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EFFECT OF MUTAGENS ON INHERITANCE OF SOME QUANTITATIVE CHARACTERS IN EGYPTIAN COTTON

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ABSTRACT

This study was conducted at Sakha Experimental Station, Agricultural Research Center during three seasons 2017- 2019. The aim was to evaluate the induced variability in some quantitative characters in an Egyptian cotton cross (Giza 86 x Giza 88) using generation mean analysis after treating with 100Gy dose of gamma rays (γ-ray) as physical mutagen and 200 ppm of Ethyl methane sulphonate (EMS) as chemical mutagen, gene effects were determined using means of the six populations: P_1, P_2, F_1, F_2, BC_1 and BC_2 to clarify the inheritance of yield, its components and fiber properties. The results indicated that the mutagen treatment decreased the mean performance for most of the studied traits and increased the variability for all traits in M_3 generation. Hybridization increased variability in both of F_2 and the back crosses of untreated populations in M_3 as compared with parents for most of the studied traits. Moreover, crossing the mutagen treated parents increased variability than crossing alone. Highly significant differences were detected among the three treatments tested in this study for most of the studied traits, with the advantageous of the control treatment that gave the best values for all traits while the chemical mutagen treatment (200 ppm, EMS) showed the most depressive effect on the mean performance. Both mutagens were effective in inducing variability as they increased the total variance in both parents as compared to the untreated population for most studied traits, EMS treatment was more effective than γ-ray treatment in this respect. Both additive and dominance gene effects estimated from the six population analysis had important role in the inheritance of the studied traits. Fiber quality traits showed that additive gene effects were significant in all treatments and larger in magnitude than dominant ones, whereas dominance effects were generally larger than additive one in plant height, cotton yield and its components. Epistatic gene interactions additive × additive (i) were significant for the studied traits with a few exceptions, additive × dominance (j) were significant for some of the studied traits and dominance × dominance (l) also showed significant role in inheritance of all traits except for boll weight and lint% in the control treatment. Mid-parents heterosis, recorded significant or highly significant positive heterosis for some traits, whereas the rest cases had highly significant negative heterosis, in most cases, values of heterosis were low in magnitude. Inbreeding depression values were significant and positive for some traits. Phenotypic and genotypic coefficients of variability estimates showed that PCV values were higher than GCV about at least two folds for most traits in all treatments, indicating the environmental important role in the expression of the studied traits. Broad-sense heritability values were generally higher for fiber traits than productivity traits and the control treatment showed higher values than the mutagen treatments, EMS treatment showed the lowest values in this respect.

Key words: ***Cotton, Mutagens, six generation analysis, Variability, gene action, heterosis, inbreeding depression, heritability.***

INTRODUCTION

Improving any crop can be facilitated through the availability of variation in the germplasm of such crop. Cotton (*Gossypium spp.* L.) breeders all-over the world have expressed concern over the narrowing genetic base of cultivated cotton and the resulting decline in both of yield and fiber quality.

Hybridization provides opportunity for increased recombination among parental chromosomes that might breakup the existing negative associations between fiber quality traits and lint yield as well as broaden the genetic base (Ulloa *et al* 2007). Most of the Egyptian cotton (*G. barbadense* L.) varieties have been bred through artificial hybridization followed by the pedigree method of selection (El-Adly *et al* 2018).

Mutation induction through physical and chemical mutagens have been used as an important tool to increase existing variability and to generate additional variability for inherited traits in cotton and played a significant role in breeding for the different attributes of cotton plant such as, earliness, dwarfness and compactness, large bolls, high ginning outturn and fiber length, high yield, high seed oil content, diseases and insect resistance, drought and salinity resistance besides induction of male sterility and creating vast genetic variability for various economic and morphological traits of cotton (Basu *et al* 1984). Moreover, mutagens proved to be an effective tool to create a wide range of phenotypic variation in cotton populations (Auld *et al* 2000).

Several studies indicated that gamma rays (γ-ray) were effective in shifting the means and increasing the genetic variance of quantitative characters in various genotypes of upland cotton (Muthusamy and Jayabalan 2011, Yue and Zou 2012, Muhammad *et al* 2015 and Khan *et al* 2017) as well as in Egyptian cotton (Srour 2006, Orabi 2009, Amer *et al* 2016, Orabi *et al* 2017 and El-Hoseiny 2018).

Creating new mutants through chemical mutagens is an alternative strategy to increase genetic variability. Ethyl methane sulphonate (EMS; $CH_3SO_2OC_2H_5$), a chemical mutagen belongs to the alkylating agents group,resulting in point mutation (Till *et al* 2007). EMS in upland cotton has shown wide range of variation in different traits of interest and could be used as an effective tool for improving cotton yield and fiber quality (Herring *et al* 2004, Lowery 2007, Muthusamy and Jayabalan 2011, Brown *et al* 2013 and Mishra 2016). Moreover, chemical mutagens in Egyptian cotton gave wider ranges as well as higher phenotypic and genotypic variations than their respective control reflecting the induced variability and the possibility to select better forms within the treated populations (Amer 2004, Srour 2006 and Amer *et al* 2016).

Mutagens of cotton genotypes combined with hybridization has been shown to be a suitable technique for creating genetic variability in different cotton attributes (Amer 2004, Orabi 2009, Amer *et al* 2016, Haidar *et al* 2016, El-Hoseiny 2018 and Patil *et al* 2018).

This study aimed to evaluate the induced variability in some quantitative characters of the Egyptian cotton as a result of using artificial hybridization and mutagens (100 Gray dose of γ- ray as physical mutagen and 200 ppm dose of EMS as chemical mutagen) each alone and/or combined with the other tool. The study also aimed to obtain useful information about the effect of mutagens on inheritance of these quantitative characters.

MATERIALS AND METHODS

The materials used in this study comprised two Egyptian cotton varieties, Giza 86 and Giza 88, both varieties were obtained by Cotton Breeding Department, Cotton Research Institute (CRI), Agricultural Research Center (ARC), Giza, Egypt.

Methods

Trials were conducted during three successful growing seasons, 2017, 2018 and 2019 at Sakha Experimental Farm, ARC., Kafr El-Sheik Governorate, Egypt.

In 2017 season, selfed seeds of each variety were divided into three parts, the first part wasexposed to 100 Gray (Gy) dose of gamma rays (γ-ray) as physical mutagen, the second part was treated with 200 ppm of Ethyl methane sulphonate (EMS) as chemical mutagen and the last part was not treated and used as a control. Three treatments of each variety were grown on 24th of April to raise plants of the M_1 generation and the control. Each treatment was arranged in four rows 4m long and 65 cm apart. The distance between hills was 50cm with one plant left per hill. At flowering time, plants in the first two rows of each treatment were artificially self-pollinated to produce seeds of the M_2 in the treated populations, the other two rows were used in artificial hybridization between both varieties using Giza 88 as a female parent pollinated by Giza 86 to obtain F_1 seeds in the control treatment and F_1M_2 in the other two treatments.

In 2018 season, parents in each treatment were self pollinated, while F_1 plants of each treatment were divided into two parts, the first part was back crossed with its two respective parents (F_1 x P_1 and F_1 x P_2) to produce the two back-crosses (BC_1 and BC_2) in each treatment, the second part of F_1 plants was selfed to produce the F_2 seeds. At the same time, crossing was made among the selfed parents of each treatment to produce F_1 seeds again.

In 2019 season, the six basic populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for each of the three treatments (control and M_3 of the two treated populations) were sown in a randomized complete block design with three replications. Each replicate consisted of 4 rows for each of the parents and F_1's, 6 rows of each back-cross and 10 rows for the F_2 populations. Rows were 4 m long and 65 cm apart and 50 cm between plants with one plant per hill. The normal cultural practices were adopted during the growing seasons.

Data were recorded on individual plants for the traits: Plant height (PH) in cm, boll weight (BW) in grams, seed cotton yield per plant (SCY/P), lint cotton yield per plant (LCY/P) both in grams and lint percentage (L%). In addition to the following fiber properties: fiber length in mm (FL); fiber fineness (FF) expressed as Micronaire instrument reading, fiber strength (FS) expressed as Pressely index. Fiber tests were performed in Cotton Technology Research Division, CRI, ARC, Giza, Egypt.

Statistical and genetic analysis

Data of the six basic populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for the three treatments were statistically analyzed using (RCBD) according to Singh and Chaudhary (1977).

Scaling tests

The scaling testes A, B, C and D were calculated for each trait to determine the adequacy of the additive-dominance model or the presence of non-allelic gene interaction according to Mather and Jinks (1982). Significance of any of these scales is taken to indicate the presence of non-allelic interaction.

Estimates of gene effects

Means of the six populations in each treatment were used to estimate the six parameters type of gene action according to Jinks and Jones (1958) and Gamble (1962) as follows:

$$M= \overline{F}_2 = ½\,\overline{P}_1 + ½\,\overline{P}_2 + 4\,\overline{F}_2 - 2\overline{BC}_1$$

$$D= \overline{BC}_1 - \overline{BC}_2$$

$$H = \overline{F}_1 + 2\,\overline{BC}_1 + 2\,\overline{BC}_2 - 4\,\overline{F}_2 - ½\;\overline{P}_1 - ½\;\overline{P}_2$$

$$i = 2\overline{BC}_1 + 2\overline{BC}_2 - 4\overline{F}_2$$

$$j = ½\overline{P}_2 + \overline{BC}_1 - ½\overline{P}_1 - \overline{BC}_2$$

$$1 = \overline{P}_1 + \overline{P}_2 + 2\overline{F}_1 + 4\overline{F}_2 - 4\overline{BC}_1 - 4\overline{BC}_2$$

Where, the parameters m, d, h, i, j and l refer to the following mean effects: F_2 mean performance, additive, dominance, additive x additive, additive x dominance and dominance x dominance gene effects, respectively.

Variances for gene effects were obtained to estimate significance of these components. Standard error of each parameter was calculated and t values were obtained and compared with tabulated t at 5% level of probability.

In case of absence of interactions as indicated by non-significance of scale test, three-parameter model is used for estimation of genetic components of variance into additive (D), dominance (H) and environmental (E) according to Mather and Jinks (1982) as follows:

$$E = \frac{1}{3}(V_{\overline{P}_1} + V_{\overline{P}_2} + V_{\overline{F}_1})$$

$$D = 2\,(V_{\overline{F}_2} - V_{\overline{BC}_1} - V_{\overline{BC}_2})$$

$$H = 4\,(V_{\overline{F}_2} - ½V_D - V_E)$$

Heterosis%

It was calculated as the percent deviation of F_1 mean performance over that of mid-parents (MP) as follows:

$$H(MP)\% = \frac{\overline{F}_1 - \overline{MP}}{\overline{MP}} \,x\,100$$

Inbreeding depression%

It was measured from the following equations:

$$ID\% = \frac{F_1 - F_2}{F_1}\,x\,100$$

Phenotypic and genotypic coefficients of variability

Phenotypic (PCV) and genotypic (GCV) coefficients of variability were calculated according to Singh and Chaudhary (1977) as follows:

$$PCV\ \% = \frac{100 * \sqrt{V\bar{F}_2}}{\bar{F}_2} \qquad GCV\ \% = \frac{100 * \sqrt{V\bar{F}_2 - V\bar{E}}}{\bar{F}_2}$$

Heritability

Estimated according to Mather and Jinks (1982) as follows:

Heritability in broad sense (h^2b) = (VF_2 – VE) / VF_2

Where: V_E is the environmental variance

V F_2 is the total phenotypic variance in F_2 generation.

RESULTS AND DISCUSSION

Analysis of variance

Mean squares resulted from the analysis of variance for the studied traits are presented in Table (1). Results revealed significant or highly significant genotypic differences among the studied populations (parents and their F_1, F_2, BC_1 and BC_2 crosses) for all traits, providing the presence of genetic variability background of the two parents and their hybrids tested in this study. In addition, the differences among the tested treatments (control, 100 Gy of γ-rays and 200 ppm of EMS) were highly significant for all traits (except for micronaire reading that was insignificant) indicating the different effect of the three treatments over all populations.

Table 1. Mean squares obtained from analysis of variance for three treatments and six cotton populations in M_3 generation for the studied traits.

		Mean Squares							
SOV	**df**	**Plant Height cm**	**Boll Weight g**	**Seed cotton Yield g/plant**	**Lint Yield g/plant**	**Lint %**	**Fiber Length mm**	**Fiber Fineness Micr.**	**Fiber Strength Press.**
Reps	**2**	**60.96**	**0.073**	**368.5**	**189.98**	**0.889**	**0.028**	**0.002**	**0.091**
Treatment (T)	**2**	**561.30 ****	**0.210 ****	**21356 ****	**3014.9 ****	**1.699 ****	**2.180 ****	**0.008**	**0.237 ****
Population (P)	**5**	**131.85 ***	**0.053 ***	**3021.5 ****	**398.75 ****	**28.360 ****	**6.181 ****	**0.434 ****	**1.326 ****
T x P	**10**	**51.06**	**0.020**	**343.81**	**142.00**	**1.461 ***	**0.089**	**0.005**	**0.131 ****
Error	**34**	**39.77**	**0.014**	**484.88**	**68.61**	**0.519**	**0.081**	**0.008**	**0.040**

*** and ** indicate significant at 5% and 1% probability levels, respectively.**

On the contrary, the treatment x population interaction was not significant for all traits (except for lint% and fiber strength) indicating that the tested populations behaved similarly over the three treatments. Similar genotypic and treatment differences were recorded by Amer 2004, Srour 2006, Orabi 2009, Muhammad *et al* 2015, Amer *et al* 2016, Orabi *et al* 2017, Ali *et al* 2018, El-Hoseiny 2018 and Ul-Allah *et al* 2019. Consequently, it permits to proceed for the future biometrical analysis to estimate genetic components and parameters for these traits.

Mean performances

Means and standard errors for the studied traits are presented in Table (2). Highly significant differences were detected among the three treatments tested in this study for all the studied traits (except for fiber fineness), with the advantageous of the control treatment that gave the best values for all traits except for fiber strength where it had the lowest value. On the contrary, the chemical mutagen treatment (200 ppm, EMS) showed the most depressive effect on the mean performance of all traits (except for fiber strength), while the physical mutagen (100 Gy of γ-rays) was intermediate for all the studied traits. Significant differences among the six population means were recorded for all traits over treatments, indicating the presence of genetic variability for these traits in the studied populations. The first parent (Giza 86) gave the higher means for the productivity traits whereas Giza 88 variety had the best fiber properties. The F_1 generation showed intermediate values between the two parents as it surpassed the lower parent in all traits but it did not reach the higher parent in most traits, while F_2 generation showed lower values than F_1 for the productivity traits, whereas it showed better fiber properties. The back crosses had intermediate values between F_1 and its respective parent in most cases. Similar genotypic differences among cotton varieties and their crosses were recorded by Nassar 2013, Yehia and Hassan 2015, Amer *et al* 2016, Ali *et al* 2018 and El-Hoseiny 2018.

Effect of hybridization and mutagens on the total variation

Data of the phenotypic variance in both parents and their cross in F_1 and F_2 in addition to the two back crosses populations were presented in Table (3). These data revealed that P_1 (Giza 86 variety) had more phenotypic variance as compared to P_2 (Giza 88 variety) in the three treatments for all the studied traits except for few cases (plant height in control treatment, lint% in both mutagen treatments and fiber fineness in EMS treatment).

Table 2. Means and standard errors of the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) in the three treatments tested in M_3 generation for the studied traits.

Trait	Treatment	P_1	P_2	F_1	F_2	BC_1	BC_2	Mean
Plant Height (cm)	Control	138.0±2.34	123.0±2.39	133.0±2.99	142.0±3.16	126.7±3.09	128.5±3.05	131.86
	γ- ray	130.5±2.85	120.7±2.59	124.8±3.09	128.8±3.23	122.3±3.17	129.5±3.23	126.11
	EMS	125.8±3.41	119.8±2.74	121.3±3.21	118.3±3.37	121.8±3.32	117.0±3.22	120.69
	LSD 5%	4.88	4.15	5.18	5.96	5.17	5.36	2.10
Boll Weight (g)	Control	3.22 ±0.06	3.06 ±0.06	3.35 ±0.06	3.16 ±0.07	3.25 ±0.06	3.16 ±0.04	3.20
	γ- ray	3.13 ±0.08	3.03 ±0.06	3.02 ±0.06	3.10 ±0.08	3.12 ±0.07	3.04 ±0.05	3.07
	EMS	3.02 ±0.09	3.03 ±0.06	2.85 ±0.07	2.93 ±0.09	3.04 ±0.07	3.02 ±0.06	2.98
	LSD 5%	0.13	0.10	0.12	0.13	0.11	0.08	0.04
Seed Cotton Yield/P (g)	Control	190.7±8.45	159.6±8.34	172.6±8.62	155.7±8.78	171.2±8.63	152.6±8.48	167.07
	γ- ray	123.6±8.57	111.1±8.42	143.4±8.97	123.7±8.97	137.7±8.71	135.8±8.59	129.22
	EMS	92.5±8.76	98.1±8.57	102.5±9.11	100.2±9.28	98.6±8.83	97.98±8.64	98.30
	LSD 5%	18.41	15.67	16.66	15.96	16.55	15.34	7.34
Lint Yield/P (g)	Control	75.66±3.46	56.12±2.99	63.25±3.26	56.30±3.30	65.43±3.29	53.71±3.07	61.74
	γ- ray	48.99±3.26	40.17±3.10	51.65±3.29	45.37±3.43	49.83±3.24	47.40±2.95	47.23
	EMS	38.05±3.74	34.98±3.19	36.62±3.28	36.53±3.46	35.05±3.21	34.32±3.17	35.93
	LSD 5%	7.32	5.64	6.18	5.96	6.39	5.47	2.76
L%	Control	39.62±0.16	35.13±0.16	36.60±0.24	36.04±0.26	38.27±0.25	35.17±0.22	36.80
	γ- ray	39.80±0.24	36.12±0.27	36.08±0.33	36.43±0.35	36.20±0.32	35.05±0.28	36.61
	EMS	40.75±0.34	35.45±0.36	35.76±0.37	36.42±0.38	35.42±0.34	34.88±0.32	36.45
	LSD 5%	0.43	0.46	0.52	0.54	0.61	0.45	0.24
Fiber Length (mm)	Control	33.11±0.14	36.02±0.08	34.47±0.15	33.95±0.21	33.05±0.11	34.46±0.17	34.18
	γ- ray	32.76±0.16	34.82±0.12	33.89±0.18	33.83±0.22	33.71±0.17	34.09±0.17	33.85
	EMS	32.07±0.14	34.42±0.15	33.61±0.19	33.82±0.24	33.04±0.19	33.92±0.16	33.48
	LSD 5%	0.29	0.28	0.30	0.35	0.28	0.28	0.09
Fiber Fineness Micr.	Control	4.23±0.04	3.65±0.04	3.98±0.05	3.97 ±0.06	4.20±0.05	3.92±0.04	3.995
	γ- ray	4.25±0.06	3.64±0.05	3.95±0.06	4.01±0.07	4.06±0.05	3.81±0.06	3.953
	EMS	4.29±0.05	3.62±0.06	3.96±0.06	4.02±0.07	4.16±0.05	3.80±0.05	3.974
	LSD 5%	0.10	0.08	0.09	0.10	0.08	0.08	-
Fiber Strength Pres.	Control	10.30±0.08	11.69±0.07	10.76±0.08	10.72±0.11	10.22±0.08	11.06±0.09	10.79
	γ- ray	10.41±0.10	11.03±0.08	10.84±0.10	10.99±0.11	10.78±0.10	11.17±0.09	10.87
	EMS	10.53±0.09	11.65±0.08	10.85±0.11	10.95±0.12	10.77±0.11	11.35±0.09	11.02
	LSD 5%	0.16	0.15	0.16	0.18	0.17	0.15	0.07

Table 3. Total variance of the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) in three treatments tested in M3 for the studied traits.

Trait	Treatment	P_1	P_2	F_1	F_2	BC_1	BC_2
Plant Height (cm)	Control	164.83	171.72	268.28	299.31	286.78	279.57
	γ- ray	243.41	200.62	287.00	313.23	302.14	301.72
	EMS	307.04	224.97	308.506	340.23	330.14	311.38
Boll Weight (g)	Control	0.125	0.098	0.103	0.133	0.141	0.105
	γ- ray	0.189	0.118	0.121	0.198	0.196	0.128
	EMS	0.201	0.124	0.151	0.217	0.234	0.147
Seed Cotton Yield/P (g)	Control	2145	2086	2232	2311	2232	2156
	γ- ray	2201	2129	2415	2415	2278	2215
	EMS	2301	2205	2492	2581	2338	2242
Lint Yield/P (g)	Control	310.77	268.14	319.06	356.83	325.20	282.28
	γ- ray	318.23	289.00	325.15	382.52	335.53	296.72
	EMS	330.45	305.98	322.27	418.97	359.42	311.03
Lint%	Control	0.731	0.720	1.753	2.024	1.849	1.462
	γ- ray	1.689	2.141	3.309	3.744	3.062	2.311
	EMS	3.366	3.402	4.033	4.365	3.554	3.738
Fiber Length (mm)	Control	0.630	0.212	0.688	1.286	0.817	0.722
	γ- ray	0.747	0.398	0.958	1.392	0.895	0.889
	EMS	0.900	0.695	1.126	1.674	1.076	0.913
Fiber Fineness Micronaire	Control	0.133	0.052	0.062	0.109	0.065	0.069
	γ- ray	0.116	0.078	0.096	0.115	0.079	0.095
	EMS	0.072	0.096	0.111	0.130	0.085	0.111
Fiber Strength Pressely	Control	0.362	0.150	0.211	0.342	0.204	0.218
	γ- ray	0.289	0.196	0.283	0.359	0.301	0.236
	EMS	0.266	0.195	0.347	0.375	0.332	0.244

Regarding the mutagen effect on phenotypic variability in both parents, it is clear that both mutagens treatment were effective in inducing variability as they increased the total variance in both parents as compared to the untreated population for all the studied traits (except for fiber fineness and fiber strength in P_1), EMS treatment was more effective than γ-ray treatment in this respect.

Concerning hybridization effect on the total variance, data presented in Table (3) for F_2 generation in the control treatment showed that the phenotypic variance in F_2 was greater than its corresponding values in both parents, moreover, the total variance for each back cross was also greater than that of its respective parent indicating that hybridization increased variability for the studied traits (except for fiber fineness and strength) which reflects the efficacy of hybridization in inducing variability in the studied materials.

The combined effect of both hybridization and mutagens in F_2 generation and the back crosses, showed that both mutagens increased the total variance as compared to the control treatment in F_2 and both parents and the back cross as compared to its respective parent for all traits in this study indicating the success of these mutagens in inducing variability in the studied materials. Hybridization between the mutagen treated parents increased variability than hybridization alone. EMS surpassed γ-ray in this respect and proved to be more effective in inducing variability in the studied materials. These findings were in harmony with those reported previously by Amer 2004, Orabi 2009, Amer *et al* 2016, Haidar *et al* 2016, El-Hoseiny 2018, Patil *et al* 2018 and Ul-Allah *et al* 2019.

The efficiency of mutagens used in increasing the total variation was emphasized by curves drawn for the total variation in F_2M_3 generation for the three treatments (Control, γ-ray and EMS) that presented in Figure 1. The studied traits showed extended variation in both negative and positive sides, except for boll weight and fiber length that showed extended variation in the negative direction only as compared to the untreated population. These results clarify the possibility to improve the studied traits throughout selecting better individual plants either in the negative direction for plant height and fiber fineness or in the positive direction for the rest of traits.

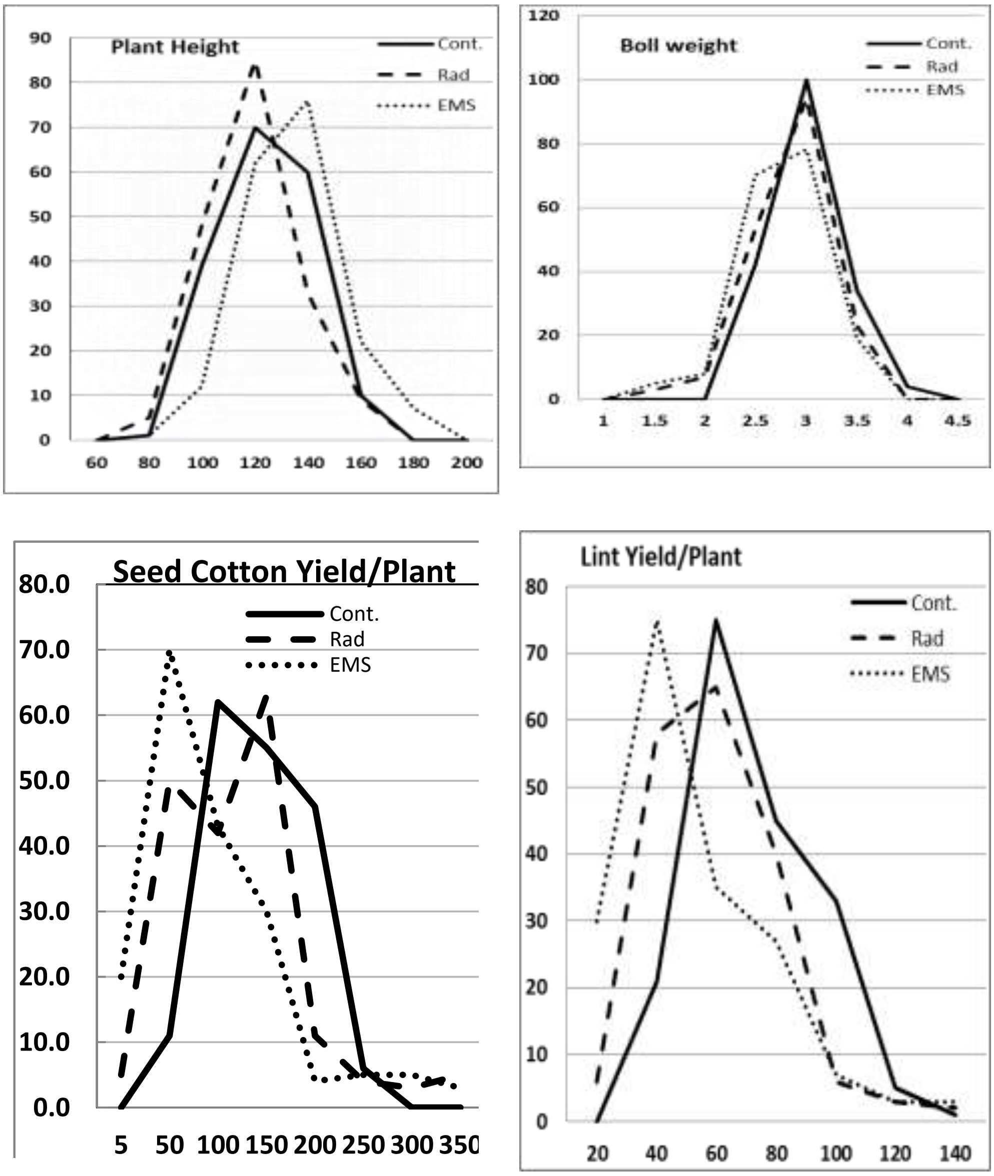

Fig. 1. Effect of the three treatments on the distribution of total variance in F_2 and F_2M_3 generation for the studied traits.

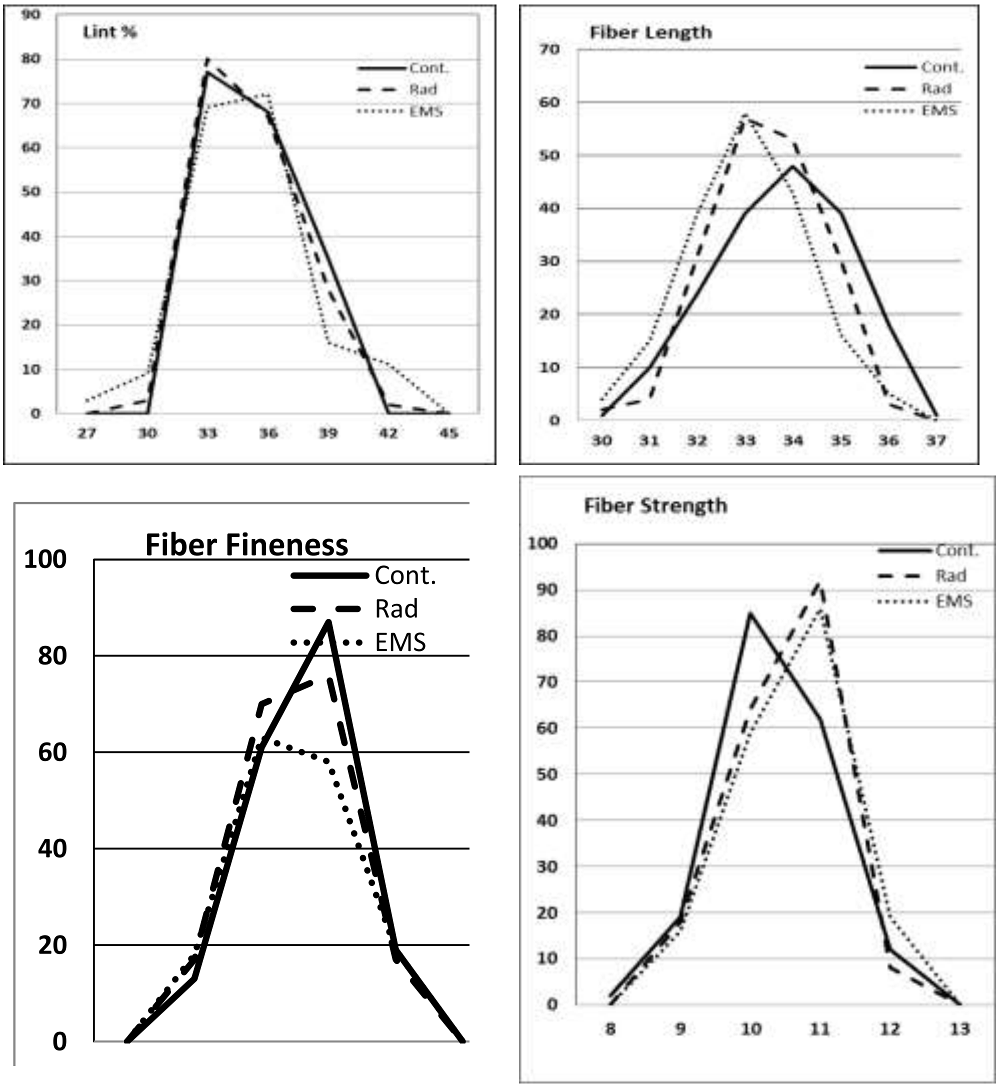

Fig. 1.Cont

Scaling test

Data of Table (4) presents the estimates of scaling tests (A, B, C and D) and their level of significance for the studied traits. Significance of any of the four scales indicates the presence of epistasis.

Table 4. Scaling tests A, B, C and D in three treatments for the studied traits.

Trait	Treatment	Scaling Test			
		A	B	C	D
Plant Height (cm)	Control	-17.67 *	1.00	41.00 **	28.83 *
	γ-ray	-10.70 *	13.47 **	14.50 *	5.87
	EMS	-3.50	-7.17 *	-15.00 *	-2.17
Boll Weight (g)	Control	-0.07	-0.10 *	-0.33**	-0.08
	γ-ray	0.09 *	0.03	0.22 *	0.05
	EMS	0.21 *	0.15 *	-0.02	-0.19 *
Seed Cotton Yield/P (g)	Control	-20.88 *	-27.15 **	-72.56 **	-12.27
	γ-ray	8.34	17.09 *	-26.79**	-26.11**
	EMS	2.32	-4.55 *	5.45 *	3.84
Lint Yield/P (g)	Control	-8.05	-11.94**	-33.07**	-6.54
	γ-ray	-0.98	2.98 *	-10.97 *	-6.48 *
	EMS	-4.58 *	-2.97	-0.16	3.70 *
Lint %	Control	0.32	-1.40 **	-3.76 **	-1.35
	γ-ray	-3.48 **	-2.10 *	-2.35 *	1.61
	EMS	-5.66 **	-1.45	-2.04	2.54 *
Fiber Length (mm)	Control	-1.48 **	-1.57 **	-2.27 *	0.39
	γ-ray	0.76 *	-0.53 *	-0.03	-0.12
	EMS	0.40 *	-0.20	1.58 *	0.69 *
Fiber Fineness Micronaire	Control	0.19	0.21	0.07	-0.16
	γ-ray	-0.08	0.03	0.24	0.14
	EMS	0.08	0.03	0.25	0.07
Fiber Strength Pressely	Control	-0.62 **	-0.32	-0.61 *	0.17
	γ-ray	0.32 *	0.47 *	0.86 **	0.03
	EMS	0.17	0.21 *	-0.06	-0.22 *

*** and ** indicate, significant at 0.05 and 0.01 probability levels, respectively.**

Gene effects:

Data in Table (4) indicated that most of scaling tests were significant for all traits (except for fiber fineness) so a simple additive-dominance model was adequate to explain the genetic variation for fiber fineness as indicated from the non-significance of all scales, indicating that selection could be practiced effectively in F_2 generation for improving this trait. While the remaining traits revealed presence of non-allelic interactions in the three treatments which mean that epistatic effects were contributed to the inheritance of such traits and suggesting that the inheritance of these traits is complex and polygenic (Warnock *et al* 1998)**,** therefore, the six parameters model was applied to determine the genetic interaction types controlling the genetic variation. Our results were in the same line with those findings reported by: Abd El-Haleem *et al* 2010, Nassar 2013, Al-Hibbiny *et al* 2015, Yehia and Hassan 2015 and Ali *et al* 2018.

The six parameters, i.e. means (m), additive (d), dominance (h), additive x additive (i), additive x dominance (j) and dominance x dominance (l) estimates were presented in Table (5). The results of mean effects (m) that reflects the contribution due to over-all mean in addition to the locus effects and interaction of the fixed loci showed highly significant mean effects for all traits in all treatments, indicating that these traits were quantitatively inherited. The untreated population showed the best values for all traits (except fiber fineness), whereas, EMS treatment had the most depressive effect on most traits, while γ-ray showed intermediate values.

Results of Table (5) indicated that, additive (d) and dominant (h) gene effects were significant for plant height, fiber length and fiber fineness in the three treatments; boll weight and fiber strength in both control and EMS treatments as well as seed cotton yield/plant and lint% in control and γ-ray treatments, in addition to lint yield/plant in control treatment, indicating that both additive and dominance had important role in the inheritance of these traits. Fiber quality traits (fiber length, fineness and strength) showed that additive gene effects (d) were significant in all treatments and larger in magnitude than dominant ones (h), indicating that additive gene action was operative for the control of these traits. For improving such traits, selection in early segregating generations would be effective; pedigree method will be useful for selecting segregates for getting superior genotypes (Jagtap 1986). Contrarily, dominance effects (h) were generally larger than additive (d) one in plant height, cotton yield and its components, indicating that dominant component of gene action was operative for the control of these traits, and hence, improving such traits need intensive selection through later segregating generations when dominant effect is diminished (Jagtap 1986).

Table 5. Estimates of six-parameter gene effects in the three treatments for the studied traits.

Traits	Treat.	Six-parameter gene effects						Type of interaction
		m	*d*	*h*	*i*	*j*	*l*	
Plant Height (cm)	Control	142.00 **	-1.83 *	-55.17 **	-57.67 **	-9.33 *	74.33 **	Duplicate
	γ-ray	128.83 **	-7.20 *	-12.48 **	-11.73 *	-12.08 *	8.97 *	Duplicate
	EMS	118.33 **	1.83 *	2.83 *	4.33 *	1.83	6.33 **	Complementary
Boll Weight (g)	Control	3.161 **	0.59 *	0.87 *	0.16 *	0.01	0.01	Complementary
	γ-ray	3.103 **	0.08	-0.15	-0.09 *	0.03 *	-0.03 *	Complementary
	EMS	2.933 **	0.43 *	0.62 *	0.39 *	0.03	-0.76 *	Duplicate
Seed Cotton Yield/P (g)	Control	155.75 **	8.67 **	22.03 **	24.53 **	3.13	23.49 **	Complementary
	γ-ray	123.69 **	11.87 *	78.21 **	52.22 **	-4.37	-77.64 **	Duplicate
	EMS	100.22 **	0.63	-0.84	-7.68 **	3.44 *	9.91 **	Duplicate
Lint Yield/P (g)	Control	56.30 **	9.13 *	25.96 **	28.61 **	-18.90 **	-13.80 *	Duplicate
	γ-ray	45.37 **	2.43	20.04 **	12.97 *	-1.98	-14.96 *	Duplicate
	EMS	36.53 **	0.73	-7.29 *	-7.39 *	-0.80	14.94 **	Duplicate
Lint %	Control	36.44 **	3.10 **	5.91 *	2.69 *	0.86 *	-1.62	Duplicate
	γ-ray	36.43 **	1.15 **	-5.11 **	-3.23 *	-0.69	8.80 **	Duplicate
	EMS	36.42 **	0.55	-7.41 **	-5.07 **	-2.10 **	12.19 **	Duplicate
Fiber Length (mm)	Control	33.95 **	-1.41 **	-0.87 *	-0.78 *	0.05	3.83 **	Duplicate
	γ-ray	33.83 **	-0.38 *	0.65 *	0.25	0.65 *	-0.47 *	Duplicate
	EMS	33.82 **	-0.88 **	-1.01 *	-1.38 *	0.30	1.18 *	Duplicate
Fiber Fineness Micr.	Control	3.98 **	-0.23 **	0.37 **	-	-	-	-
	γ-ray	4.01 **	-0.85 **	1.62 **	-	-	-	-
	EMS	4.18 **	-0.25 **	0.49 **	-	-	-	-
Fiber Strength Pres.	Control	10.72 **	-0.47 *	-0.85 **	-0.33 *	-0.15 *	1.27 **	Duplicate
	γ-ray	10.99 **	-0.39 **	0.05	-0.07	-0.07	-0.73 *	Duplicate
	EMS	10.95	-0.58 **	0.70 *	0.44 *	-0.02	-0.82 *	Duplicate

m= Mean of F_2, d= Additive effect, h= Dominance effect, i= Additive x Additive, j= Additive x Dominance and l= Dominance x Dominance interactions.

The sign of (h) also plays important role, positive sign suggests its enhancing effects on performance of the trait. The sign for dominance effects is a function of the F_1mean value in relation to the mid parental value and indicates which parent is contributing to the dominance effect (Cukadar and Miller 1997). However, the insignificant (h) would indicate no dominance or presence of ambidirectional dominance between parents and the dominant effects was not important in the genetic control of such cases. With regard to the negative values observed either in the main effects; (d) and (h) or the non-allelic interactions; (i), (j) and (l), indicated that the alleles responsible for less value of traits were over dominant over those controlling high value. Our results were agreed with those of Nassar 2013, Yehia and Hassan 2015, Ali *et al* 2018 and Hussain *et al* 2019 and disagreed with AL-Hibbiny *et al* 2015 and Amer *et al* 2016 who found that additive effects was smaller than dominance one in all cases of their studies.

Epistatic gene interactions additive × additive (i) were significant for the studied traits except for fiber length and fiber strength in γ-ray treatment, additive × dominance (j) were significant for some of the studied traits and dominance × dominance (l) also showed significant role in inheritance of the studied traits except for boll weight and lint % in the control treatment. Nidagundi *et al* (2012) reported that the prevalence of additive x dominance epistatic effect (highest magnitude) for the trait suggesting delayed selection and intermating the segregates followed by recurrent selection for improving this trait. Moreover, EL-Refaey and Abd El-Razek (2013) and Srinivas and Bhadru (2015) stated that when epistatic effects were significant for a trait, there is possibility of obtaining desirable segregates through intermating in early segregating generations by breaking undesirable linkage oritissuggested to practice recurrent selection for rapid improvement in such trait.

The signs of dominance (h) and dominance x dominance (l) gene effects were opposite with few exceptions (plant height in EMS treatment, boll weight in both control and γ-ray treatments and seed cotton yield in the control treatment), suggesting duplicate type of non-allelic interaction which will deceit impediment to plant breeder in selection in long run (Mather and Jinks 1982). The prevalence of (h) and (l) type of gene effects revealed that the expression of the studied traits was largely controlled by many genes having small effects and also dominant in their action. However, (h), (j) and

(l) which refer to non-additive genetic variance were significant for most traits, indicating that these traits were greatly affected by dominance as main effect and their non-allelic interactions as epistatic effects. These results were agreed with those of Abd El-Haleem *et al* 2010, Nassar 2013, Deore *et al* 2014 and Srinivas and Bhadru 2015**.**

The complementary type of gene interaction especially (h) and (l) enhance the effect of dominance, while the duplicate type oppose the effect of dominance, therefore, heterosis is likely to be expressed with greater magnitude in crosses showing complementary type, while it may not be observed at all in crosses showing duplicate type (Jinks and Jones 1958). Presence of dominance and epistasis for different traits in all treatments would slow down the progress of selection. Hence, it would be suggested the use of intermating of selectors followed by visual selection in early segregating generations, which would simultaneously exploit both types of gene effects. Further, this approach is likely to break some undesirable linkages resulting in the establishment of rare useful recombinations.

Genetic Parameters

Data concerning the genetic parameters (mid-parents heterosis, inbreeding depression, phenotypic and genotypic coefficients of variability and heritability in broad sense of the three treatments were presented for the studied traits in Table (6). Regarding mid-parents heterosis (H), results recorded significant or highly significant positive heterosis relative to mid-parents for plant height and boll weight in the control treatment, seed and lint cotton yields and fiber length in both γ-ray and EMS treatments as well as fiber fineness and fiber strength in all treatments, Whereas the rest cases had highly significant negative heterosis. However, in most cases, values of heterosis were low in magnitude which may be ascribed to the duplicate type of epistasis recorded for most of the studied traits and treatments.

Inbreeding depression (I.D) values were significant and positive for the traits, plant height in EMS treatment; boll weight, lint %, fiber length and fiber strength in the control treatment; fiber length in both control and γ-ray treatments as well as seed and lint cotton yields in all treatments. While the rest cases showed significant or insignificant negative values.

Table 6. Estimates of some genetic parameters in the three treatments for the studied traits.

Traits	Treatment	H %	I.D %	P.C.V %	G.C.V %	h^2b
Plant Height (cm)	Control	1.88 **	-6.77**	12.18	6.96	32.64
	γ-ray	-0.71	-8.82**	13.03	6.12	25.05
	EMS	-1.24**	2.47 **	15.59	5.75	23.60
Boll Weight (g)	Control	6.22 **	5.59 **	11.54	4.96	26.47
	γ-ray	-1.82	-2.64	13.98	7.09	25.75
	EMS	-6.04**	-2.84	15.89	7.78	23.97
Seed Cotton Yield/P (g)	Control	-1.45	9.78 **	30.87	8.05	29.81
	γ-ray	18.11 **	13.89 **	39.78	10.33	26.74
	EMS	7.02 **	2.18 **	50.69	15.72	22.62
Lint Yield/P (g)	Control	-4.18**	10.98 **	32.11	5.94	33.42
	γ-ray	12.74 **	12.37 **	41.02	5.51	31.80
	EMS	3.29*	3.25**	51.86	8.39	29.62
Lint %	Control	-2.13	1.51 **	3.95	2.71	31.24
	γ-ray	-5.32**	-1.03	5.31	3.22	33.76
	EMS	-6.54**	-1.84**	5.74	2.12	29.71
Fiber Length (mm)	Control	-0.26	1.52 **	3.34	2.44	53.35
	γ-ray	0.16 *	0.06	3.48	2.45	50.48
	EMS	1.10 **	-0.62*	3.83	2.74	48.21
Fiber Fineness Micronaire	Control	0.92 **	0.00	8.30	4.15	34.99
	γ-ray	0.59 **	-1.10	8.59	3.71	33.64
	EMS	0.38*	-1.52**	8.99	4.82	32.76
Fiber Strength Pressely	Control	0.53 *	0.31 **	5.45	2.96	39.50
	γ-ray	0.35 *	-1.48**	5.43	2.91	38.66
	EMS	0.44 *	-0.98 **	5.59	2.96	38.11

H: heterosis mid-parents; ID: inbreeding depression; P.C.V: phenotypic coefficient of variability; G.C.V: genotypic coefficient of variability and h^2b: broad sense heritability.

The positive values for I.D% is expected as the expression of heterosis in F_1 will be followed by respective reduction in F_2 due to the direct effect of homozygosity, while the negative values may be suggested that genes controlling these traits were not completely segregated. Significant positive or negative heterosis and inbreeding depression in cotton traits were previously recorded by Nassar 2013, Deore *et al* 2014, Srinivas and Bhadru 2015, Yehia and Hassan 2015 and Hussain *et al* 2019.

Phenotypic and genotypic coefficients of variability (PCV and GCV) estimates were presented in Table (6). PCV values were higher than their corresponding values of GCV about at least two folds for most of the studied traits in all treatments, these results proved that the environment had an important role in the expression of the studied traits. The highest values of PCV and GCV were recorded by lint and seed cotton yields, respectively; whereas the lowest values were recorded by fiber length. These results were in agreement with the previous studies on Egyptian cotton reported by Esmail 2007, Abd El-Haleem *et al* 2010, Nassar 2013, Yehia and Hassan 2015 and Amer *et al* 2016 the results disagreed with those of AL-Hibbiny *et al* 2015 who found that both PCV and GCV values were much close, and the major proportion of the observed variation was contributed by genetic factors in additive manner for the studied traits in two cotton crosses**.**

Broad-sense heritability (h^2b) values were generally higher for fiber traits than productivity traits. Moreover, control treatment showed higher values than the mutagen treatments, whereas EMS treatment had the lowest values. High h^2b values (exceeded 50%) were recorded for fiber length in both of control and γ-ray treatments (53.35 and 50.48%, respectively), indicating that effective selection could be practiced on individual plant basis during early segregating generations for improving this trait. On the other hand, moderate h^2b values (30–50%) were recorded for the traits fiber fineness and fiber strength in the three treatments; lint yield/plant and lint % in both control and γ-ray treatments; plant height in the control treatment and fiber length in EMS treatment. On the contrary, low h^2b values (less than 30%) were observed for boll weight and seed cotton yield/plant in all treatments, plant height in both γ-ray and EMS treatments as well as lint yield/plant and lint% in EMS treatment which reflecting the great effects of environment on these traits and hence environmental fluctuations had a share in the expression of such traits, therefore, improving such traits needs intensive selection during later generations. Our findings were in agreement with those reported by, Abd El-Haleem *et al* 2010, Nassar 2013, AL-Hibbiny *et al* 2015, Yehia and Hassan 2015 and Amer *et al* 2016.

CONCLUSION

Out of this study, it could be concluded that hybridization and both mutagen treatments (γ-ray, 100 Gy and EMS, 200 ppm) increased the total variance for the studied traits, EMS treatment was more effective than γ-ray treatment in this respect. Moreover, the combined effect (hybridization between mutagen treated parents) was greater than the effect of each tool alone in inducing variability. Both additive and dominance had important role in the inheritance of the studied traits, additive gene effects were more important for the control of fiber quality traits, whereas, dominance effects were more important for the control of plant height, cotton yield and its components.

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تأثير المطفرات على توارث بعض الصفات الكميه فى القطن المصرى

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اقيمت هذه الدراسة بمحطة التجارب الزراعية التابعة لمركز البحوث الزراعية بسخا محافظة كفر الشيخ خلال ٣ مواسم ٢٠١٧ – ٢٠١٩ بهدف تقييم التباين المستحدث فى بعض الصفات الكمية للقطن المصرى نتيجة استعمال التهجين الصناعى والمطفرات (١٠٠جراى من أشعة جاما و ٢٠٠ جزء فى المليون من الايثايل ميثان سلفونيت) وكذلك لتقدير بعض القياسات الوراثية التى توضح توارث صفات المحصول ومكوناته وكذلك صفات جودة التيلة عن طريق تحليل العشائر السته. وقد أظهرت النتائج المتحصل عليها ان المعاملة بالمطفرات أدت الى انخفاض متوسطات معظم الصفات المدروسة بينما زاد التباين لكل الصفات. كما ادى التهجين الى زيادة التباين لمعظم الصفات، وأدى التهجين بين الآباء المعاملة بالمطفرات الى زيادة التباين المستحدث عنه فى حالة التهجين بين الآباء غير المعاملة. وقد اختلفت المعاملات الثلاثة المستعمله فى الدراسه معنويا فى كل الصفات المدروسه وأعطت المعاملة الكنترول افضل المتوسطات بينما أعطت المعاملة بالمطفر الكيماوي أقل المتوسطات، وأظهر كلا من المطفرين فعالية فى استحداث التباين وكان المطفر الكيماوي أكثر فعالية عن الأشعاع. أظهر كلا من التباين الإضافي والتباين السيادي دورا هاما فى وراثة الصفات المدروسة، وكان للتباين الإضافي الدور الأهم فى وراثة صفات جودة التيلة حيث أعطى معنوية عالية وكانت قيمته أعلى من قيمة التباين السيادي بينما العكس فى صفات المحصول ومكوناته حيث كان التباين السيادي هو الأهم فى توارث هذه الصفات وكانت قيمته أعلى من التباين الإضافي. كما أظهرت تفاعلات التفوق الثلاثة الإضافي × الإضافي، الإضافي × السيادي، السيادي × السيادي أهمية في توارث الصفات المدروسة باستثناء وزن اللوزة وتصافى الحليج. وبالنسبه للقياسات الوراثية فقد أظهرت قوة الهجين عن متوسط الأبوين قيما معنوية موجبة لبعض الصفات بينما أظهرت معظم الصفات قيما معنوية سالبة وكانت قيم قوة الهجين منخفضة لمعظم الصفات. كذلك فان الإنخفاض الناتج عن التربية الداخلية كان معنويا وموجبا لقليل من الصفات بينما كانت القيمة سالبه ومعنوية أو غير معنوية لمعظم الصفات. اظهر معامل التباين المظهري قيما أعلى من معامل التباين الوراثي لكل الصفات مما يدل على ان البيئة لها دور هام فى التعبير عن هذه الصفات. كانت القيمة الوراثية أعلى لصفات جودة التيلة عنها فى صفات الإنتاجية كما أدت المعاملة بالمطفرات الى انخفاض القيمة الوراثية عن الكنترول وأعطت المعاملة بالمطفر الكيماوى أقل القيم.

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