

Inheritance of Fruit Length, Diameter and Number of Fruit Ridges in Okra (*Abelmoschus esculentus* L.) Landraces of Jordan

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ABSTRACT

Nine landraces of okra were evaluated for fruit length, diameter and number of ridges per fruit. Crosses between the diverse parents for each character were made to study the inheritance of such traits in P₁, P₂, F₁, F₂, BC₁ and BC₂ generations. It is reported that fruit length, diameter and number of ridges are quantitatively inherited traits. Mean generation analysis showed that dominance is the major contribution to variation in fruit length and number of ridges per fruit, while additive gene effect was predominant over dominance gene effect for fruit diameter. Significant dominance estimate was obtained toward thin fruit diameter over wide fruit diameter and toward high ridges over low number of ridges. Broad sense heritability estimates ranged from 20.3 to 78% for fruit length, 37.8 to 99% for immature fruit diameter, 40.5 to 96.5% for mature fruit diameter and from 12 to 81.2% for number of ridges. Minimum number of genes ranged from 3 to 10 for fruit length, 0.7 to 3.16 for immature fruit diameter, and 0.7 to 4.9 for mature fruit diameter and from 0.99 to 3.7 for number of ridges, indicating effectiveness of selection in early generation.

Keywords: *Abelmoschus esculentus*, Fruit Length, Diameter, Number of Ridges, Heritability.

1. INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is an annual, self-pollinated with hermaphrodite flowers, belongs to the malvaceae family (Düzyaman, 1997). It is an important vegetable crop commercially grown in most of tropics and subtropics with an extension to the Mediterranean climate (Düzyaman and Vural, 2003), and provides an important input of vitamins and mineral salts including calcium, which are often lacking in the

diet of developing countries (Hamson et al., 1990). Despite being a minor crop, Okra has gained considerable interest as an alternative to more traditional vegetables in many countries throughout the world (Düzyaman, 2006). The origin of okra remains unclear, but centers of genetic diversity include West Africa, India and Southern Asia (Hamon and van Sloten, 1989).

In Jordan, okra occupied an area of 5357.9 dunums, which comprise 1.5% of the total area planted with vegetables in 2003. The area increased in 2004 up to 6197.1 dunums with a total production of 8666.8 tons (Department of General Statistics, 2003- 2004). Landraces of okra are becoming extinct from all parts of the country, and they are very rapidly replaced by “improved” cultivars developed and introduced from abroad. Landraces or primitive cultivars are possible source for successful

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development of improved cultivars by exploiting genetic complexes governing adaptation, or adaptability to the often very extreme environmental conditions (Kuckuck et al., 1991).

Many efforts have been made during the last four decades to enrich okra variability. Genetic resources of okra have also been utilized in new cultivars that are adapted to a wide range of agro-climatic conditions and cropping patterns, possess better fruit yield and quality (Rana and Thomas, 1990). Pod shape and flowering behavior are reported to account for most of the observable phenotypic variation among okra genotypes (Marin et al., 1981; Ariyo, 1987; Düzyaman, 2005).

The purpose of this study is to investigate the inheritance of length, diameter and number of ridges of fruit in some okra landraces collected from Jordan as critical characters affecting the marketing of this crop especially in the Mediterranean region including Jordan.

2. MATERIALS AND METHODS

Plant Material and Cultural Practices

About 55 accessions of okra were collected from different parts of Jordan and conserved in the Genetic Resource Unit at the National Center for Agriculture Research and Technology Transfer (NCARTT). For the current study, the inbred accessions were selected and planted in a Randomized Complete Block Design (RCBD) with three replications at Maru Agricultural Station. Nine diverse parents for fruit character were selected to be the parents for this study. Different crosses between the diverse parents were made, for each cross, P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 populations were developed. Seeds of all populations of all crosses were sown in the field at the Jordan University Experimental Station in the Jordan Valley. The experiment layout was the same as mentioned above. The plants were spaced 40 cm within

the row and 100 cm between the rows. Black plastic mulch and drip irrigation system with drippers placed along the laterals at 40 cm were used. Irrigation commenced at the time of planting and continued as needed.

Data Collection

Data were obtained from individual plants of P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 populations for each cross and the following characters were recorded:

1. Immature fruit diameter measured at marketing stage.
2. Mature fruit diameter measured when the fruit turns yellow.
3. Length of the mature fruit measured when the fruit turns yellow.
4. Number of ridges per fruit measured when the fruit turns yellow.

Statistical and Genetic Analysis

Frequency distributions, means and standard deviations for populations of each cross were calculated for all crosses studied according to formula outlined by Steel and Torrie (1981). Gene effects for fruit length and fruit diameter were determined according to Gamble notation (1961).

Mean effect, additive, dominance and the three types of digenic epistatic effect were calculated according to:

$$m \text{ (mean effect)} = \overline{F_2}$$

$$a \text{ (additive effect)} = \overline{BC_1} - \overline{BC_2}$$

$$d \text{ (dominance effect)} =$$

$$\overline{F_1} + 2\overline{BC_1} + 2\overline{BC_2} - \frac{1}{2}\overline{P_1} - \frac{1}{2}\overline{P_2} - 4\overline{F_2}$$

$$aa \text{ (additive} \times \text{ additive effect)} =$$

$$2\overline{BC_1} + 2\overline{BC_2} - 4\overline{F_2}$$

$$ad \text{ (additive} \times \text{ dominance)} =$$

$$(0.5)\overline{P_2} + \overline{BC_1} - (0.5)\overline{P_1} - \overline{BC_2}$$

dd (dominance × dominance effect) =

$$\overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F} - 4\overline{BC_1} - 4\overline{BC_2}$$

The variance of these estimates is obtained in the usual manner for example:

$$\sigma^2 d = \sigma^2 \overline{F_1} + 4\sigma^2 \overline{BC_1} + 4\sigma^2 \overline{BC_2} + \frac{1}{4}\sigma^2 \overline{P_1} + \frac{1}{4}\sigma^2 \overline{P_2} + 16\sigma^2 \overline{F_2}$$

Broad sense heritability (HBS) was calculated according to Walter (1987) formula:

$$HBS = \frac{VG}{VF_2}$$

where:

V_G = The genotypic variance = $V_{F_2} - V_E$.

V_{F_2} = Total phenotypic variance within F_2 individuals.

V_E = Environmental variance = $(V_{F_1} + V_{P_1} + V_{P_2})/3$.

V_{F_1} = variance of F_1 .

V_{P_1} = variance of P_1 .

V_{P_2} = variance of P_2 .

Minimum Number of Genes (N)

The minimum number of genes (N) controlling the expression of each character was calculated using the following formula by Castle and Wright (1921):

$$N = \frac{R^2}{8(V_{F_2} - V_{F_1})}$$

Where:

R = The range between extreme phenotypes in the F_2 plants.

V_{F_2} = phenotypic variance of F_2 plants.

V_{F_1} = phenotypic variance of F_1 plants.

3. RESULTS

Fruit Length

Frequency distribution, means, and standard deviations of P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 progenies in twelve crosses of okra for fruit length are presented in Table 1. In all crosses, fruit length ranged from 9 to 23 cm. In cross I between parent (48) and parent (C), the average fruit length for parents was 10.8 and 17.2 cm, respectively. This difference in fruit length among parents indicating the presence of genetic variability, and so they are suitable for genetic study of this character. Fruit length of plants in F_1 generation ranged from 11-16 cm with an average of 13.5 cm. The mean of fruit length in the F_1 is closer to the parent (48) than the parent (C) indicating partial dominance effect toward short fruit length in this cross. Plants of the F_2 generation segregated from 9 to 15 cm with an average of 12 cm. The continuous variation of progeny indicated that fruit length is a quantitative trait with probably few genes involved in controlling this trait. The mean of the F_2 fell between mid-parent and short parent, and the distribution skewed toward short fruit parent indicating that fruit length is partial dominant toward short fruit. In addition, the narrow distribution of progeny may indicate that few genes are involved in the control of this trait. The plants of BC_1 (F_1 backcrossed to P_1) segregated from 9 to 15 cm with an average of 11.9 cm, while plants of the BC_2 (F_1 backcrossed to P_2) segregated for fruit length from 15 to 19 cm with an average of 16.3 cm. The results of BC_1 and BC_2 again support that fruit length inherited quantitatively with partial dominance of fruit length toward the short fruit 1.

The same trend was observed in cross II where there was a partial dominance effect toward shorter fruit.

In cross III between parents (12) and (49), fruit

length ranged from 16 to >20 cm for parent (12), and from 18 to > 20 cm for parent (49). The average fruit length was 18.9 and 18.3 cm for parents (12) and (49) respectively. Fruit length in the F₁ generation ranged from 18 to 22 cm with an average of 19.81, the mean of the fruit length in F₁ is relatively larger than the mean of the parents, indicating that those parents may have different gene/s for fruit length. In the F₂ generation, plants ranged from 15 to 22 cm with an average of 18.2 cm, the F₂ plants segregated in classes out range of the parents indicating that these parents may possess different gene/s for fruit trait. The results of BC₁ and BC₂ generations again support the possible existence of different gene/s controlling the fruit length in the two parents.

The same trend was observed in cross IV.

Dominance gene effect was the major contribution to variation in fruit length indicated by the relative magnitude of parameter (d) to parameter F₂ mean (m) supporting the results of plant segregation of different crosses in Table 2. In most crosses, we have positive dominance effect; however, significant additive gene effect was also found indicating the presence of both additive and dominance genetic variation for fruit length. In addition, we have significant additive genetic variation and non-significant dominance in crosses III, which maybe due to the low diversity between parents. In most crosses, we have significant epistatic effect (additive x additive, additive x dominance, and dominance x dominance) which indicate that the epistatic effect have important role in the inheritance of fruit length in okra. Broad sense heritability estimates for fruit length in okra were relatively high (Table 3) for most crosses especially those contain diverse parents such as crosses I and III which have 69.6% and 78% heritability values, respectively. In general, heritability estimates ranged from 21.4% to 78 %, the low values

may be due to low diversity between the parents or due to the environmental effect.

The effective factors affecting the fruit length ranged from 3 to 10 (Table 3).

Immature Fruit Diameter

In cross I (Table 4) between parent (8) and parent (12), the average immature fruit diameter for parents was 1.30 and 1.36 cm, respectively. Immature fruit diameter in F₁ generation ranged from 1.2 to 1.8 cm with an average of 1.45 cm. The mean of F₁ generation exceeded the mean of the two parents indicating that parents may possess different gene/s for immature fruit diameter. The plants of F₂ generation ranged from 1.0 to 1.8 cm with an average of 1.43 cm. The segregation's of the immature fruit in F₂, BC₁ and BC₂ generation were in a range out side that of parents supporting the results of F₁. In cross II between parent (8) and parent (C), the average immature fruit diameter for the parents was 1.30 and 1.87cm, respectively. The plants of F₁ generation ranged from 1.0 to 2 cm with an average of 1.45 cm. The mean of F₁ generation is closer to the mean of the narrow immature fruit parent suggesting possible dominance toward narrow immature fruit diameter. In the F₂, plants segregated in few classes ranged from 1.0 to 1.8 cm with an average of 1.51 cm. The continuous variation in few classes indicated that immature fruit diameter is quantitatively inherited with probably few genes involved in controlling this trait. Also, the segregation was skewed toward narrow fruit diameter and fell between narrow diameter and mid-parent supporting that this trait is dominant toward narrow fruit diameter. The BC₁ and BC₂ segregation was toward their perspective parent confirming the results of F₁ and F₂ generations.

In cross IV between parent (48) and parent (C). The average immature fruit diameter for the two parents was

1.75 and 1.87 cm, respectively. Fruit diameter of F_1 ranged from 1.8 to 2.4cm with an average of 2.04 cm. The higher fruit diameter of F_1 plants than the parents support that the genes controlling immature fruit diameter in the both parents are different. Segregation of fruit diameter for plants in the F_2 generation ranged from 1.6 to 2.6 cm with an average of 2.23cm. The segregation of F_2 plants out range of parents again support the results of F_1 . The mean and distribution of BC_1 and BC_2 also were toward the perspective parent.

The estimates of the six parameter for the various gene effects are presented in Table 2. In cross II, additive gene effect was the major contribution to variation in the immature fruit diameter indicated by the relative magnitude of parameter (a) to parameter F_2 (m). Significant negative estimate for dominance was found in cross I indicating dominance effect for thin immature fruit diameter, and this support the results of F_1 , F_2 , BC_1 and BC_2 segregations. Crosses I, III and IV exhibit significant additive x additive gene effect, while additive x dominance was significant in cross II and III. On the other hand, all crosses showed significant dominance x dominance. Broad sense heritabilities for immature fruit diameter are presented in Table 3. High heritability estimate (99.0%) was found in cross IV, while low estimate (37.8%) was found for cross II, and intermediate estimates (63.6% , 70.3%) were found in cross III and II, and this again support that the parents in cross III are more diverse than those in cross I. The effective factors affecting fruit diameter ranged from 0.7 to 3.16 (Table 3).

Mature Fruit Diameter

Mature fruit diameter of parents and all generations under study was increased (Table 5) as compared to those of immature fruit diameter (Table 4). In cross I between parent (8) and parent (12), the average mature

fruit diameter for parents was 2.46 and 2.36 cm, respectively. Mature fruit diameter of plants in F_1 generation ranged from 2.2 to 2.8 cm with an average of 2.52cm. The mean of F_1 generation exceeded the mean of the two parents. The plants of F_2 generation segregated in classes ranged from 2.0 to 3.0 cm with an average of 2.54 cm. The segregations of F_2 , BC_1 and BC_2 generation were out range of parents supporting the results of F_1 . The same trend of immature fruit diameter for crosses II, III and IV were observed in mature fruit diameter.

Broad sense heritability estimates for mature fruit diameter are presented in (Table 3). High heritability estimates (96.5%, 97.7%) were found in cross I and IV, which mean that selection for this trait can be made in early generation. Medium estimates of 40.5%, 48.7% were found in cross III and II, respectively. The different estimates of heritability between crosses may be due to low diversity between parents, and/or to the environmental factors. The effective factors affecting fruit diameter ranged from 0.7 to 4.9 (Table 3).

Fruit Ridges

In cross I (Table 6) between parent (48) and parent (C), the average number of fruit ridges for the two parents was 8.3 and 6.6, respectively. The plants of F_1 ranged from 8 to 9 with an average of 8.1 which is closer to the mean of high number of fruit ridges suggesting strong dominance toward high number of ridges over medium number of ridges. Number of ridges in progeny of F_2 was distributed from 6 to 10. The continuous variation and lack of distinct phenotypic classes indicate that this trait is quantitative. The mean of F_2 plants was 8.28, which is closer to the mean of high fruit ridges over medium number of ridges supporting the strong dominance of high number of ridges over low number. The fruits of BC_1 distributed from 7 to 10 with an

average of 8.39, while fruits of BC₂ plants ranged from 6 to 10 with an average of 7.39. The results of BC₁ and BC₂ also support the results of F₂.

In cross III between two small numbered ridges 8 and 12, average number for the both parents was 5. In the F₁ the plants distributed from 5 to 7 with an average of 5.9 which exceeds the mean of the two parents. In F₂ generation, the progeny ranged from 5 to 7 with an average of 6.2. Plants of F₂, BC₁ and BC₂ segregated outside the range of parents. The same trend for the inheritance of number of ridges was found in the rest of crosses. The estimates of six parameter for gene effect in the number of ridges in okra are shown in Table 2.

4. DISCUSSION

The differences in the studied parameters among parents indicating the presence of genetic variability. Phenotypically diverse genotypes, presumably of diverse origins, are regarded as to be more effective in obtaining promising crosses (Düzyaman and Vural, 2002). It was found that dominance gene effect was the major contribution to variation in fruit length; however significant additive gene effect was also found indicating the presence of both additive and dominance genetic variation in fruit length, this result agreed with those of Singh (1982) who reported that pod length in okra is affected by both additive and dominance genes. Bas and Koludar (2001) found also a considerable variation in fruit shape and partly length of the mature fruits.

Chheda and Fatokun (1990) found that fruit length exhibited a wide variation range from 9 cm to 18 cm. High heritability estimates for fruit length of okra were found by Lal et al. (1977), Kirti et al. (1974), Ngag and Graham (1977) and Singh (1974). High heritability values and genetic advance estimate were obtained for fruit length of okra (Kirti et al., 1974). The inheritance of fruit length in okra was obtained as partial dominance

(Partap et al., 1980; Stino et al., 1970), additive gene effect (Thaker et al. 1983) and both additive and dominance gene action (Singh, 1982). Overdominance was also observed in fruit length suggesting that hybrid vigor can be exploited in okra for increasing yield (Sharma and Mahajan, 1978). The Yield was influenced directly and /or indirectly by pod weight and pod length suggesting that these traits would be the most useful as selection criteria in breeding for yield improvement (Palel and Dalal, 1994; Düzyaman and Vural, 2003).

To obtain unbiased estimation of minimum number of genes, this method requires the following assumptions to be fulfilled: a) linkage is absent b) one parent contributes only plus factors and the other only minus factors c) all genes are equally important d) degree of dominance of all plus factors is the same, and e) there is no epistasis. Since one or more of these assumptions may not exist in the crosses, the actual number may be difficult to estimate.

The broad sense heritability for immature fruit diameter ranged from low (37.8%) to very high (99.0%) which indicate that the parents used in this study are diverse regarding this character. Singh and Singh (1979) indicated that heritability estimate for fruit width of okra was high and genetic advances were moderate to low. Similar results were found by Lal et al. (1977), Kirti et al. (1974) and Mishra and Chhonkar, (1979). Partap et al. (1980) indicated that the okra pod diameter is controlled by complete dominance. Stino et al. (1970) demonstrated that pod width is controlled by partial dominance.

Dominance gene effect was the major contribution to variation in the number of ridges indicated by the relative magnitude of parameter (d) to parameter (m). In most crosses, dominance is significant and positive indicating that positive dominance of gene effect is important in the inheritance of fruit ridges in the

generation means studied. The estimate of parameter (a), additive gene effect, is quite small in magnitude relative to the parameter (m). Eight of crosses exhibited significant additive gene effect, indicating that genetic variation is present for number of ridges. Seven crosses exhibited significant additive x additive gene effect. Significant additive x dominance and dominance x dominance gene effects are presented in 8 and 5 crosses, respectively. Only crosses VII and VIII exhibited significant estimate for all three types of epistasis.

The additive x additive and additive x dominance gene effect appear to be relatively more important than dominance x dominance gene effect. Broad sense

heritability estimates for fruit ridges (Table 3). Cross I, broad sense heritability was 66.9% reach to 81.2% in cross II, and it varies from 12.2% in cross (VIII) to 79.7% in cross (IV). The effective factors affecting the fruit ridge ranged from 0.99 to 3.7 (Table 3). The high heritability estimates and low number of genes for number of ridges in okra fruit may indicate the effectiveness of selection in early generation. Studying pod characteristics as pod weight and diameter is very important since it has been found that both characteristics affect the total yield positively (Düzüyman and Vural, 2003).

Table (1): Frequency distributions, means and standard deviations of mature fruit length in P₁, P₂, F₁, F₂, BC₁ and BC₂ generations of different crosses of okra (*Abelmoschus esculentus* L.).

Cross	Population	Classes of mature fruit length (cm)												n	$\bar{X} \pm s.d$
		9-10	10-11	11-12	12-13	13-14	14-15	15-16	16-17	17-18	18-19	19-20	>20		
I	48	3	5	6	1									15	10.81±0.84
	C								5	6	4			15	17.26±0.75
	48 x C (F1)			1	4	6	7	2						20	13.57±0.9
	F1selfing(F2)	10	24	24	22	19	17	1						117	12.04±1.5
	BC1(F1x48)	6	11	17	11	6	7							58	11.89±1.33
	BC2(F1x C)							17	24	13	4			58	16.34±1.17
II	12								1	1	4	6	3	15	18.97±1.16
	C								5	6	4			15	17.26±0.75
	12 x C (F1)						1	4	10	4	1			20	17.48±0.83
	F1selfing(F2)							25	34	30	25	4		118	16.92±1.2
	BC1(F1x12)							2	11	18	15	7		58	18.11±1.27
	BC2(F1x C)							12	16	16	13	1		59	17.01±1.32
III	12								1	1	4	6	3	15	18.97±1.16
	49										11	3	1	15	18.33±0.97
	12 x49 (F1)										4	8	8	20	19.81±0.88
	F1selfing(F2)							16	19	26	20	19	18	117	18.17±2.16
	BC1(F1x12)							12	7	12	5	8	14	58	18.24±2.06
	BC2(F1x49)							10	13	14	11	7	4	59	17.40±1.58
IV	8								4	3	5	3		15	17.74±0.52
	C								5	6	4			15	17.26±0.78
	8 x C (F1)									7	6	6		19	18.44±1.01
	F1selfing(F2)							23	24	31	24	11	4	117	17.26±0.95

Cross	Population	Classes of mature fruit length (cm)												n	$\bar{X} \pm s.d$
		9-10	10-11	11-12	12-13	13-14	14-15	15-16	16-17	17-18	18-19	19-20	>20		
	BC1(F1x12)							12	15	19	7	4	1	58	17.14 ± 0.86
	BC2(F1x C)							7	13	21	10	6	1	58	17.57 ± 0.68

Table (1 cont.):Frequency distributions ,means and standard deviations of mature fruit length in P₁ ,P₂ ,F₁ ,F₂ ,BC₁ and BC₂ generations of different crosses of okra (*Abelmoschus esculentus* L.).

Cross	Population	Classes of mature fruit length (cm)									n	$\bar{X} \pm s.d$
		13-14	14-15	15-16	16-17	17-18	18-19	19-20	>20			
V	8				4	3	5	3		15	17.74 ± 1.03	
	12				1	1	4	6	3	15	18.97 ± 1.16	
	8 x 12(F1)				6	8	4	2		20	17.63 ± 0.88	
	F1selfing(F2)		2	37	29	24	14	11		117	18.75 ± 1.33	
	BC1(F1x8)			7	8	32	7	5		59	17.47 ± 1.39	
	BC2(F1x12)			14	18	16	8	2		58	16.89 ± 1.11	
VI	8				4	3	5	3		15	17.74 ± 1.03	
	52				5	6	4			15	17.26 ± 0.75	
	8 x 52 (F1)			3	6	4	6			19	17.14 ± 1.04	
	F1selfing(F2)			28	33	37	20	1		119	16.69 ± 1.07	
	BC1(F1x8)			5	9	11	13	16	4	58	18.13 ± 1.34	
	BC2(F1x52)			13	22	12	10	1		58	16.83 ± 1.11	
VII	1			3	6	5	1			15	16.62 ± 0.77	
	52				5	6	4			15	17.29 ± 0.86	
	1 x 52 (F1)		1	2	8	5	3			19	16.88 ± 0.97	
	F1selfing(F2)			28	31	30	18	7	3	117	16.94 ± 1.36	
	BC1(F1x1)			14	24	10	9	1		59	16.77 ± 1.24	
	BC2(F1x52)			18	16	15	8	2		59	16.63 ± 1.13	
VIII	1			3	6	5	1			15	16.62 ± 0.77	
	42				7	4	3	1		15	17.33 ± 0.97	
	1 x 42(F1)					8	8	4		20	18.29 ± 0.86	
	F1selfing(F2)			21	30	30	16	16	5	118	17.30 ± 1.47	
	BC1(F1x1)			18	19	15	3	3		58	16.74 ± 1.00	
	BC2(F1x42)			14	21	17	5			58	16.61 ± 0.99	
IX	1			3	6	5	1			15	16.62 ± 0.77	
	C				5	6	4			15	17.26 ± 0.75	
	1 x C (F1)			5	7	8				20	16.52 ± 0.69	
	F1selfing(F2)			29	31	30	24	3		117	16.84 ± 1.13	
	BC1(F1x 1)			11	15	16	13			58	17.16 ± 1.2	
	BC2(F1x C)			15	20	16	8			59	16.62 ± 0.98	

Classes of mature fruit length (cm)											
Cross	Population	13-14	14-15	15-16	16-17	17-18	18-19	19-20	>20	n	$\bar{X} \pm s.d$
X	7					8	5	2		15	17.83 ± 0.71
	34				5	6	4			15	17.29 ± 0.86
	7 x 34 (F1)			2	8	6	4			20	17.17 ± 0.94
	F1selfing(F2)			34	36	32	15	3	1	117	16.62 ± 0.94
	BC1(F1x7)			17	19	11	7			58	16.72 ± 1.35
	BC2(F1x34)		1	17	19	19	3			59	16.57 ± 0.94
XI	52				5	6	4			15	17.29 ± 0.86
	49						11	3	1	15	18.33 ± 0.97
	52 x 49 (F1)			1	6	3	7	4		21	17.72 ± 1.21
	F1selfing(F2)			12	22	17	34	16	16	117	18.0 ± 1.73
	BC1(F1x52)			11	14	16	12	5		58	17.23 ± 1.31
	BC2(F1x49)			9	18	15	11	4	2	59	16.99 ± 1.17
XII	1			3	6	5	1			15	16.62 ± 0.77
	12				1	1	4	6	3	15	18.97 ± 1.16
	1 x 12 (F1)					1	7	7	4	19	19.25 ± 0.94
	F1selfing(F2)			13	22	31	25	18	8	117	17.8 ± 1.71
	BC1(F1x1)			13	18	12	13	1	1	58	16.96 ± 1.308
	BC2(F1x12)			12	10	23	5	5	4	59	17.23 ± 1.6

Table (2): Mean generation estimate of six gene effect for fruit length in 12 crosses of okra (*Abelmoschus esculentus* L.).

Cross No.	Cross	m	a	d	aa	ad	dd
I	48 x C	12.04±1.51*	-4.44±0.23*	7.87±0.77*	8.33±0.73*	-1.22±0.27*	-9.59±1.2*
II	12 x C	16.92±1.20*	1.11±0.24*	1.91±0.7*	2.54±0.65*	0.26±0.29	-1.59±1.17
III	12 x 49	18.51±2.16*	1.04±0.34*	-1.35±1.08	-2.75±1.05*	0.00±0.39	7.39±1.67*
IV	8 x C	17.26±1.37*	-0.57±0.25*	1.80±0.76*	0.08±0.70	-0.80±0.30*	4.29±1.25*
V	8 x 12	16.75±1.33*	0.58±0.23*	0.98±0.70	1.71±0.67*	1.19±0.30*	1.55±1.16
VI	8 x 52	16.69±1.07*	1.30±0.22*	2.77±0.67*	3.13±0.60*	1.06±0.28*	-3.46±1.15*
VII	1 x 52	16.94±1.36*	0.14±0.21	-1.04±0.72	0.04±0.67	0.47±0.26	1.82±1.15
VIII	1 x 42	17.30±1.47*	0.13±0.18	-1.19±0.70	2.51±0.66*	0.48±0.24	6.34±1.04*
IX	1 x C	16.84±1.13*	0.54±0.20*	-0.24±0.62	0.19±0.58	0.87±0.25*	-0.83±1.00
X	7 x 34	16.63±0.95*	0.15±0.22	-0.31±0.61	0.08±0.56	-0.12±0.26	2.79±1.07*
XI	52 x 49	18.0±1.73*	0.23±0.23	-1.07±0.85	-3.54±0.78*	0.23±0.28	5.14±1.28*
XII	1 x 12	17.79±1.71*	-0.27±0.27	0.77±0.88	-2.81±0.83*	0.90±0.31*	8.51±1.37*

Table (3): Broad sense heritability (HBS) and minimum number of genes for fruit length diameter and number of ridges in different crosses of okra (*Abelmoschus esculentus* L.).

Cross	Length		No. of ridges		Immature diameter		Mature diameter	
	HBS	No. of genes	HBS	No. of genes	HBS	No. of genes	HBS	No. of genes
48 x C	69.6%	2.9	66.9%	3.5	70.3%	1.7	97.7%	0.7
8 x 12	40.2%	6.7	81.2%	0.85	37.8%	3.16	40.5%	3.5
8 x 52	47.8%	5.0	79.7%	1.09	99%	2.3	96.5%	4.9
3 x 1	26.8%	8.5	59.8%	1.4	63.6%	0.7	48.7%	1.08
12 x C	40.1%	7.8	64.4%	1.32				
1 x 42	65%	3.4	48.6%	1.78				
8 x C	21.4%	9.8	72.7%	1.77				
1 x 52	59%	5.1	58.7%	1.18				
3 x 12	70.7%	3.7	12.2%	3.7				
7 x 34	20.3%	7.0	67.8%	0.99				
1 x C	57.3%	4.0	53.4%	1.3				
1 x 12	68%	3.0	49.4%	2.9				
52 x 49	65%	3.0	60.6%	2.4				
12 x 49	78%	2.0	51.9%	2.7				

Table (4): Frequency distribution, means and standard deviations for immature fruit diameter in P₁, P₂, F₁, F₂, BC₁ and BC₂ generations for 4 crosses of Okra (*Ablemoschus esculentus* L.).

Cross No.	Population	Classes of immature fruit diameter (cm)									n	X ± s.d
		< 1.0	1.0-1.2	1.2-1.4	1.4-1.6	1.6-1.8	1.8-2.0	2.0-2.2	2.2-2.4	2.4-2.6		
I	8		3	9	3						15	1.302 ± 0.094
	12			10	5						15	1.362 ± 0.098
	8 x 12 (F ₁)			9	4	4					17	1.45 ± 0.163
	F ₁ selfing(F ₂)		8	43	51	17					118	1.425 ± 0.155
	BC ₁ (F ₁ x8)		13	17	23	6					59	1.37 ± 0.141
	BC ₂ (F ₁ x12)		9	22	15	9	4				60	1.45 ± 0.152
II	8		3	9	3						15	1.302 ± 0.094
	C					5	7	3			15	1.87 ± 0.127
	8 x C (F ₁)		1	7	10		1				19	1.45 ± 0.134
	F ₁ selfing(F ₂)		1	34	43	40					118	1.505 ± 1.209
	BC ₁ (F ₁ x8)		7	29	23						59	1.35 ± 0.121
	BC ₂ (F ₁ x C)			6	7	26	21				60	1.71 ± 0.149
III	3		2	10	3						15	1.32 ± 0.099
	1		1	9	3	2					15	1.38 ± 0.141
	3 x 1 (F ₁)			2	3	11	3				19	1.67 ± 0.195

Classes of immature fruit diameter (cm)												
Cross No.	Population	< 1.0	1.0-1.2	1.2-1.4	1.4-1.6	1.6-1.8	1.8-2.0	2.0-2.2	2.2-2.4	2.4-2.6	n	$\bar{X} \pm s.d$
	F ₁ selfing(F ₂)		3	45	58	11					117	1.43 ± 0.25
	BC ₁ (F ₁ x3)			27	26	6					59	1.42 ± 0.121
	BC ₂ (F ₁ x1)		4	5	29	22					60	1.54 ± 0.118
IV	48					12	3				15	1.75 ± 0.058
	C					5	7	3			15	1.87 ± 0.127
	48x C (F ₁)						11	5	2	1	19	2.04 ± 0.123
	F ₁ selfing(F ₂)					1	13	42	48	13	117	2.23 ± 0.197
	BC ₁ (F ₁ x48)					12	24	23			59	2.03 ± 0.273
	BC ₂ (F ₁ x C)				3	14	22	20			59	1.97 ± 0.257

Table (5):Frequency distributions , means and standard deviations for mature fruit diameter in P₁ ,P₂ ,F₁ ,F₂, BC₁ and BC₂ generations for 4 crosses of okra (*Abelmoschus esculentus* L.).

Classes of mature fruit diameter (cm)												
Cross No.	Population	< 2.0	2.0-2.2	2.2-2.4	2.4-2.6	2.6-2.8	2.8-3.0	3.0-3.2	3.2-3.4	3.4-3.6	n.	$\bar{X} \pm s.d$
I	8			8	6	1					15	2.46 ± 0.275
	12		1	8	6						15	2.36 ± 0.123
	8 x 12 (F ₁)			4	7	6					17	2.52 ± 0.139
	F ₁ selfing(F ₂)	1	5	15	46	38	14				118	2.54 ± 0.249
	BC ₁ (F ₁ x8)		8	28	14	9					59	2.34 ± 0.198
	BC ₂ (F ₁ x12)		16	26	6	5	6				60	2.37 ± 0.13
II	8			8	6	1					15	2.46 ± 0.275
	C				2	3	6	2	2		15	2.90 ± 0.227
	8 x C (F ₁)				4	8	6	1			19	2.75 ± 0.158
	F ₁ selfing(F ₂)			6	35	43	30	4			118	2.65 ± 0.22
	BC ₁ (F ₁ x8)		6	19	20	14					59	2.43 ± 0.175
	BC ₂ (F ₁ x C)				12	11	28	9			60	2.85 ± 0.218
III	3		2	3	6	3	1				15	2.47 ± 0.201
	1		1	5	7	2					15	2.48 ± 0.151
	3 x 1 (F ₁)					3	5	2	8		19	3.11 ± 0.296
	F ₁ selfing(F ₂)		12	38	51	16					117	2.42 ± 0.31
	BC ₁ (F ₁ x3)		5	15	23	10	6				59	2.48 ± 0.184
	BC ₂ (F ₁ x1)			4	7	28	20				60	2.74 ± 0.186
IV	48				1		1	2	6	6	15	3.29 ± 0.25
	C				2	3	6	2	2		15	2.90 ± 0.227
	48x C (F ₁)							2	7	10	19	3.42 ± 0.153
	F ₁ selfing(F ₂)					1	7	18	43	48	117	3.46 ± 1.407
	BC ₁ (F ₁ x48)						19	30	10		59	3.37 ± 0.272
	BC ₂ (F ₁ x C)				1	3	15	40			59	3.17 ± 0.212

Table (6) : Frequency distributions ,means and standard deviations for number of fruit ridges in P₁,P₂,F₁,F₂,BC₁ and BC₂ generations of different crosses of okra (*Abelmoschus esculentus* L.).

Classes of number of fruit ridges									
Cross No.	Population	5	6	7	8	9	10	n.	$\bar{X} \pm s.d$
I	48(P ₁)				10	5		15	8.30 ± 0.63
	C(P ₂)		6	9				15	6.60 ± 0.51
	48 x C (F ₁)				15	5		20	8.10± 0.27
	F ₁ selfing(F ₂)		4	31	47	28	6	116	8.28 ± 0.63
	BC ₁ (F ₁ x P ₁)			11	27	16	5	58	8.39 ± 0.44
	BC ₂ (F ₁ x P ₂)		10	24	16	7	1	58	7.39 ±0.53
II	12(P ₁)	15						15	5.00 ± 0.00
	C(P ₂)		6	9				15	6.60 ± 0.51
	12 x C (F ₁)	1	9	10				20	6.45 ± 0.61
	F ₁ selfing (F ₂)	56	39	22				117	5.71 ± 0.77
	BC ₁ (F ₁ x P ₁)	26	13	21				60	5.92 ± 0.89
	BC ₂ (F ₁ x P ₂)	12	22	24				58	6.20 ± 0.74
III	12(P ₁)	15						15	5.00 ±0.00
	49(P ₂)	15						15	5.00 ± 0.00
	8 x 12 (F ₁)	6	9	5				20	5.94 ±0.64
	F ₁ selfing(F ₂)	32	27	58				117	6.22 ±0.85
	BC ₁ (F ₁ x P ₁)	20	30	10				60	5.80 ±0.78
	BC ₂ (F ₁ x P ₂)	20	34	6				60	5.76 ±0.58
IV	8(P ₁)	15						15	5.00 ±0.00
	C(P ₂)		6	9				15	6.60 ±0.51
	8 x 52 (F ₁)	10	5	4				19	5.68 ±0.48
	F ₁ selfing(F ₂)	33	36	45	4			118	6.20 ±0.89
	BC ₁ (F ₁ x P ₁)	12	30	15	3			60	6.15 ±0.71
	BC ₂ (F ₁ x P ₂)	4	23	33				60	6.48 ±0.60

n.: total number of plants.

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