

**GENETIC ANALYSIS OF YIELD, YIELD COMPONENTS  
AND SOME CHEMICAL CONSTITUENTS IN SIX  
EGYPTIAN COTTON CROSSES (*Gossypium*  
*barbadense* L.) UNDER RAS-SUDR  
CONDITIONS**

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**ABSTRACT:** Six populations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub>) of six cotton crosses, namely 1) Giza 89 × Dandara, 2) Giza 83 × Ashmoni, 3) Giza 45 × Giza 70, 4) Giza 45 × Giza 83, 5) Giza 80 × Giza 86 and 6) Giza 89 × Ashmoni were raised in a randomized complete block design during the three successive summer seasons of 2000, 2001 and 2002 at Ras-Sudr Agriculture Research Station of Desert Research Center, South Sinai. The aim of the study was to determine the adequacy of genetic model and gene action controlling yield and its components i.e., number of fruiting branches/plant, number of open bolls/plant, boll weight, seed cotton yield/plant and some chemical constituents such as potassium, magnesium and sodium concentrations as well as proline content. The collected data were subjected to two-way analysis of variance according to Steel and Torrie (1980). The results indicated that the scaling test (A, B and C) provide evidence of non-allelic interaction in controlling number of fruiting branches/plant, number of open bolls/plant, boll weight and seed cotton yield/plant in all crosses and for chemical components potassium concentration in 1<sup>st</sup>, 2<sup>nd</sup>, 4<sup>th</sup> and 6<sup>th</sup> crosses; magnesium concentration in 1<sup>st</sup>, 5<sup>th</sup> and 6<sup>th</sup> ones; sodium concentration in 1<sup>st</sup>, 4<sup>th</sup>, 5<sup>th</sup> and 6<sup>th</sup> crosses and proline content in 1<sup>st</sup>, 2<sup>nd</sup> and 5<sup>th</sup> ones. The simple genetic model was adequate for explaining the inheritance of potassium concentration in 3<sup>rd</sup> and 5<sup>th</sup> crosses; magnesium

concentration in 2<sup>nd</sup>, 3<sup>rd</sup>, and 4<sup>th</sup> ones; sodium concentration in 2<sup>nd</sup> and 3<sup>rd</sup> crosses as well as proline content in 3<sup>rd</sup>, 4<sup>th</sup> and 6<sup>th</sup> ones. The additive gene effect (d) was more important in the inheritance of number of fruiting branches/plant in 1<sup>st</sup>, 2<sup>nd</sup>, 3<sup>rd</sup>, 5<sup>th</sup> and 6<sup>th</sup> crosses; boll weight in 1<sup>st</sup> and 2<sup>nd</sup> ones; potassium concentration in 2<sup>nd</sup>, 5<sup>th</sup> and 6<sup>th</sup> crosses; magnesium concentration in 1<sup>st</sup>, 3<sup>rd</sup> and 4<sup>th</sup> crosses; sodium concentration in the 2<sup>nd</sup> and 3<sup>rd</sup> crosses and proline content in 2<sup>nd</sup>, 3<sup>rd</sup>, 4<sup>th</sup> and 6<sup>th</sup> ones. The additive × additive (i) interaction type was important in the genetics of number of open bolls/plant and seed cotton yield/plant in 6<sup>th</sup> cross as well as boll weight in 4<sup>th</sup> and 6<sup>th</sup> crosses; however both additive and additive × additive interactions types were important in the genetic system controlling potassium concentration in 4<sup>th</sup> and 6<sup>th</sup> crosses and proline content in 5<sup>th</sup> one. The dominance (h) and its digenic interaction type, dominance × dominance (I) were involved in the inheritance of boll weight and seed cotton yield/plant in 6<sup>th</sup> cross; number of open bolls/plant in 1<sup>st</sup> and 6<sup>th</sup> crosses; potassium concentration in 4<sup>th</sup> one; magnesium concentration in 6<sup>th</sup> cross sodium concentration in 5<sup>th</sup> cross and proline content in 1<sup>st</sup> one. Also, the dominance gene action played an important role in the genetics of potassium and magnesium concentration in 3<sup>rd</sup> cross sodium concentration in 5<sup>th</sup> cross and proline content in 1<sup>st</sup> one. Additive × dominance (j) was significant for number of fruiting branches/plant in 2<sup>nd</sup>, 4<sup>th</sup> and 6<sup>th</sup> crosses; number of open bolls/plant in 3<sup>rd</sup> cross only; boll weight in 1<sup>st</sup> and 3<sup>rd</sup> crosses and seed cotton yield/plant in 3<sup>rd</sup> one. Narrow sense heritability was high (>50%) for number of fruiting branches/plant in 3<sup>rd</sup> cross, potassium concentration in 5<sup>th</sup> cross and magnesium concentration in 2<sup>nd</sup> one. Whereas; it ranged from low to moderate for number of fruiting branches/plant, number of open bolls/plant, boll weight, seed cotton yield/plant, sodium concentration and proline content.

**Key words:** Cotton, varieties, gene action, heritability, chemical constituents.

## INTRODUCTION

Cotton is considered as the major fiber crop of global important through the world.

Improvement of cotton production in Egypt could be achieved by developing high yielding cultivars tolerant to environmental stresses to increase cultivated area

(throughout newly reclaimed soil), and improving the agronomic practices. It is worthy to mention that some of the newly reclaimed soils in Egypt are desert and have limited quantity of water irrigation and high level of salinity. Cotton in this respect is classified as a salt tolerant crop and variation in salt tolerance has become observed among different varieties (Mass and Hoffman, 1977 and Afiah and Ghoneim, 1999). Also, resistance of cotton to salinity may differ according to climatic conditions (El-Sheik, 1961).

Regulation of transport and distribution of ions in various plant parts and within cells is an important feature of the mechanism of salt tolerance (Flowers et al., 1977 and Greenway and Munns, 1980). AS much as the specific accumulation of  $\text{Na}^+$  and/or  $\text{Cl}^-$  in plant tissues is toxic and found as one of the major causes of growth reduction under saline conditions (Greenway and Munns, 1980; Wyn Jones, 1981; Yeo and flowers, 1984 and Ashraf, 1994). However, proline function in plant tissues is to protect several enzymes against inactivating effects of stress. So, high values of proline content indicate that, plants are tolerant,

while the low values reveal that the plants are sensitive to salinity (Paleg *et al.*, 1981).

Therefore, studying the type of gene action controlling yield and its components along with chemical constituents accounted the major importance in cotton breeding program. Since, decision making about the effective breeding procedure to be used is mainly dictated by the type of gene action controlling chemical constituents. Thus, the genetic information obtained from multigeneration are reliable compared with those based on one generation. Thus six populations ( $\bar{P}_1$ ,  $\bar{P}_2$ ,  $\bar{F}_1$ ,  $\bar{F}_2$ ,  $\bar{B}_1$  and  $\bar{B}_2$ ) are considered the one which may give detailed information about type of gene action that control the studied characters.

Many investigators indicated the importance of genetic variance in the genetics of quantitative traits. Most of these genetic variances were due to the additive variance in some traits i.e., number of open bolls/plant, boll weight, lint percentage and seed index [Abul-Naas *et al.*, 1983; Gomma and Shaheen, 1995] showed that dominance and additive  $\times$  additive gene effects were important in

controlling yield and yield attributes. In this concern, Kassem *et al.* (1981) reported that the additive, dominance and epistatic gene effects were involved in the inheritance of most yield and yield attributes. On the other hand, Atta *et al.* (1982), El- Okkia *et al.* (1989) and Hendawy (1994) reported that both additive and non-additive gene effects were important in the inheritance of seed cotton yield, number of open bolls/plant, boll weight, seed index and lint percentage. The non-additive and environmental variances were larger in magnitude than the additive one in some cases.

So, the present study was carried out to investigate the nature of gene action and some genetical parameters for seed cotton yield/plant, number of

fruiting branches/plant, number of open bolls/plant, boll weight and chemical components i.e., potassium, magnesium, sodium concentrations as well as proline content in cotton leaves under Ras Sudr conditions.

## MATERIALS AND METHODS

### 1. Description of the Studied Materials and Experimental Layout

The present investigation was conducted during the three successive summer growing seasons; 2000, 2001 and 2002 at Ras Sudr Agricultural Research Station of Desert Research Center, South Sinai. Six cotton crosses, derived from eight diverse parental cotton genotypes Table 1 have been used in the present study.

**Table 1: The pedigree and origin of the cotton varieties under investigation**

Genotype	Pedigree	Origin
1-Giza 45	Giza 28 (Sakha 3 × Sakha 4) × Giza 7 (Ashmouni)	Egypt
2-Giza 70	Giza59a(Giza36×Giza44)×Giza 56(Giza36×Giza40)	Egypt
3-Giza 80	Giza 66 × Giza 73	Egypt
4-Giza 83	Giza 67 × Giza 72	Egypt
5-Giza 85	Giza 67 × C.B. 58	Egypt
6-Giza 86	Giza 75 × Giza 81	Egypt
7-Giza 89	Giza 75 × R. 6022	Egypt
8-Ashmouni	Progenatore of Egyptian cotton cultivars	Egypt
9-Dandara	selected from Giza 3	Egypt
10-Karshenseki-2	Russian variety ( <i>G. barbadense L.</i> )	Russian

These genotypes were used to obtain the following six crosses: 1) Giza 89 x Dandara, 2) Giza 83 x Ashmoni, 3) Giza 45 x Giza 70, 4) Giza 45 x Giza 83, 5) Giza 80 x Giza 86 and 6) Giza 89 x Ashmoni.

In the first Season of 2000, the eight parental cotton genotypes were evaluated in a randomized complete block design with three replications, at the meantime pair crosses were performed to obtain  $F_1$ s seeds. In the second season, 2001, six  $F_1$  cross seeds were sown to produce  $F_1$  plants. Each of the  $F_1$  plants were back crossed to their respective parents to produce first  $BC_1$  ( $F_1 \times P_1$ ) and second  $BC_2$  ( $F_1 \times P_2$ ) back crosses. In the meantime, pair crosses were made to produce more  $F_1$  seeds.  $F_1$  plants were selfed to produce  $F_2$  seeds. In the third season, 2002, the obtained seeds of six populations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $B_1$  and  $B_2$ ) for each of the six cotton crosses were sown and evaluated under normal condition of salinity (2000 ppm) using a randomized complete block design with three replications. Cotton seeds were sown on 26 March. Ridges were 3 m length and 60 cm apart with 20 cm between hills. Each hill was thinned to two plants. The experimental plot consisted of 15 ridges (5 ridges for  $F_2$  generation

and 2 ridges for each of the parents,  $F_1$  and back crosses). In each year, the calcified soil was prepared before sowing and fertilized with 24 unit  $P_2O_5$  that equal about 150 kg. superphosphate/ fed. Fertilization with nitrogen and potassium were carried out after 30, 60 and 90 days of sowing, however in each fertilization date, 20 kg N/fed as ammonium sulphate (20.6% N) and 10 Kg  $K_2O$ /fed. (48%  $k_2O$ ) as potassium sulphate were applied.

## 2. Recorded Data

### a- Chemical analysis

At the beginning of flowering random three samples of leaves from each entry were taken and oven dried according to A. O. A. C. (1975) to determine the chemical constituents, i.e., potassium, magnesium and sodium concentrations (Johnson and Ulich, 1959 and Allen *et al.*, 1974) and proline content (Bates *et al.*, 1973).

### b- Agronomic characters

At harvest, data of yield and yield attributes (i.e., number of fruiting branches/plant, number of open bolls/plant, boll weight and seed cotton yield/plant) were collected on guarded individual plants (i. e., 10 plants for each of the parents and  $F_1$ 's 15 plants for back cross progenies and 30 plants

for  $F_2$  generation) in each replicate from the six populations.

### 3. Biometrical Analysis

#### Testing the genetic model

Two way analysis of variance was performed before biometrical analysis. The A, B and C scaling tests as outlined by Mather (1949) and Hayman and Mather (1955) were applied to test the presence of non-allelic interaction as follows;

$$A = 2\bar{B}_1 - \bar{P}_1 - \bar{F}_1, B = 2\bar{B}_2 - \bar{P}_2 - \bar{F}_1$$

and  $C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2$ . Due to the unknown biased effect of non-allelic interaction, the simple genetic model (m, d and h) was applied when epistasis was absent using the formula by outlined Jinks and Jones (1958) as follows;

$$\text{Mean (m)} = \left[ \frac{1}{2}\bar{P}_1 + \frac{1}{2}\bar{P}_2 + 4\bar{F}_2 - 2\bar{B}_1 - 2\bar{B}_2 \right]$$

Additive

$$(d) = \frac{1}{2}\bar{P}_1 - \frac{1}{2}\bar{P}_2 \text{ and}$$

Dominance

$$(h) = 6\bar{B}_1 + 6\bar{B}_2 - 8\bar{F}_2 - \bar{F}_1 - \frac{3}{2}\bar{P}_1 + \frac{3}{2}\bar{P}_2.$$

Whereas, in the presence of non-allelic interaction, the analysis was proceeded to compute the interaction types involved using the six parameters genetic model of Jinks and Jones (1958) as follows:

m = Mean of  $\bar{F}_2$ .

d = additive effect =  $\bar{BC}_1 - \bar{BC}_2$ .

h = Dominance effect =  $\bar{F}_1 - 4\bar{F}_2 - \frac{1}{2}\bar{P}_1 - \frac{1}{2}\bar{P}_2 + 2\bar{BC}_1 + 2\bar{BC}_2$ .

I = Additive  $\times$  additive type of gene interaction =  $2\bar{BC}_1 + 2\bar{BC}_2 - 4\bar{F}_2$ .

J = Additive  $\times$  dominance type of gene interaction =  $\bar{BC}_1 - \frac{1}{2}\bar{P}_1 - \bar{BC}_2 + \frac{1}{2}\bar{P}_2$ .

L = Dominance  $\times$  dominance type of gene interaction =

$$\bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\bar{F}_2 - 4\bar{BC}_1 - 4\bar{BC}_2$$

The significancy of the genetic components were tested using the "t" test where:

$$\pm t = \frac{\text{Effect}}{\sqrt{\text{variance of effect}}}$$

The estimates of genetic components variance and heritability value in both broad and narrow senses ( $T_{(b)}$  and  $T_{(n)}$ ) were determined according to Mather and Jinks (1982) as follows:

$$E = \frac{1}{3}(\bar{V}_P + \bar{V}_E + \bar{V}_F)$$

$$D = 4\bar{V}_E - 2(\bar{V}_{BC} + \bar{V}_{BQ})$$

$$H = 4(\bar{V}_E - \frac{1}{2}\bar{V}_{D-E})$$

$$T_{(b)} = \frac{\frac{1}{2}D + \frac{1}{4}H}{\frac{1}{2}D + \frac{1}{4}H + E} \quad \text{and} \quad T_{(n)} = \frac{\frac{1}{2}D}{\frac{1}{2}D + \frac{1}{4}H + E}$$

## RESULTS AND DISCUSSIONS

### 1. Mean Performance

#### A- Yield and its components

The reliability of genetic components estimates depend mainly on the amount of the genetic variability among the studied genotypes. Thus, before proceeding to the biometrical analysis, the "t" statistical test was applied to the studied genotypes for the different characters. The results indicated significant differences between parental cotton genotypes, providing evidence for the presence of considerable amount of genetic variability which could be used for further biometrical analysis.

Mean and standard error of the six populations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) of six cotton crosses for the studied characters are given in Table 2. According to the mean of  $F_1$ 's as compared with its respective parental genotypes. Results revealed that, the  $F_1$ 's exceeding the high performing parent for number of fruiting branches/plant in all crosses, except the 4<sup>th</sup> one; and boll weight and seed cotton yield/plant in 1<sup>st</sup> cross only. These results provide

evidence for the presence of overdominant gene effects and the increasing alleles were more frequent than decreasing ones in the genetic constitution of parental cotton genotypes.

While, the  $F_1$ 's mean were less than the lower parent for number of open bolls/plant in 1<sup>st</sup>, 2<sup>nd</sup> and 4<sup>th</sup> crosses; boll weight in 6<sup>th</sup> cross and seed cotton yield/plant in 3<sup>rd</sup>, 4<sup>th</sup> and 6<sup>th</sup> crosses, providing evidence for predominant of decreasing alleles and negative heterotic effects.

The  $F_1$ 's means were equal to the lower parent for number of open bolls/plant in 3<sup>rd</sup> cross and boll weight in 4<sup>th</sup> one, showing complete dominance for these characters.

The  $F_2$ 's of the six studied crosses in each character ranged from  $9.623 \pm 0.393$  (cross 1) to  $14.451 \pm 0.526$  (cross 2) for number of fruiting branches/plant;  $6.766 \pm 0.335$  (cross 5) to  $14.378 \pm 0.799$  (cross 2) for number of open bolls/plant;  $1.742 \pm 0.185$  (cross 5) to  $2.121 \pm 0.132$  (cross 1) for boll weight and  $11.171 \pm 0.580$  (cross 5) to  $32.683 \pm 0.832$  (cross 1) for seed cotton yield/plant. Such wide range indicate the presence of appreciable amount of genetic

**Table 2: Mean  $\pm$  S.E. for the six populations for seed cotton yield/plant(g), number of fruiting branches /plant; number of open bolls/plant and boll weight(g) at Ras Sudr Agriculture Research Station during summer season of 2002**

Characters crosses population	Seed cotton yield/plant(g)						Number of fruiting branches/plant					
	1	2	3	4	5	6	1	2	3	4	5	6
<b>P<sub>1</sub></b>	22.736	28.246	30.743	30.798	16.434	23.116	8.711	11.222	11.200	11.278	11.311	8.701
	$\pm 0.202$	$\pm 0.118$	$\pm 0.119$	$\pm 0.062$	$\pm 0.119$	$\pm 0.138$	$\pm 0.113$	$\pm 0.041$	$\pm 0.041$	$\pm 0.034$	$\pm 0.044$	$\pm 0.036$
<b>P<sub>2</sub></b>	25.453	36.636	10.440	40.493	14.300	37.062	10.962	13.480	9.600	9.901	9.530	13.400
	$\pm 0.025$	$\pm 0.040$	$\pm 0.117$	$\pm 0.037$	$\pm 0.056$	$\pm 0.018$	$\pm 0.162$	$\pm 0.028$	$\pm 0.035$	$\pm 0.030$	$\pm 0.036$	$\pm 0.037$
<b>F<sub>1</sub></b>	28.365	17.806	23.038	23.673	14.950	20.300	13.406	14.600	14.233	10.650	12.461	15.600
	$\pm 0.114$	$\pm 0.049$	$\pm 0.135$	$\pm 0.013$	$\pm 0.088$	$\pm 0.145$	$\pm 0.136$	$\pm 0.049$	$\pm 0.058$	$\pm 0.028$	$\pm 0.036$	$\pm 0.030$
<b>F<sub>2</sub></b>	32.683	27.944	20.689	18.995	11.171	12.659	9.623	14.451	11.000	13.300	11.852	13.333
	$\pm 0.832$	$\pm 2.071$	$\pm 1.282$	$\pm 0.733$	$\pm 0.588$	$\pm 0.557$	$\pm 0.393$	$\pm 0.526$	$\pm 0.465$	$\pm 0.379$	$\pm 0.372$	$\pm 0.388$
<b>BC<sub>1</sub></b>	19.845	23.670	15.724	23.264	14.152	38.039	9.010	8.401	13.761	11.455	12.268	10.201
	$\pm 0.855$	$\pm 1.410$	$\pm 0.391$	$\pm 0.475$	$\pm 0.424$	$\pm 1.366$	$\pm 0.072$	$\pm 0.035$	$\pm 0.045$	$\pm 0.054$	$\pm 0.022$	$\pm 0.026$
<b>BC<sub>2</sub></b>	30.325	16.359	15.602	15.257	11.310	36.575	9.714	14.346	8.615	11.280	10.600	13.712
	$\pm 1.412$	$\pm 0.261$	$\pm 1.166$	$\pm 1.157$	$\pm 0.528$	$\pm 1.724$	$\pm 0.045$	$\pm 0.030$	$\pm 0.054$	$\pm 0.037$	$\pm 0.022$	$\pm 0.033$



Table 2: Cont.

Characters crosses population	Number of open bolls/plant						Boll weight(g)					
	1	2	3	4	5	6	1	2	3	4	5	6
P1	11.922	18.084	15.080	15.428	8.700	9.492	1.910	1.570	2.270	2.032	1.693	2.644
	±0.116	±0.230	±0.191	±0.059	±0.298	±0.422	±0.032	±0.015	±0.008	±0.004	±0.004	±0.003
P2	14.068	12.760	4.350	16.400	11.023	12.244	1.813	2.986	1.183	2.493	1.313	3.043
	±0.163	±0.150	±0.079	±0.110	±0.211	±0.112	±0.004	±0.003	±0.004	±0.011	±0.003	±0.013
F1	10.501	9.329	4.533	11.600	9.286	11.023	2.722	2.181	1.450	2.040	1.502	1.853
	±0.139	±0.070	±0.097	±0.072	±0.119	±0.322	±0.024	±0.017	±0.018	±0.014	±0.003	±0.003
F2	11.551	14.338	10.353	11.014	6.766	7.250	2.121	1.932	2.063	1.833	1.742	1.775
	±0.462	±0.799	±0.546	±0.455	±0.335	±0.356	±0.132	±0.209	±0.184	±0.159	±0.185	±0.144
BC1	10.083	11.600	11.284	12.667	8.700	16.286	1.983	2.034	1.465	2.006	1.683	2.317
	±0.361	±0.707	±0.412	±0.224	±0.317	±0.427	±0.093	±0.030	±0.059	±0.053	±0.132	±0.100
BC2	11.600	8.230	8.700	7.752	6.505	16.240	2.598	2.268	1.769	1.868	1.789	2.299
	±0.483	±0.265	±0.500	±0.480	±0.265	±0.653	±0.131	±0.064	±0.414	±0.132	±0.072	±0.176

variability. Hereby, offer breeder great opportunity for isolating promising cotton genotypes.

The back cross population means are the mid-way between the  $F_1$  and the parental genotypes for number of fruiting branches/plant, number of open bolls/plant, boll weight and seed cotton yield/plant in most studied crosses. These results suggested absence of dominance and genes controlling these characters are independently segregated. But, it deviated from the mid value of parents and their respective  $F_1$  for number of fruiting branches/plant in 4<sup>th</sup> cross; number of open bolls/plant in 5<sup>th</sup> and 6<sup>th</sup> crosses; boll weigh in 3<sup>rd</sup>, 4<sup>th</sup> and 5<sup>th</sup> crosses and seed cotton yield/plant in 1<sup>st</sup>, 4<sup>th</sup> and 5<sup>th</sup> crosses. These results suggest that, polygenic genes are more pronounced for these characters.

#### **B- Chemical constituents**

Data of mean performance of chemical composition of 6 crosses and its components Table 3 revealed that, the  $F_1$ 's exceeding the high performing parent for potassium concentration in 3<sup>rd</sup> and 5<sup>th</sup> crosses; magnesium concentration in 4<sup>th</sup> cross; sodium concentration in 1<sup>st</sup> and 4<sup>th</sup> crosses

and proline content in 2<sup>nd</sup> and 6<sup>th</sup> crosses. The results indicated the presence of overdominance gene effects and positive heterotic effects which may result in adequate genetic base for further improvement.

While, the  $F_1$ 's mean were less than the lower parent for potassium concentration in 1<sup>st</sup>, 2<sup>nd</sup> and 4<sup>th</sup> crosses; magnesium concentration in 3<sup>rd</sup> and 5<sup>th</sup> crosses; sodium concentration in 2<sup>nd</sup>, 3<sup>rd</sup>, 5<sup>th</sup> and 6<sup>th</sup> crosses and proline content in 4<sup>th</sup> and 5<sup>th</sup> crosses, providing evidence for the predominance of decreasing alleles and negative heterotic effect in these crosses for the studied characters.

The  $F_2$  of the six studied crosses in each character ranged from  $68.788 \pm 0.943$  (cross 3) to  $78.707 \pm 1.399$  (cross 5) for potassium concentration;  $103.800 \pm 0.772$  (cross 3) to  $112.300 \pm 1.350$  (cross 1) for magnesium concentration;  $43.506 \pm 1.088$  (cross 6) to  $50.117 \pm 0.769$  (cross 3) for sodium concentration and from  $0.705 \pm 0.149$  (cross 5) to  $1.228 \pm 0.206$  (cross 2) for proline content. Such wide range indicate the presence of a fair amount of genetic variability. Thus, offer the

**Table 3: Mean  $\pm$  S.E. for the six populations for chemical composition potassium, magnesium, sodium concentration and proline content at Ras Sudr Agriculture Research Station during summer season of 2002**

Character Crosses population	Potassium concentration(gm/100gm)						Magnesium concentration(gm/100gm)					
	1	2	3	4	5	6	1	2	3	4	5	6
P1	70.313	68.520	68.410	68.300	78.360	70.320	107.450	105.331	105.303	105.370	108.390	107.333
	$\pm 0.217$	$\pm 0.147$	$\pm 0.192$	$\pm 0.170$	$\pm 0.139$	$\pm 0.124$	$\pm 0.133$	$\pm 0.171$	$\pm 0.172$	$\pm 0.141$	$\pm 0.174$	$\pm 0.134$
P2	80.500	77.550	69.263	77.410	76.450	77.300	114.360	113.499	106.280	113.282	112.320	114.360
	$\pm 0.228$	$\pm 0.188$	$\pm 0.174$	$\pm 0.148$	$\pm 0.150$	$\pm 0.165$	$\pm 0.180$	$\pm 0.158$	$\pm 0.192$	$\pm 0.140$	$\pm 0.168$	$\pm 0.192$
F1	68.866	65.317	71.366	65.487	80.336	75.270	113.291	110.363	104.380	114.388	105.250	109.346
	$\pm 0.181$	$\pm 0.190$	$\pm 0.238$	$\pm 0.196$	$\pm 0.187$	$\pm 0.179$	$\pm 0.188$	$\pm 0.208$	$\pm 0.170$	$\pm 0.142$	$\pm 0.174$	$\pm 0.171$
F2	76.612	70.700	68.788	72.100	78.707	78.100	112.300	110.200	103.800	109.501	104.217	108.811
	$\pm 1.435$	$\pm 1.399$	$\pm 0.943$	$\pm 1.574$	$\pm 1.399$	$\pm 1.418$	$\pm 1.350$	$\pm 1.814$	$\pm 0.772$	$\pm 1.746$	$\pm 0.952$	$\pm 1.373$
BC1	71.740	68.329	70.563	64.311	80.815	73.205	107.863	106.505	104.686	110.101	104.766	104.500
	$\pm 2.246$	$\pm 0.895$	$\pm 1.003$	$\pm 0.684$	$\pm 0.696$	$\pm 1.769$	$\pm 1.332$	$\pm 1.708$	$\pm 0.686$	$\pm 1.215$	$\pm 1.536$	$\pm 1.167$
BC2	76.555	74.200	70.896	69.644	77.947	79.938	114.226	111.602	104.804	112.761	107.000	108.847
	$\pm 1.612$	$\pm 0.712$	$\pm 0.573$	$\pm 1.551$	$\pm 1.197$	$\pm 1.858$	$\pm 0.471$	$\pm 0.763$	$\pm 0.416$	$\pm 0.668$	$\pm 1.633$	$\pm 1.705$

Table 3: Cont.

Characters Crosses population	Sodium concentration(gm/100gm)						Proline content ( $\mu$ moles/gm f.w.)					
	1	2	3	4	5	6	1	2	3	4	5	6
P1	48.150	50.520	50.260	50.363	47.210	48.311	1.057	0.648	1.376	1.375	1.674	1.057
	$\pm 0.181$	$\pm 0.240$	$\pm 0.092$	$\pm 0.137$	$\pm 0.173$	$\pm 0.171$	$\pm 0.005$	$\pm 0.002$	$\pm 0.002$	$\pm 0.002$	$\pm 0.002$	$\pm 0.003$
P2	47.180	49.522	52.400	46.326	47.271	47.222	0.668	0.973	0.890	1.141	1.217	0.975
	$\pm 0.218$	$\pm 0.177$	$\pm 0.155$	$\pm 0.149$	$\pm 0.261$	$\pm 0.149$	$\pm 0.002$	$\pm 0.003$	$\pm 0.011$	$\pm 0.001$	$\pm 0.002$	$\pm 0.003$
F1	49.791	47.491	48.400	52.360	44.400	45.274	0.989	1.966	1.332	0.799	0.429	1.148
	$\pm 0.155$	$\pm 0.175$	$\pm 0.164$	$\pm 0.115$	$\pm 0.146$	$\pm 0.161$	$\pm 0.008$	$\pm 0.006$	$\pm 0.005$	$\pm 0.002$	$\pm 0.003$	$\pm 0.003$
F2	46.455	48.954	50.117	48.500	45.303	43.506	1.057	1.228	1.125	0.876	0.705	1.013
	$\pm 0.340$	$\pm 0.831$	$\pm 0.767$	$\pm 0.969$	$\pm 0.817$	$\pm 1.088$	$\pm 0.151$	$\pm 0.206$	$\pm 0.193$	$\pm 0.102$	$\pm 0.149$	$\pm 0.161$
BC1	46.711	48.600	48.104	48.771	44.813	45.000	1.104	0.896	1.080	1.156	1.314	1.185
	$\pm 0.473$	$\pm 0.452$	$\pm 0.586$	$\pm 0.831$	$\pm 0.975$	$\pm 1.155$	$\pm 0.218$	$\pm 0.173$	$\pm 0.189$	$\pm 0.200$	$\pm 0.136$	$\pm 0.179$
BC2	47.721	47.218	50.368	46.304	43.110	45.244	1.219	1.372	1.116	1.157	1.288	1.314
	$\pm 0.495$	$\pm 1.191$	$\pm 0.518$	$\pm 1.291$	$\pm 1.197$	$\pm 1.237$	$\pm 0.178$	$\pm 0.141$	$\pm 0.187$	$\pm 0.200$	$\pm 0.180$	$\pm 0.136$

breeder great opportunity for effective selection to isolate specific patterns of cotton genotypes. The  $F_2$  values for potassium, magnesium, sodium concentrations and proline content tended to be decreased from  $F_1$  to  $F_2$ , indicating inbreeding depression and accumulation of decreasing alleles.

The back cross population means are in the mid-way between the  $F_1$  and the parental genotypes for potassium, magnesium, sodium concentrations and proline content in most studied crosses. But, it deviated from the mid value of parents and their respective  $F_1$  for the same characters in some crosses. Thus, polygenic effect is more pronounced.

## **2. Assessment the Types of Gene Action Using First Degree Statistic (Six Population Model)**

In the present study, scaling test (A, B and C) was employed to test the presence of epistasis. For this purpose, six populations biometrical approach have been applied in six cotton crosses for yield and its components and some chemical constituents.

### **A- Yield and its attributes**

In this investigation (A, B and

C) scaling tests were employed to test the presence of epistasis. The results in Tables 4 and 5 indicated significant non-allelic interactions for number of fruiting branches/plant, number of open bolls/plant, boll weight and seed cotton yield/plant in all crosses. These results indicate the presence of epistasis, and may be taken as an evidence for the failure of simple genetic model to ascertain the genetic variation for these characters in the corresponding crosses. In this respect, the inheritance of number of fruiting branches/plant, number of open bolls/plant and seed cotton yield/plant were under complex genetic control for the studied crosses in cotton genotypes (Awaad and Hassan, 1996). Moreover, Younis (1999) and Allam (2003) indicated the presence of non-allelic interaction in controlling seed cotton yield. In addition El-Disouqi and Zeina (2001) reported that the complex genetic model played a great role in the inheritance of number of open bolls/plant, seed cotton yield/plant and boll weight.

The adequacy of genetic model, Table 4 and 5 indicated that, the additive gene effect (d) was the main type controlling the

inheritance of number of fruiting branches/plant in 1<sup>st</sup>, 2<sup>nd</sup>, 3<sup>rd</sup>, 5<sup>th</sup> and 6<sup>th</sup> crosses and boll weight in 1<sup>st</sup> and 2<sup>nd</sup> ones, indicating that, superior genotypes could be identified from its phenotypic expression. In the respect, additive gene action played a major role in determining the inheritance of no. of fruiting branches/plant [Awaad and Hassan; 1996] seed cotton yield/plant, number of open bolls/plant and boll weight (Gomaa, 1997; Esmail *et al.*, 1999; El-Disouqi and Zeina, 2001; El-Adly, 2004 and Abd El-Hadi *et al.*, 2005).

On the other hand, the interaction type of gene action additive  $\times$  additive was positive and significant for number of open bolls/plant and seed cotton yield/plant in 6<sup>th</sup> cross as well as boll weight in 4<sup>th</sup> and 6<sup>th</sup> crosses; while in the 3<sup>rd</sup> only it was negative and significant. Therefore, phenotypic selection was effective for improving the foregoing characters in the corresponding crosses. Similar findings were obtained by Khalil and Khattab (1997); Abd El-Gelil, (2001) and Allam, (2003) for seed cotton yield/plant.

The dominance (h) and its digenic interaction type,

dominance  $\times$  dominance (1) were significant and involved in the inheritance of boll weight and seed cotton yield/plant in 6<sup>th</sup> cross only as well as number of open bolls/plant in the 1<sup>st</sup> and 6<sup>th</sup> crosses; The considerable amount of non fixable gene action type displayed by these characters in the corresponding crosses may suggest that, improving these characters could be achieved through hybrid breeding method. Similar trends were reported by Khalil and Khattab (1997) for number of open bolls/plant; Esmail *et al.* (1999) and Abd El-Hadi *et al.* (2005) for seed cotton yield/plant and boll weight and Allam (2003) for seed yield/plant.

Moreover, the interaction type additive  $\times$  dominance (j) was negative and significant for number of fruiting branches/plant in 2<sup>nd</sup>, 4<sup>th</sup> and 6<sup>th</sup> crosses; number of open bolls/plant in 3<sup>rd</sup> cross only; boll weight in 1<sup>st</sup> and 3<sup>rd</sup> crosses and seed cotton yield/plant in 3<sup>rd</sup> one, showing more frequent of decreasing alleles over increasing ones. In this respect, Allam (2003) indicated that the interaction type additive  $\times$  dominance was negative and significant for seed cotton

Table 4: Scaling tests, gene effects and heritability for seed cotton yield/plant(g) and number of fruiting branches/plant using six populations in six cotton crosses at Ras Sudr Agriculture Research Station during summer season of 2002

Character Cross	Seed cotton yield/plant(g)						Character Cross	Number of fruiting branches/plant					
	1	2	3	4	5	6		1	2	3	4	5	6
<b>Scaling test</b>							<b>Scaling test</b>						
A	-3.90	0.44	-2.60*	-2.90*	-0.90	11.30**	A	-4.1**	-9.0**	2.1**	1.0**	0.8**	-3.6**
B	2.40	-7.50**	4.30	-11.6**	-2.20	5.40	B	-4.9**	0.6*	-6.6**	1.9**	-0.7**	-1.6**
C	8.90*	8.40	8.40*	-14.9**	-5.30*	-17.50**	C	-8.1	3.8	-5.2	10.9*	1.6	-0.2
<b>Appropriate genetic model</b>							<b>Appropriate genetic model</b>						
m	11.27*	9.60	7.10**	6.60**	3.90**	4.30**	m	9.6**	14.4**	11.0**	13.0**	11.8**	13.3**
d	-3.60	2.50	0.04	2.80	0.98	0.50	d	-0.7**	-5.9**	5.2**	0.2	1.6**	-3.5**
h	-8.90*	-15.90*	-11.0**	-3.70	2.01*	30.90**	h	2.6	-9.9	4.4	-7.9	0.4	0.9
i	10.50*	10.90	-6.80	0.36	2.20	34.20**	i	-0.9	-12.2	0.6	-8.0	-1.7	-5.4
j	-3.20	3.97*	-3.50*	4.30**	0.63	2.90	j	0.4	-4.8**	4.3**	-0.5*	0.8**	-1.2**
l	11.90	17.90	5.20	14.20	0.98	-50.90**	l	10.0**	20.6**	4.0	5.1	1.7	10.9*
T <sub>(b)</sub>	16.71	20.69	12.13	17.22	17.15	12.15	T <sub>(b)</sub>	40.11	56.64	74.74	68.62	65.59	36.59
T <sub>(n)</sub>	11.16	15.41	6.29	11.70	12.15	6.30	T <sub>(n)</sub>	22.68	43.51	72.19	45.12	43.19	23.08

**Table 5: Scaling test, gene action and heritability for Number of open bolls/plant and boll weight(g) using six populations in six cotton crosses at Ras Sudr Agriculture Research Station during summer season of 2002**

Character Cross	Number of open bolls / plant						Character Cross	Boll weight (g)					
	1	2	3	4	5	6		1	2	3	4	5	6
<b>Scaling test</b>							<b>Scaling test</b>						
A	-0.9	-1.4	0.9	-1.3*	-0.2	4.4*	A	-0.67*	0.23**	-0.55**	-0.06	0.17	0.14
B	3.8*	-2.0**	3.0*	-4.4**	-2.6**	3.2*	B	0.91**	-0.63**	0.91*	-0.80*	0.76**	-0.29
C	-0.5	2.6	4.3	-4.1**	-4.0**	-4.8**	C	-0.68	-1.19	2.14	-1.27*	0.96	-2.30**
<b>Appropriate genetic model</b>						<b>Appropriate genetic model</b>							
m	3.9**	4.9**	3.5**	3.7**	2.3**	2.5**	m	2.10**	1.90**	2.10**	1.80**	1.70**	1.80**
d	-0.6	1.2	0.8	1.4	0.8	2.8	d	-0.61**	-0.23**	-0.30	0.14	-0.11	0.12
h	-5.7**	-8.1*	-2.3	-3.1	1.0	12.6**	h	1.50**	0.78	-1.94**	0.19	0.03	1.10*
i	-0.8	-6.0	-0.4	-1.6	1.2	12.4**	i	0.66	0.88	-1.78**	0.42*	-0.02	1.80**
j	-0.25	9.3	-1.1*	1.6*	1.2*	0.6	j	-0.66**	0.47**	-0.73**	0.37	-0.30	0.22
l	2.1*	9.4*	-3.5	7.3*	1.6	-20.0**	l	-0.64	-0.56	1.40	0.44	-0.91*	-1.97*
T <sub>(b)</sub>	38.92	42.71	35.04	26.61	26.21	32.01	T <sub>(b)</sub>	46.40	43.13	26.56	31.39	24.96	20.09
T <sub>(n)</sub>	32.91	31.42	29.44	21.09	22.65	26.25	T <sub>(n)</sub>	42.20	39.35	21.17	26.83	19.96	14.76



yield/plant and El-Adly (2004) for number of open bolls/plant and seed cotton yield/plant.

Heritability estimates depends on the magnitudes of its components part; additive (D) and dominance (H) gene effects. In this respect, narrow sense heritability (Tn) was varied from low to moderate for number of fruiting branches/plant; number of open bolls/plant; boll weight and seed cotton yield/plant in most studied crosses with a few exceptions, indicating great effect of environmental changes on the gene expression. Whereas, it was high (72.19%) for number of fruiting branches/plant in 3<sup>rd</sup> cross. In this connection, low to moderate heritability estimates in narrow sense are reported for seed cotton yield and its attributes by several investigators [Khalil and Khattab, 1997; El-Disouqi and Zeina, 2001; Nassar, 2002 and Allam, 2003]. On the contrary, high heritability values in narrow sense were obtained by Gomaa (1997) for seed cotton yield/plant and boll weight; Younis (1998) for number of open bolls/plant; Esmail *et al.* (1999) for number of open bolls/plant and seed cotton/plant and Younis (1999) for boll weight.

## B- Chemical constituents of cotton leaves

The results in Tables (6 and 7) indicate significant non-allelic interaction for potassium concentration in 1<sup>st</sup>, 2<sup>nd</sup>, 4<sup>th</sup> and 5<sup>th</sup> crosses; magnesium concentration in 1<sup>st</sup>, 5<sup>th</sup> and 6<sup>th</sup> crosses, sodium concentration in 1<sup>st</sup>, 4<sup>th</sup>, 5<sup>th</sup> and 6<sup>th</sup> crosses and proline content in 1<sup>st</sup>, 2<sup>nd</sup> and 5<sup>th</sup> crosses. These results showed the presence of epistasis and the simple genetic model was failed to ascertain the genetic variation for these characters in the corresponding crosses. In this respect, Hassan (2000) and Moursi (2003) concluded that the complex genetic model played a great role in the inheritance of leaves proline content.

The insignificancy of non-allelic interaction was observed in potassium concentration in 3<sup>rd</sup> and 5<sup>th</sup> crosses; magnesium concentration in 2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup> crosses; sodium concentration in 2<sup>nd</sup> and 3<sup>rd</sup> crosses as well as proline content in 3<sup>rd</sup>, 4<sup>th</sup> and 6<sup>th</sup> ones. The previous results indicated that, the simple additive-dominance genetic model proved to be satisfactory in explaining the inheritance of the foregoing characters. In this connection, simple genetic model was adequate for explaining the inheritance of proline content .

The adequacy of genetic model Table (6 and 7) indicated that, the additive gene effect (d) was the main type controlling the inheritance of potassium concentration in 2<sup>nd</sup>, 5<sup>th</sup> and 6<sup>th</sup> crosses; magnesium concentration in 1<sup>st</sup>, 3<sup>rd</sup> and 4<sup>th</sup> crosses; sodium concentration in the 2<sup>nd</sup> and 3<sup>rd</sup> crosses and proline content in 2<sup>nd</sup>, 3<sup>rd</sup>, 4<sup>th</sup> and 6<sup>th</sup> crosses. Meanwhile, the additive (d) and additive × additive (i) interaction type were important in the genetic system controlling potassium concentration in 4<sup>th</sup> and 6<sup>th</sup> crosses and proline content in 5<sup>th</sup> one. These results indicated that, the superior genotypes could efficiently identified from its phenotypic expression. Therefore, phenotypic selection was more effective for improving these characters for such cross. Similar findings were obtained by Moursi (2003) who concluded that the additive genetic variance was significant for proline content.

The dominance (h) and its digenic interaction type, dominance × dominance (l) were significant and involved in the inheritance of potassium concentration in 4<sup>th</sup> cross and magnesium concentration in 6<sup>th</sup> cross. Sodium concentration in 5<sup>th</sup>

cross and proline content in 1<sup>st</sup> one. Also, the dominance gene action played an important role in the genetics of sodium concentration in 5<sup>th</sup> cross and proline content in 1<sup>st</sup> cross. The considerable amount of non fixable gene action type displayed by these characters in the corresponding crosses may suggest that improving these characters could be achieved through hybrid breeding method. In this connection, dominance gene action played a major role in determining the inheritance of potassium concentration (Mahassen *et al.*, 1999); sodium and potassium concentrations (Mahgoub and Sayed-Ahmed, 1999) and proline content (Hassan, 2002).

It is worthy to mention that both additive and dominance gene effects were significant and involved in the inheritance of potassium concentration in 1<sup>st</sup> and 4<sup>th</sup> crosses and magnesium concentration in 6<sup>th</sup> cross. Thus, potassium concentration and magnesium concentration as salinity tolerance criteria could be improved simultaneously through crossing and selection (pedigree method) to make the utmost of the type of gene effects.

**Table 6: Scaling test, gene action and heritability for potassium concentration and magnesium concentration using six populations in six cotton crosses at Ras Sudr Agriculture Research Station during summer season of 2002**

Character Cross	Potassium concentration(gm/100gm)						Character Cross	Magnesium concentration(gm/100gm)					
	1	2	3	4	5	6		1	2	3	4	5	6
<b>Scaling test</b>							<b>Scaling test</b>						
A	4.38	2.78	1.23	-5.17**	2.91	0.81	A	-5.14*	-2.66	-0.08	0.45	4.44	-7.63**
B	3.80	5.55**	0.98	-3.60	-0.98	7.23**	B	0.75	-0.65	-1.06	-2.26	-3.57	-6.06*
C	18.00**	6.13	-5.59	11.75**	-0.67	14.24**	C	0.81	1.29	-5.14	-9.41	-14.41**	-5.09
Appropriate genetic model							Appropriate genetic model						
m	76.60**	70.70**	61.04**	72.10**	74.81**	78.10**	m	112.30**	113.99**	102.19**	101.72**	104.20**	108.80**
d	-4.80*	-5.9**	-0.43	-5.30**	0.96**	-6.70**	d	-6.40**	-4.10**	-0.49	-3.96**	-2.40	-4.30*
h	-16.50**	-5.54	20.29*	-27.91**	10.06	4.74	h	-2.82	-11.55	4.25*	18.45	1.29	-10.15*
i	-9.90	2.20		-20.52**		-6.20**	i	-5.20				6.40*	-8.60
j	0.25	-1.39		-0.79		-3.21	j	-2.95				0.44	-0.79
l	1.80	-10.53*		29.29**		-1.84	l	9.59*				1.61	22.29**
T <sub>(b)</sub>	18.15	31.61	46.42	15.54	80.09	26.66	T <sub>(b)</sub>	45.09	54.73	67.36	52.95	13.68	14.04
T <sub>(n)</sub>	12.69	23.36	32.23	11.44	64.74	21.66	T <sub>(n)</sub>	41.48	51.75	45.43	49.74	7.91	12.24

**Table 7: Scaling test, action and heritability for sodium concentration and proline content using six populations in six cotton crosses at Ras Sudr Agriculture Research Station during summer season of 2002**

Character Cross	Sodium concentration(gm/100gm)						Character Cross	Proline content ( $\mu$ moles/gm. f.w)					
	1	2	3	4	5	6		1	2	3	4	5	6
Scaling test							Scaling test						
A	-4.54**	-0.79	-2.46	-5.32**	-2.02	-3.58	A	0.162	-0.822*	-0.548	0.140	0.525	0.165
B	-1.57	-2.61	-0.20	-6.08**	-5.48*	-2.09	B	0.781*	-0.195	0.010	0.374	0.930*	0.247
C	-9.41**	0.80	0.94	-7.40	-2.10	12.07**	C	0.525	-0.641	-0.430	-0.610	-0.929	-0.276
Appropriate genetic model							Appropriate genetic model						
m	46.50**	45.17**	45.93**	48.50**	45.3**	43.50**	m	1.057**	1.228**	1.241	0.136	0.705**	0.07
d	-1.00	-4.52**	-1.07**	2.40	1.70	-0.20	d	-0.115	-0.476*	0.243**	0.117**	0.026	0.041**
h	5.12	-14.32	-12.79	0.02	-8.23*	3.91	h	-1.779*	-1.489	-0.555	2.297	-1.235	2.694
i	3.00			-4.00	-5.40	6.40*	i	0.418	-0.376			2.384*	
j	-1.49			0.38	1.73	-0.75	j	-0.310	-0.314			-0.203	
l	3.11*			15.40*	12.90**	-0.73	l	-1.361*	1.394*			-3.839*	
T <sub>(b)</sub>	17.24	30.82	69.87	17.28	19.02	16.73	T <sub>(b)</sub>	26.84	23.91	46.29	31.96	26.66	33.84
T <sub>(n)</sub>	11.85	20.63	48.80	5.93	15.53	14.48	T <sub>(n)</sub>	16.36	12.50	34.13	26.75	14.41	27.03

Narrow sense heritability "Tn" reflects fixable type of gene action transmissible from the parents to the progeny or from generation to another, was high (>50%) for potassium concentration in 5<sup>th</sup> cross and magnesium in 2<sup>nd</sup> one. These results allowing for considerable progress in salt tolerance through selection for both characters. In this regard, high heritability estimate in narrow sense (>50%) was recorded for Potassium concentration (Mahassen *et al.*, 1999). While, heritability in narrow sense "Tn" ranged from low to moderate for the other characters in the corresponding crosses. In this respect, Hassan (2002) obtained narrow sense heritability value ranged from 28.8 to 46.4% for leaf proline content. While Moursi (2003) reported high narrow sense heritability (>50%) for leaf proline content.

### Conclusion

It could be concluded that gene action of such cotton character varied according to the parents involved in cotton crosses. However, the additive gene effects played an important role in the inheritance of number of fruiting branches/ plant and the

concentration of potassium, magnesium and proline in cotton leaves of most crosses, indicating the efficiency of phenotypic selection in improving these characters. Otherwise, the dominant gene effects and its digenic type played the major role in the inheritance of seed cotton yield, number of open bolls/plant and boll weight in almost crosses, indicating the efficiency of hybrid breeding method for developing these characters.

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السلوك الوراثي للمحصول ومساهماته وبعض المكونات الكيميائية في ستة هجن من القطن المصري تحت ظروف وأرض مختبرية  
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أجريت هذه الدراسة بمحطة بحوث راس سدر (محافظة جنوب سيناء) التابعة لمركز بحوث الصحراء خلال الموسم الصيفي لآعام ٢٠٠٠، ٢٠٠١، ٢٠٠٢. مستخدماً نظام الستة عشائر لستة هجن من القطن هي: (١) جيزة ٨٩ × نندرة ٢، جيزة ٨٣ × اشمونى ٣، جيزة ٤٥ × جيزة ٧٠، ٤، جيزة ٤٥ × جيزة ٨٣، ٥، جيزة ٨٠ × جيزة ٨٦، ٦، جيزة ٨٩ × اشمونى بهدف معرفة النظام الوراثي وطبيعة الفعل الجيني المتحكم فى صفات المحصول ومساهماته (عدد الأفرع الثمرية للنبات، عدد اللوز المتفتح للنبات، وزن اللوزة، ومحصول القطن الزهر للنبات) بالإضافة إلى بعض المكونات الكيميائية مثل تركيزات البوتاسيوم، الماغنسيوم والصوديوم ومحتوى البرولين تحت تركيز ملوحة ٢٠٠٠ جزء فى المليون وكان التصميم التجريبي المستخدم قطاعات كاملة العشوائية فى ثلاث مكررات. ويمكن تلخيص أهم النتائج فيما يلى:- أظهرت نتائج اختبار المقياس (A, B & C) أن الموديل الوراثي غير البسيط هو الملائم لتفسير وراثه صفات عدد الأفرع الثمرية للنبات، عدد اللوز المتفتح للنبات، وزن اللوزة ومحصول القطن الزهر للنبات فى كل الهجن وصفة

تركيز البوتاسيوم في الهجين الأول، الثاني، الرابع والسادس، تركيز الماغنسيوم في الهجين الأول، الخامس والسادس، تركيز الصوديوم في الهجين الأول، الرابع، الخامس والسادس ومحتوى البرولين في الهجين الأول، الثاني والخامس.

كان الموديل الوراثي البسيط هو الملائم لتفسير وراثة صفات تركيز البوتاسيوم في الهجين الثالث والخامس، تركيز الماغنسيوم في الهجين الثاني والثالث والرابع، تركيز الصوديوم في الهجين الثاني والثالث ومحتوى البرولين في الهجين الثالث والرابع والسادس.

كان الفعل الجيني المضيف هو الأكثر أهمية في وراثة صفات عدد الأفرع الثمرية للنبات في الهجين الأول، الثاني، الثالث، الخامس والسادس، وزن اللوزة في الهجين الأول والثاني، تركيز البوتاسيوم في الهجين الثاني، الخامس والسادس، تركيز الماغنسيوم في الهجين الأول، الثالث والرابع وتركيز الصوديوم في الهجين الثاني والثالث ومحتوى البرولين في الهجين الثاني، الثالث، الرابع والسادس. كما كان الفعل الجيني (المضيف × المضيف) ذو أهمية في وراثة صفات ارتفاع النبات، عدد اللوز المتفتح للنبات ومحصول القطن الزهر للنبات في الهجين السادس ووزن اللوزة في الهجين الرابع والسادس. وكان الفعل الجيني المضيف والتفاعل (المضيف × المضيف) ذو أهمية في وراثة صفات تركيز البوتاسيوم في الهجين الرابع والسادس ومحتوى البرولين في الهجين الخامس.

كما كان الفعل الجيني السيادة والتفاعل (السيادة × السيادة) هو المتحكم في وراثة صفات وزن اللوزة ومحصول القطن الزهر للنبات في الهجين السادس، عدد اللوز المتفتح للنبات في الهجين الأول والسادس، تركيز البوتاسيوم في الهجين الرابع وتركيز الماغنسيوم في الهجين السادس، تركيز الصوديوم في الهجين الخامس ومحتوى البرولين في الهجين الأول. وكان الفعل الجيني السيادة ذو أهمية في وراثة صفات تركيز الصوديوم في الهجين الخامس ومحتوى البرولين في الهجين الأول.

كانت كفاءة التوريث بالمعنى المحدود عالية (> 50%) لصفات عدد الأفرع الثمرية للنبات في الهجين الثالث، تركيز البوتاسيوم في الهجين الخامس وتركيز الماغنسيوم في الهجين الثاني. بينما تراوحت قيم كفاءة التوريث بالمعنى المحدود منخفضة إلى متوسطة لصفات عدد الأفرع الثمرية للنبات، عدد اللوز المتفتح للنبات، وزن اللوزة، محصول النبات من القطن الزهر، تركيز الصوديوم ومحتوى البرولين.