims to study gene action mode of some quantitative traits as well as various genetic parameters, which involved phenotypic coefficient of variation, genotypic coefficient of variation, heritability and expected genetic advance under selection in the three okra crosses.

MATERIALS AND METHODS

Experimental design: Six basic sets of generations namely P_1, P_2, F_1, F_2, BC_1 and BC_2 were derived from three crosses involving six contrasting genotypes of okra. Two local cultivars i.e., Cairo Red (HK) and Romy (R) were used in this study as well as four genetically divergent parents of okra that previously in 2009 created and developed by Soher El-Gendy (El-Gendy, 2012). These four genetically divergent parent lines are: P_1, P_6, P_7 and P_9. The crosses were referred as: $Cross_1$ (HK X R), $Cross_2$ (P_1 X P_7) and $Cross_3$ (P_6 X P_9). These crosses among the accessions were sown during summer seasons through 2010 at El-Baramon experimental farm, horticultural institute (Mansoura Research Station, ARC). In summer of 2011, F_1 seeds were planted in the field to produce F_2 seeds; subsequent flower buds were back crossed to produce the first backcross (BC_1) and second backcross (BC_2) generations. Parents, F_1, F_2, BC_1 and BC_2 from each of the three crosses were sown in a complete randomized block design (RCBD) with three replications during summer season 2012 at El-Baramon experimental farm of the horticultural institute (Mansoura Research Station, ARC).

Data from these six generations were recorded on three plants chosen at random from each plot for the following traits: Number of seeds/pod (N. S/p); Weight of 100 seeds (W100 sec g) Number of days to 50% flowering (N. DF); Plant height (PH cm); Number of Branches/plant (NB/p); Number of leaves/plant (N. L/p); Fruit Diameter (FD cm); fruit length (FL cm) and total yield per plant (TY/p kg).

Statistical and genetic analysis: Using SAS software (SAS 9.1), analyses of variances were done for six populations (The two parents, F_1, F_2, BC_1 and BC_2) within each cross with respect to all the studied traits. In addition, analysis of variance according to (RCBD) analysis of variance for the studied traits was made to detect the significance of the observed differences among and within crosses (Singh and Narayanan, 2000).

Estimation of heterosis (H_): Estimates of Heterosis (%) were computed as the percent deviation of F_1 mean performance over that either mid or better parent as follows according to Abd El-Haleem *et al.* (2010):

Heterosis from the mid-parents:

$$H_{\overline{Mp}}(\%) = \frac{\overline{F_1} - \overline{Mp}}{\overline{Mp}} \times 100 = \frac{\overline{F_1} - \frac{\overline{P_1} + \overline{P_2}}{2}}{\frac{\overline{P_1} + \overline{P_2}}{2}} \times 100$$

where, Heterosis deviation = $\overline{F_1} - \overline{Mp}$ and Variance of heterosis deviation:

$$V_{F1} + \frac{1}{4}(V_{P1} + V_{P2})$$

Heterosis from the better-parent:

$$H_{\overline{Bp}}(\%) = \frac{\overline{F_1} - \overline{Bp}}{Bp} \times 100$$

where, Heterosis deviation = $\overline{F_1} - \overline{Mp}$ and Variance of heterosis deviation = $V_{F1}+V_{Bp}$.

The t values of T-test were computed as follows:

$$\pm t_H = \frac{\text{Heterosis deviation}}{\sqrt{\text{Variance of heterosis deviation}}}$$

Estimation of Inbreeding depression (I.D.): Its value was computed as the percent deviation of F_2 mean than their the corresponding F_1 mean from the following equation according to Abd El-Haleem *et al.* (2010):

$$I.D.(\%) = \frac{\overline{F_1} - \overline{F_2}}{\overline{F_1}} \times 100$$

The t values of T-test of I.D. were computed as follows:

$$\pm t_{I.D.} = \frac{\overline{F_1} - \overline{F_2}}{\sqrt{V_{F1} + V_{F2}}}$$

The scaling tests (A, B and C) and their variances were computed for each trait for testing deviations of segregation from the additive and dominance model of gene effects were computed according to Mather and Jinks (1982) as follows:

$$A = 2\overline{BC_1} - \overline{P_1} - \overline{F_1} \text{ and } VA = 4V_{BC_1} + V_{P_1} + V_{F_1}$$
$$B = 2\overline{BC_2} - \overline{P_2} - \overline{F_1} \text{ and } VB = 4V_{BC_2} + V_{P_2} + V_{F_1}$$
$$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2} \text{ and } VC = 16V_{F_2} + 4V_{F_1} + V_{P_1} + V_{P_2}$$

where, V_{P1}, V_{P2}, V_{F1}, V_{F2}, V_{BC1} and V_{BC2} were estimated according to Scheffe (1959).

The t vales of T-test are calculated as follows:

$$\pm t = \frac{\text{Deviation}}{\text{Stan dard error}} = \frac{\text{Deviation (value of A or B or C)}}{\sqrt{\text{Variance of deviation}}}$$
$$t_A = \frac{A}{\sqrt{VA}} \text{ and } t_B = \frac{B}{\sqrt{VB}} \text{ and } t_C = \frac{C}{\sqrt{VC}}$$

In each test, the degrees of freedom is sum of the degrees of freedom of various generations involved. Also, the significance of any one of these scales is taken to indicate the presence of non-allelic interaction (Singh and Chaudhary, 1977).

Therefore, the six parameter model is used for estimating various genetic components i.e., m, a, d, aa, ad and dd, which stand for mean effects, additive, dominance, additive×additive, additive×dominance and dominance×dominance gene effect, respectively. These genetic components and their variances were computed according to Jinks and Jones (1958) and Khodambashi *et al*. (2012) as follows:

$$[m] = \overline{F_2}$$
$$V_m = V_{F_2}$$
$$[a] = \overline{BC_1} - \overline{BC_2}$$
$$V_a = V_{BC_1} + V_{BC_2}$$
$$[d] = \overline{F_1} - 4\overline{F_2} - \frac{1}{2}\overline{P_1} - \frac{1}{2}\overline{P_2} + 2\overline{BC_1} + 2\overline{BC_2}$$
$$V_d = V_{F_1} + 16V_{F_2} + \frac{1}{4}V_{P_1} + \frac{1}{4}V_{P_2} + 4V_{BC_1} + 4V_{BC_2}$$
$$[aa] = 2\overline{BC1} + 2\overline{BC_2} - 4\overline{F_2}$$
$$V_{aa} = 4V_{BC_1} + 4V_{BC_2} + 16V_{F_2}$$
$$[ad] = \overline{BC_1} - \frac{1}{2}\overline{P_1} - \overline{BC_2} + \frac{1}{2}\overline{P_2}$$
$$V_{ad} = V_{BC_1} + \frac{1}{4}V_{P_1} + V_{BC_2} + \frac{1}{4}V_{P_2}$$
$$[dd] = \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{BC_1} - 4\overline{BC_2}$$
$$V_{dd} = V_{P_1} + V_{P_2} + 4V_{F_1} + 16V_{F_2} + 16V_{BC_1} + 16V_{BC_2}$$

Standard error of these parameters and calculated "t" values were estimated according to Gamble (1962) and Singh and Chaudhary (1977) in a similar manner as done in case of scaling test.

In the absence of non-allelic interaction, the additive-dominance model is adequate. Thus, m, a and d their variances were estimated according to Jinks and Jones (1958) as follows:

$$[m] = \frac{1}{2}\overline{P_1} + \frac{1}{2}\overline{P_2} + 4\overline{F_2} - 2\overline{BC_1} - 2\overline{BC_2}$$
$$V_m = \frac{1}{4}V_{P_1} + \frac{1}{4}V_{P_2} + 16V_{F_2} + 4V_{BC_1} + 4V_{BC_2}$$
$$[a] = \frac{1}{2}\overline{P_1} - \frac{1}{2}\overline{P_2}$$
$$V_a = \frac{1}{4}V_{P_1} + \frac{1}{4}V_{P_2}$$
$$[d] = 6\overline{BC_1} + 6\overline{BC_2} - 8\overline{F_2} - \overline{F_1} - \frac{3}{2}\overline{P_1} - \frac{3}{2}\overline{P_2}$$
$$V_d = 36V_{BC_1} + 36V_{BC_2} + 64V_{F_2} + V_{F_1} + \frac{9}{4}V_{P_1} + \frac{9}{4}V_{P_2}$$

Significance of the genetic effects is tested in a similar manner as done in case of scaling test.

Estimation of genetic parameters

Phenotypic coefficient of variability (pcv) and genotypic coefficient of variability (gcv): Its values were computed according to Singh and Chaudhary (1977) as follows:

$$PCV = \frac{\sqrt{V_{F_2}}}{\overline{F_2}} \times 100 \text{ and } GCV = \frac{\sqrt{V_{F_2} - V_E}}{\overline{Fl}} \times 100$$

Heritability in broad sense (H^2_{bs}) was computed according to Mather and Jinks (1982) using the following equation:

$$H^2_{bs} = \frac{V_{F_2} - V_E}{V_{F_2}} \times 100 = \frac{V_{F_2} - \frac{V_{F_1} + V_{P_2} + V_{P_1}}{3}}{V_{F_2}} \times 100$$

where, V_E is environmental variance.

Heritability in narrow sense (H^2_{ns}) was computed for the characters using the following equation (Adeniji and Kehinde, 2012):

$$H^2_{ns} = \frac{2V_{F_2} - (V_{BC_1} + V_{BC_2})}{V_{F_2}} \times 100$$

Expected Genetic advance under selection (GA%): The estimate of expected genetic advance (response to selection) expressed as percentage of mean at 5% selection intensity (i) (selection differential, K = 2.06) was computed by the following formula according to Eshghi and Akhundova (2010) and Deb and Khaleque (2009):

$$GA(\%) = \frac{k \times \sqrt{V_{F_2}} \times h^2_{ns}}{\overline{F_2}}$$

RESULTS AND DISCUSSION

In this study, yield and other traits were investigated. Therefore, several analyses of variances were made in

order to test the significance of differences among crosses as well as populations within crosses. The results of the analysis of variance and the mean squares of yield and other traits of crosses and their populations are presented in Table 1.

The obtained results revealed that most generations within all crosses had significant differences of all studied traits indicating the existence of genetic variation and possibility of selection for yield and yield components. This finding indicates that the further partition of genetic variance to its components and the comparisons between means are valid with respect to the traits under study. In fact the development of any plant breeding program is dependent upon the existence of genetic variability. Furthermore, the efficiency of selection and expression of heterosis also depends largely upon the magnitude of genetic variability present in the plant population (Singh and Narayanan, 1993; Singh and Chaudhary, 1999).

Therefore, the means and standard deviations of the six generations as well as heterosis and inbreeding depression with respect to the three crosses for all studied traits are presented in Table 2.

The variance estimates from data of standard deviation for all studied traits in segregating generations were greater than that of F_1 and the parents. This showing that genetic variability does exist among the generation means in all studied crosses. Similar results were obtained by Adeniji and Kehinde (2012).

The results indicated that line P_6 was the best parent compared to the crosses and its generations in most studied traits, especially in total yield per plant with the mean value of 1.51 kg. Also, indicated that the local cultivar R was the earlier genotype with the mean value of 43.7.

Meanwhile, all of F_1's were lower than the better-parent or mid-parents value for number of seeds/pod, number of branches/plant, fruit diameter and total yield per plant. These results led to the negative heterosis values for these traits in all studied crosses which indicate that dominance direction was toward the low respective parent in these traits. However, heterosis above the better parent for weight of 100 seeds, plant height, number of leaves/plant and fruit length in cross 1, indicated that the dominance direction was toward the best parent in this cross with respect to these traits. These results were in agreement with those obtained by Abd El-Haleem *et al.* (2010).

Also, these results showed desirable negative values of heterosis over mid-parents for number of days to 50% flowering trait of all studied crosses. However the cross 2 only showed desirable negative and highly significant of heterosis over mid-parents and better-parent with values of -14.58 and -13.03%, respectively. This result indicates that the dominance direction was toward the best parent in this cross with number of days to 50% flowering trait.

Positive and significant inbreeding depression was observed for plant height trait in cross 1 and cross 3 with values of 30.7 and 30.1%, respectively. This indicates the role of dominant gene action in the inheritance of this trait. This result disagreed those obtained by Khanorkar and Kathiria (2010), while it was in agreement with the result obtained by Senthil Kumar *et al.* (2005). Also, the positive and significant inbreeding depression was observed for number of days to 50% flowering in cross 3 with value of 18.29%. This indicates the possibility to obtain desirable segregants for earliness in subsequent segregating generations of this cross. This result was in agreement with the results obtained by Khanorkar and Kathiria (2010).

On the other hand, insignificant positive or negative inbreeding depression values were registered in the other traits for all crosses. These indicated that the presence of vigor in F_2 can be attributed to additive and epistatic gene action. Such crosses in these traits are expected to give segregants superior to the better parent in these traits, which may be handled through pedigree breeding method. Similar results were obtained by Surendira Kumar *et al.* (2004). Low inbreeding depression suggests that increased retention of vigor in F_2's is expected to be mainly due to accumulation of favorable additive genes (Shukla and Gautam, 1990).

Table 1: Analysis of variance and mean squares for all studied traits of crosses and their populations

S.O.V.	D.F.	N. S/p	W100s g	N. DF	PH (cm)	N. B/p	N. L/p	FD (cm)	FL (cm)	TY/p kg
Replication (Reps.)	r-1 = 2	360	0.91*	0.2	568	1.46	260	0.27	1.27	0.010
Crosses (Crs.)	c-1 = 2	483*	1.72**	96.0**	2316**	0.62	5501**	3.43**	0.35	0.183**
Rep. within Crs. (E_a)	(r-1) (c-1) = 4	59	0.14	2.2	25	2.41	221	0.07	0.14	0.016
Populations (Pops.) within Crs.	c(p-1) = 15	2730**	0.60*	71.7**	4338**	7.20**	5543**	1.03*	1.66*	0.154**
Pops. within cross 1	(p-1) = 5	6809**	1.52**	40.4**	7693**	8.83**	993	1.80	4.35**	0.025
Pops. within cross 2	(p-1) = 5	5663**	0.95*	178.2**	5027**	17.13**	10600**	2.54	1.44	0.318**
Pops. within cross 3	(p-1) = 5	3906**	1.12**	211.4**	13308**	17.23**	21668**	1.86	4.19**	0.578**
Reps. within pops. x Crs. (E_b)	c(r-1) (p-1) = 30	109	0.26	0.7	221	1.83	610	0.57	0.75	0.023
Reps. Within pops. x cross 1	(r-1) (p-1) = 10	164	0.51	0.5	353	1.93	1082	1.00	1.59	0.059
Reps. Within pops. x cross 2	(r-1) (p-1) = 10	246	0.34	1.6	381	6.32	1577	1.48	1.16	0.042
Reps. Within pops. x cross 3	(r-1) (p-1) = 10	245	0.71	1.9	595	2.74	1003	0.93	1.74	0.034

*,**Significant at 0.05 and 0.01 levels probability, respectively, D.F: Days to 50% flowering, NS/p: Number of seeds/pod, W100s g: Weight of 100 seeds, N. DF: Number days to 50% flowering, PH (cm): Plant height, N. B/p: Number of branches plant, N. L/p: Number of leaves/plant, FD (cm): Fruit diameter, FL (cm): Fruit length, TY/p kg: Total yield per plant

Table 2: Mean performance and standard deviations of parents, F_1, F_2 and backcross generations in three okra crosses as well as heterosis and inbreeding depression for all studied traits

Traits	N. S/p			W100s g			N. DF		
Generations	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$
P_1	124.3±12.9	110.8±7.10	82.3±10.4	6.3±0.2	6.2±0.2	5.3±0.4	51.0±0.9	55.0±1.3	56.5±0.5
P_2	59.5±12.5	76.2±6.60	79.7±5.80	6.5±0.4	6.9±0.2	5.9±0.3	43.7±1.6	57.0±1.3	56.0±0.9
F_1	73.7±2.70	90.8±4.50	60.0±11.7	7.3±0.4	6.4±0.3	5.4±0.5	44.7±1.6	47.8±1.2	54.7±0.8
F_2	117.2±24.7	124.7±17.1	117.5±27.2	6.4±1.0	6.0±1.0	6.3±0.9	45.0±1.5	44.2±1.5	44.7±1.6
BC_1	46.2±19.1	46.5±15.4	47.3±19.9	5.7±0.8	5.7±0.6	5.8±0.7	45.3±0.5	45.0±1.3	45.0±1.3
BC_2	53.0±19.1	55.2±9.80	55.2±21.1	6.3±0.7	6.3±0.8	6.3±0.7	45.7±2.1	46.2±1.5	45.2±1.3
$LSD_{0.05}$	19.7	13.1	20.8	0.75	0.69	0.72	1.74	1.55	1.34
H_{Mp}(%)	-19.85	-2.85	-25.93	13.82	-2.93	-4.46	-5.63	-14.58**	-2.81
H_{Bp}(%)	-40.75**	-18.05*	-27.13	12.50	-8.19	-9.58	2.29	-13.03**	-2.38
I. D.(%)	-59.05	-37.25	-95.83	12.03	5.51	-17.13	-0.75	7.67	18.29**
Traits	PH (cm)			N. B/p			N. L/p		
Generations	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$
P_1	202±14	263±4	296±17	6.0±0.9	9.2±1.2	9.2±1.0	156±33	237±25	289±13
P_2	223±17	238±7	246±10	8.0±0.9	6.8±1.0	6.0±0.9	160±15	205±32	200±14
F_1	282±7	232±4	286±11	6.0±0.6	6.0±0.6	7.0±0.0	161±23	189±6	188±6
F_2	196±25	198±25	198±27	7.3±2.3	7.3±2.6	7.3±2.3	143±38	146±42	142±40
BC_1	192±23	196±20	196±21	4.5±1.2	4.0±1.3	4.0±1.1	131±38	130±34	130±37
BC_2	188±18	192±16	192±21	6.3±2.1	6.7±2.5	6.7±2.2	138±33	142±34	138±34
$LSD_{0.05}$	21.6	17.8	22.0	1.72	2.00	1.72	36.5	36.4	32.4
H_{Mp}(%)	32.7**	-7.5**	5.3	-14.29	-25.00	-7.69	2.1	-14.2	-23.3**
H_{Bp}(%)	26.7 **	-11.9 **	-3.6	-25.00	-34.55*	-23.64	0.5	-20.0	-35.1 **
I. D.(%)	30.7 **	14.8	30.1*	-22.22	-22.22	-4.76	11.2	23.0	24.3
Traits	FD (cm)			FL (cm)			TY/p kg		
Generations	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$
P_1	5.5±0.3	6.5±0.5	4.9±0.3	3.2±0.6	4.2±0.6	6.1±0.4	0.90±0.22	1.35±0.20	1.51±0.22
P_2	4.3±0.4	6.3±0.2	5.8±0.2	5.4±0.7	3.7±0.1	3.7±0.5	0.71±0.18	1.03±0.26	1.01±0.12
F_1	4.8±0.8	5.7±0.2	4.6±0.2	5.5±0.3	4.4±0.3	3.9±0.8	0.77±0.23	1.09±0.06	0.73±0.15
F_2	5.7±1.5	6.2±2.3	5.5±1.8	4.7±1.4	5.0±2.0	4.8±1.5	0.77±0.30	0.79±0.29	0.74±0.27
BC_1	4.5±1.2	4.9±1.7	4.5±1.2	5.0±1.1	4.8±1.5	5.0±1.1	0.74±0.31	0.78±0.29	0.74±0.31
BC_2	5.3±1.2	5.2±1.5	5.4±1.3	5.0±1.2	5.0±1.4	4.9±1.1	0.77±0.20	0.79±0.20	0.77±0.09
$LSD_{0.05}$	1.17	1.57	1.25	1.13	1.41	1.14	0.29	0.27	0.25
H_{Mp}%	-1.87	-10.65	-14.33*	29.55*	11.53	-19.59	-3.55	-8.09	-42.20*
H_{Bp}%	-12.16	-11.79	-21.43**	2.80	4.72	-34.99	-13.70	-18.94	-51.85*
I. D.%	-17.65	-8.72	-20.73	15.11	-12.03	-21.19	0.77	27.53	-1.70

*,**Significant at 0.05 and 0.01 levels probability, respectively, D.F: Days to 50% flowering, NS/p: Number of seeds/pod, W100s g: Weight of 100 seeds, N. DF: Number days to 50% flowering, PH (cm): Plant height, N. B/p: Number of branches plant, N. L/p: Number of leaves/plant, FD (cm): Fruit diameter, FL (cm): Fruit length, TY/p kg: Total yield per plant

The results of the A, B and C scaling tests for assessing the validity of additive-dominance models are given in Table 3. The values of the A, B and C scaling tests were not significant for all crosses in weight of 100 seeds, fruit diameter, fruit length and total yield per plant traits. The same results recorded for cross 1 with number branches/plant and number of leaves/plant traits and in cross 3 for number of seeds/pod trait. These findings indicate the absence of epistasis (non-allelic interaction) and the additive-dominance model was adequate to demonstrate the genetic variation. Thus, it is important in the inheritance of the above mentioned studied traits in such crosses. The result of weight of 100 seeds trait is in agreement with those obtained by Adeniji *et al.* (2007). On the other hand, the results of fruit length and total yield per plant traits were opposite with that obtained by Akhtar *et al.* (2010).

The additive gene effects (a) were significant in cross 2 for weight of 100 seeds traits as well as in cross 1 and 3 for fruit diameter and fruit length traits, while the dominance gene effect (d) was significant in cross 3 for number of seeds/pod trait. This finding, explain the role of both additive and dominance gene effects in inheritance of these traits in such crosses.

The non-allelic interactions were found to be operating in the control of genetic variation among the six generations for all crosses in number of days to 50% flowering and plant height traits. The same result was recorded for cross 2 and 3 with number of branches/plant and number of leaves/plant traits and for cross 1 and 2 with number of seeds/pod trait. These findings indicate the presence of epistasis (non-allelic interaction) and the results were in agreement with those obtained by Akhtar *et al.* (2010).

The mean effect [m] was significant for all crosses in number of seeds/pod, number of days to 50% flowering, plant height, number of branches/plant and number of leaves/plant traits, except cross 1 for number of

Table 3: The scaling test and estimates of the genetic components: additive, dominance and interaction parameters as well as standard errors in three okra crosses for all studied traits

Traits / Scaling test and parameters	N. S/p			W100s g			N. DF		
	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$
A	-106±40*	-109±32**	-48±43	-2.16±1.57	-1.05±1.32	0.97±1.49	-5.0±2.1*	-12.8±3.1**	-21.2±2.7**
B	-27±40	-57±21*	-29±44	-1.11±1.56	-0.63±1.58	1.30±1.55	3.0±4.7	-12.5±3.4**	-20.3±2.9**
C	138±101	130±70	188±112	-1.73±4.00	-1.78±3.89	3.17±3.69	-4.0±7.2	-31.0±6.6**	-43.2±6.8**
m	117±25**	125±17**	346±123**	7.93±4.44	6.44±4.32	6.50±4.05	45.0±1.5**	44.2±1.5**	44.7±1.6**
a	-7±27	-9±18	1±6	-0.07±0.23	-0.38±0.13*	-0.32±0.25	-0.3±2.1	-1.2±1.9	-0.2±1.8
d	-289±113*	-298±78**	-628±279 *	-5.45±10.06	-1.68±9.73	0.22±9.26	-0.7±7.8	-2.5±7.2	0.1±7.6
aa	-270±113*	-295±78**	-	-	-	-	2.0±7.5	5.7±7.1	1.7±7.5
ad	-39±29	-26±19	-	-	-	-	-4.0±2.3	-0.2±2.1	-0.4±1.9
dd	403±148*	461±101**	-	-	-	-	0.0±11.2	19.7±10.2	39.8±10.0**
Traits / Scaling test and parameters	PH (cm)			N. B/p			N. L/p		
	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$
A	-100±48	-104±40*	-191±46**	-3.0±2.7	-7.2±2.9*	-8.2±2.4**	-56±86	-165±73*	-216±75*
B	-130±40**	-85±34*	-148±45**	-1.3±4.3	0.5±5.1	0.3±4.4	-47±71	-110±76	-112±70
C	-208±105	-174±101	-315±110**	3.3±9.2	1.3±10.5	0.2±9.1	-66±161	-237±171	-296±162
m	196±25**	198±25**	200±26**	14.7±10.2	7.3±2.6*	7.3±2.3*	195±182	146±42*	142±40*
a	4±29	3±26	4±30	-1.0±0.6	-2.7±2.8	-2.7±2.4	-2±18	-12±48	-8±50
d	47±118	-34±113	-9±122	-20.7±23.1	-10.0±11.8	-8.6±10.2	-173±430	-70±193	-89±190
aa	-23±117	-15±113	-24±121	-	-8.0±11.8	-8.0±10.2	-	-39±192	-32±189
ad	15±31	-9±26	-21±31	-	-3.8±2.9	-4.3±2.5	-	-28±52	-52±51
dd	253±156	204±144	363±162*	-	14.7±15.4	15.8±13.3	-	314±258	361±259
Traits / Scaling test and parameters	FD (cm)			FL (cm)			TY/p kg		
	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$
A	-1.50±2.5	-2.43±3.50	-0.52±2.5	1.27±2.25	0.90±3.08	0.05±2.41	-0.20±0.69	-0.90±0.61	-0.77±0.68
B	1.28±2.5	-1.63±3.10	0.42±2.7	-0.95±2.44	1.78±2.77	2.20±2.42	0.06±0.49	-0.55±0.48	-0.20±0.27
C	2.81±6.2	0.63±9.10	2.27±7.2	-0.82±5.87	3.05±8.01	1.42±6.11	-0.08±1.32	-1.40±1.20	-1.01±1.15
m	7.94±6.9	11.12±10.2	7.72±8.1	3.13±6.57	4.34±8.95	4.06±6.67	0.85±1.42	1.25±1.35	1.22±1.27
a	0.58±0.3*	0.08±0.30	-0.48±0.2*	-1.11±0.47*	0.26±0.31	1.16±0.30**	0.09±0.14	0.16±0.16	0.25±0.13
d	-6.18±15.6	-14.15±22.7	-5.60±18.1	3.84±14.94	2.41±20.09	2.96±15.14	-0.27±3.30	-1.66±3.14	-1.43±2.95
aa	-	-	-	-	-	-	-	-	-
ad	-	-	-	-	-	-	-	-	-
dd	-	-	-	-	-	-	-	-	-

The scaling tests (A, B and C), M = Mean, [a] = Additive effects, [d] = Dominance effects, [aa] = Additive×additive effects, [ad] = Additive×dominance effects, [dd] = Dominance×dominance effects *, **: Significant at 5 and 1% level of probability, respectively,D.F: Days to 50% flowering, NS/p: Number of seeds/pod, W100s g: Weight of 100 seeds, N. DF: Number days to 50% flowering, PH (cm): Plant height, N. B/p: Number of branches plant, N. L/p: Number of leaves/plant, FD (cm): Fruit diameter, FL (cm): Fruit length, TY/p kg: Total yield per plant

branches/plant and number of leaves/plant traits. These results indicated that the above mentioned studied traits in such crosses were quantitavely inherited exactly as what was found in accordance with (Abd El-Haleem *et al*., 2010).

The magnitude of additive gene effects (a) was small relative to the corresponding dominance effects (d) in most cases, suggesting that pedigree selection method is a useful breeding program for improving these populations. However, the negative value of (d) observed in most cases except in fruit length trait indicated that the alleles responsible for less value of the trait were dominant over the alleles controlling high value. These results are in harmony with those obtained by Alake *et al.* (2012), Adeniji *et al*. (2007) and Khattab *et al*. (2010).

The results indicated that the dominance×dominance effects were greater in magnitudes than additive×additive and additive×dominance in all cases which recorded non-allelic interaction except in case of cross 1 for number of days to 50% flowering trait. When non-additive portion is larger than additive, the improvement of these traits needs intensive selection through later generations (Khattab *et al*., 2010).

The dominance gene effect (d) was significant in all crosses for number of seeds/pod trait. These results indicated that the dominance effect (d) was important in the inheritance of this trait. Also, in this trait the additive×additive (aa) and dominance×dominance (dd) gene effect were significant in cross 1 and 2, which may lead to hinder the progress of selection leading to losses of favorable genotypes during the early generation of selection. According to (Mather and Jinks, 1982), opposite signs of additive×additive and dominance×dominance indicated prevalence of duplicate epistasis and complementary

Table 4: Magnitude of phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance in three okra crosses for all studied traits

Traits	N.S/p			W100s g			N. DF		
Genetic parameters	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$
PCV	21.10	13.71	23.14	15.25	15.95	14.08	3.44	3.33	3.660
GCV	19.10	12.79	21.63	14.27	15.46	12.52	1.33	1.82	3.230
H^2_{bs}	81.97	87.03	87.37	87.67	93.91	79.01	14.81	29.74	77.920
H^2_{ns}	80.49	85.97	86.34	84.52	91.67	74.96	11.11	26.15	73.750
GA(%)	34.98	24.29	41.15	26.55	30.12	21.74	0.79	1.80	5.550
Traits	PH (cm)			N. B/p			N. L/p		
Genetic parameters	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$
PCV	12.98	12.74	13.26	30.69	35.21	30.69	26.21	28.47	28.22
GCV	11.05	12.48	11.52	28.60	32.71	28.86	19.82	23.46	27.06
H^2_{bs}	72.43	95.96	75.41	86.84	86.33	88.38	57.18	67.89	91.95
H^2_{ns}	72.27	95.87	75.06	86.18	82.00	84.21	21.17	64.87	41.37
GA (%)	19.33	25.16	20.51	54.49	59.47	53.25	11.43	38.05	24.05
Traits	FD (cm)			FL (cm)			TY/p kg		
Genetic parameters	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$	$Cross_1$	$Cross_2$	$Cross_3$
PCV	26.59	36.32	32.46	30.72	40.08	30.77	39.24	36.16	36.37
GCV	24.67	35.98	32.14	28.12	39.28	28.28	28.16	26.73	28.02
H^2_{bs}	86.05	98.12	98.03	83.78	96.07	84.50	51.50	54.65	59.35
H^2_{ns}	79.96	97.91	97.72	80.88	95.42	83.74	50.90	52.88	52.26
GA (%)	43.80	73.27	65.35	51.18	78.78	53.07	41.15	39.39	39.15

D.F: Days to 50% flowering, NS/p: Number of seeds/pod, W100s g: Weight of 100 seeds, N. DF: Number days to 50% flowering, PH (cm): Plant height, N. B/p: Number of branches plant, N. L/p: Number of leaves/plant, FD (cm): Fruit diameter, FL (cm): Fruit length, TY/p kg: Total yield per plant

epistasis. The complementary effect will produce new recombinants capable of improving yield. Therefore, the improving of this character could be achieved through hybrid breeding method.

The phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability in broad sense (H^2_{bs}), heritability in narrow sense (H^2_{ns}) and expected genetic advance (GA%) were calculated as percent of F_2 mean for all traits are presented in Table 4.

The magnitude of PCV was higher than that of GCV for all the traits indicating that these traits are more sensitive to the environmental conditions (Abd El-Haleem *et al*., 2010). The GCV and PCV were high for number of branches/plant, number of lecules/pod, fruit diameter, fruit length, total yield per plant and number of seeds/pod for cross 3, ranged from 23.14 (in case of cross 3 for number of seeds/pod trait) to 40.08 (in case of cross 2 for fruit length trait) for PCV and ranged from 19.82 (in case of cross 1for number of leaves/plant trait) to 39.28 (in case of cross 2 for fruit length trait) for GCV. These results indicated that the maximum variability among the genotypes selected for evaluation and thus these traits provide a better selection chance of desirable genotypes (Jindal *et al*., 2010). Meanwhile, the GCV and PCV were moderate for number of seeds/pod except in cross 3, weight of 100 seeds and plant height ranged from 12.74 to 21.10 for PCV and from 11.05 to 19.10 for GCV. Also, low GCV and PCV were recorded for number of days to 50% flowering.

Heritability was estimated in each of broad and narrow sense. Estimation of broad-sense heritability indicated higher importance of genetic effects in control of traits. Comparison between broad and narrow-sense heritabilities revealed equal importance of additive and non-additive effects in genetic control of traits (Reza, 2012). The higher values of narrow sense heritability for a particular character indicated that it is controlled largely by genes acting in an additive fashion (Khanorkar and Kathiria, 2010). Thus, expected genetic advance is yet another important genetic parameter that aid breeder in a selection program (Shukla *et al*., 2004). The knowledge of heritability along with expected genetic advance aids in drawing valuable conclusions for selection of breeding methods to be employed for further improvement of the traits.

From Table 4, the results of heritabilities and expected genetic advance indicated that the heritability in broad and narrow sense were generally found to be high in magnitudes in all crosses for number of seeds/pod, weight of 100 seeds, plant height, number of branches/plant, fruit diameter and fruit length, ranged from 72.43% (in case of cross 1 for plant height trait) to 98.03% (in case of cross 3 for fruit diameter trait) for heritability in broad sense and ranged from 72.27 to 97.72% (in the above mentioned cases) for heritability in narrow sense. The analysis of expected genetic advance in percentage of mean for the above mentioned studied traits in all crosses showed that highest expected genetic advance (more than 19%) indicated good response to selection. High heritability estimates accompanied with high estimates of expected genetic advance expected in

the next generation for these traits, indicated the preponderance of additive gene action for the expression of these traits which is fixable in subsequent generations. This also provides the evidence that larger proportion of phenotypic variance has been attributed to genotypic variance and reliable selection could be made for these traits on the basis of phenotypic expression (Bello *et al*., 2012).

Moderate heritability (ranged from 51.50 to 59.35% in broad sense and from 50.90 to 52.88% in narrow sense) accompanied with high expected genetic advance (ranged from 39.15 to 41.15%) were recorded for total yield per plant trait in all crosses, providing little chance for its further improvement. However, care must be taken while breeding for this complex trait as it is considerably influenced by environmental factors. It seems a limited scope of improvement could be achieved for this trait within these genotypes (Bello *et al*., 2012).

Also, moderately high to low heritability (ranged from 77.92 to 14.81% in broad sense and from 73.75 to 11.11% in narrow sense) accompanied with low expected genetic advance (ranged from 0.79 to 5.55%) were observed for number of days to 50% flowering, which might be due to non-additive gene effects. Hence, little improvement by selection is likely in this trait. This result is in line with those reported by Abdelmageed (2010). Straight forward selection from the segregation population of this trait does not seem to be possible, the genetic variation existed in this trait could be improved successfully following reciprocal recurrent selection. Furthermore, this trait in which over dominance was involved may advantageously be utilized by the breeders to develop hybrid, as suggested by Ojaghi and Akhundova (2010).

From the above mentioned results, high and moderately high GCV, PCV, heritability and GA% of mean in most crosses for all studied traits except number of days to 50% flowering suggested that these traits could be transmitted to the hybrid progeny and phenotypic selection based on these would be effective. Also, reported low GCV, PCV, heritability and GA% for number of days to 50% flowering. This finding was due to the influence of environment on this trait.

CONCLUSION

Variations observed in this research study for all studied traits were indicative of the differences in the genetic constitution of used okra genotypes. These differences led to better chance and large scope of selection and breeding programs. Applying generation mean analysis to three special okra crosses made it possible to conclude that there was very high direct genotypic effects especially additive and non-additive variances that were found to be important in the genetic control of all studied traits. Additive-dominance model was adequate to demonstrate the genetic variation and it is important in the inheritance for yield and yield component studied traits. While, non-allelic interactions were found in the other traits for most crosses. Also, High and moderately high GCV, PCV, heritability and GA% of mean in most crosses for most studied traits except number of days to 50% flowering suggested that the phenotypic selection could be effective for improving these traits.

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