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GENE ACTION OF EARLINESS AND SOME MORPHOLOGICAL TRAITS IN COTTON UNDER DIFFERENT ENVIRONMENTAL CONDITIONS

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ABSTRACT

This study aimed to investigate the type of gene action and the relative amount of genetic variance components as well as their interaction by locations using eight Egyptian cotton varieties. These varieties were: Ashmouni (Giza-19), Giza-70, Giza-45, Giza-85, Giza-86 , Giza- 89 (P6), American-Egyptian; Pima-S6 and Creamy type of [Bahteem 105 x Giza-67] x [Giza-72 x Delsero]. These varieties and their 15 F_1 hybrids, which produced using 3 x 5 factorial mating designed were evaluated at two different locations for some earliness and morphological characters. The obtained results could be summarized in the following:

The mean squares of genotypes were highly significant for all studied earliness and vegetative traits which included first fruiting node, days to first flower, days to first opening boll, earliness index, number of fruiting branches per plant and plant height. Also, the locations and genotypes by location interaction mean square were highly significant for these traits. These results indicated the presence of real differences between these genotypes for these traits and gave also different performances at the different environmental conditions.

The results showed that the means of F_1 hybrids were decreased towards earliness over their mid-parents with respect to first fruiting node, days to first flower and days to first opining boll. Thus, negative heterosis values over mid-parents were observed for these traits.

The results revealed that additive effects play a major role in the expression of studied traits, while dominance effects had a minor role. Genetic parameters by location interactions also revealed that the magnitude of non-additive by locations interaction (σ^2_{DL}) were positive and larger in magnitude than their corresponding values of additive by locations interaction (σ^2_{AL}) for all studied earliness and vegetative traits except for first fruiting node. These results suggested that additive effects were more stable over the environments than non-additive effects with respect to most of studied earliness and vegetative traits. The importance of additive genetic variance (σ^2_A) over the dominance genetic variance (σ^2_D) was verified once again by the dominance degree ratio, which was less than one for first fruiting node, number of fruiting branches per plant and plant height or equal zero for days to first flower, days to first opening boll and earliness index.

It could be concluded that the investigated traits are mainly controlled by additive genetic variance, while non-additive and its interactions with epigenetic factors play a minor role in the inheritance of these traits. Thus, the selection program could be a proper tool to produce earlier genotypes.

INTRODUCTION

Although Egyptian cotton is famous for its advantage as extra fine long staple cotton varieties, earliness in cotton is needed to harvest the crop during periods of more favorable weather. It also help in reducing water requirements, escaping from diseases and insects injury. On the other hand, genotypes by environment interactions usually hamper selection of such genotype, due to the failure of genotype to show the same characteristics in different environmental conditions. Since, environmental factors are usually in continuous state of changing, the partitioning of genotypes and their interaction with environment variances to its components in plant breeding is a matter of major importance. In this respect, some investigators studied the nature of gene action for earliness in cotton, among them Kosba *et al* (1991), Al-Kaddoussi and Eissa (1994), Gomaa and Shaheen (1995) Kosba *et al* (1999). They indicated that both additive and non additive gene action were important in the expression of days to first flower, first fruiting node and earliness index traits. They also revealed that additive genetic variance was predominated over dominance genetic variance in the inheritance of these traits. In addition, El-Helw (1990) and Hendawy (1994-a) found that the GCA as well as SCA variances and their interaction with environments were highly significant for plant height and number of fruiting branches per plant. Although, additive genetic variance plays a major role in the inheritance of plant height, non additive genetic variance was predominated in the case of number of fruiting branches per plant.

Therefore, this investigation aimed to determine the genetic variance components and their interactions with two different environments for earliness and some morphological traits.

MATERIALS AND METHODS

This investigation was carried out at two different locations during two successive seasons. These locations were: Sakha Experimental Station at Kafer El-Sheikh and El-Serw Experimental Station at Domitta. The genetic material used in the present investigation included eight cotton varieties belonging to *Gossypium barbadense* L. These varieties were Ashmouni; Giza-19 (P1), Giza-70 (P2), Giza-45(P3), Giza-85 (P4), Giza-86 (P5), Giza-89 (P6), American-Egyptian; Pima-S6 (P7) and Creamy type of [Bahteem 105 x Giza-67] x [Giza-72 x Delsero] (P8). The seeds of these varieties were obtained from Cotton Breedig Section, Cotton Research Institute, Agriculture Research Center, Giza, Egypt. In the growing season of 1998, selfed seeds of these parental varieties were sown at Sakha Agriculture Station and single crosses between the eight parents were made according to Factorial Mating Design. In this respect, the three varieties (Ashmouni; Giza-19, Giza-70 and Giza-45) were used as male parents. Whereas, Giza-85, Giza 86, Giza-89, Pima-S6 and Creamy type were used as female parents in order to obtain 15 F_1 hybrids. In the second growing season of 1999, eight parental varieties and their 15 F_1 hybrids were evaluated in a field trial experiments at Sakha and El-Serw Experimental Stations in a randomized complete blocks design with four replications at each location. Each block was consisted of 23 plots. Each plot was represented by one row 4 m. long and 60 cm. wide. Hills were 20 cm apart to insure 20 hills per row. At the seedling stage, hills were thinned to keep a constant stand of two plants per hill. Land preparation, fertilizer applications and other culture practices were applied in at the proper time as recommended for cotton crop.

Data were recorded on ten guarded randomly chosen plants per plot for all entries at each location on the following traits: First fruiting node (FFN), days to first flower (DFF), days to first opening boll (DFOB), earliness index (EI), number of fruiting branches per plant (NFB/P) and plant height (PH).

From the data combined over both locations, the combined analyses of variances were conducted for all studied traits as outlined by Singh and Chaudhary (1979). The mean squares of genotypes, locations and genotypes by locations interaction for studied traits were tested for significance according to the regular "F" test.

The amount of heterosis was determined as the percentage deviation of the F_1 hybrids over the average of the mid-parents (M.P) or above the better-parent (B.P). To detect significance of heterosis, differences were measured by the least significant difference values (L.S.D) at 0.05 and 0.01 levels of probability as suggested by Steel and Torrie (1960).

An analysis of variance utilizing the F_1 hybrids was mad according to the analysis of variance of 3 x 5 factorial mating design as outlined by Comstock and Robinson (1952) and defined as design II, with a modification for combined data over both locations. The form of the analysis and the expectation of mean squares are presented in Table 1. Then, the estimates of the different variance components were calculated for each studied trait. Subsequently, these estimates could be expressed in terms of covariance among the two types of relatives in a factorial mating design according to Cockerham (1963). General combining ability variance is equivalent to the covariance among half sibs (HS), and specific combining ability variance is equivalent to the covariance among full sibs (FS) minus twice the covariance of half sibs.

Since, the covariance of half sibs (HS) estimates:

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the covariance of full sibs (FS) estimates:

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Where, if the inbreeding coefficient of the paternal (Fm) and maternal (F_f) lines assumed to having the same inbreeding coefficient equal to one. Therefore, the genetic parameters could be estimated as following:

$2\sigma^2_m = 2\ Cov_{HS(m)} = VA + \frac{1}{2}\ VAA + \ldots;\ \ 2\sigma^2_f = 2\ Cov_{HS(f)} = VA + \frac{1}{2}\ VAA + \ldots$

$\sigma^2_m + \sigma^2_f = Cov_{HS(m)} + Cov_{HS(f)} = VA + \frac{1}{2}\ VAA + \ldots\ldots..$

$\sigma^2_{mf} = Cov_{FS} - [Cov_{HS(m)} + Cov_{HS(f)}] = VD + VAD + VDD + \ldots\ldots\ldots$

Table 1: Form of the analysis of variance and expectation of mean squares of a factorial mating design from the data combined over locations

S.O.V	Df	MS	EMS
Locations (Loc)	L – 1		
Rep./Loc.	L(r-1)		
Crosses	mf – 1	M_c	$\sigma^2_e + + r\sigma^2_{cl} + rL\sigma^2_c$
Males (M)	m – 1	M_m	$\sigma^2_e + r\sigma^2_{mfl} + rL\sigma^2_{mf} + rf\sigma^2_{ml} + rfL\sigma^2_m$
Females (F)	f – 1	M_f	$\sigma^2_e + r\sigma^2_{mfl} + rL\sigma^2_{mf} + rm\sigma^2_{fl} + rml\sigma^2_f$
M x F	(m-1)(f-1)	M_{mf}	$\sigma^2_e + r\sigma^2_{mfl} + rL\sigma^2_{mf}$
Crosses x Loc.	(mf-1)(L- 1)	M_{cl}	$\sigma^2_e + r\sigma^2_{cl}$
M x Loc.	(m-1)(L-1)	M_{ml}	$\sigma^2_e + r\sigma^2_{mfl} + rf\sigma^2_{ml}$
F x Loc.	(f-1)(L-1)	M_{fl}	$\sigma^2_e + r\sigma^2_{mfl} + rm\sigma^2_{fl}$
M x F x Loc.	(m-1)(f-1)(L-1)	M_{mfl}	$\sigma^2_e + r\sigma^2_{mfl}$
Error	L(r-1)(mf-1)	Me	σ^2_e

Where:
L, r, m, f and c: are number of locations, replications, male parents, female parents and crosses, respectively. σ^2_e , σ^2_m , σ^2_f , σ^2_{mf} , σ^2_{ml} , σ^2_{fl} and σ^2_{mfl} are error , males, females, males x females, male x locations, female x locations and males x females x locations variances, respectively.

In addition, estimates of heritabilities in both broad and narrow sense were caculated as follows:

Heritaiblity in broad sense (h^2_b):

$$h^2_b = \frac{\sigma^2_m + \sigma^2_f + \sigma^2_{mf}}{\sigma^2_m + \sigma^2_f + \sigma^2_{mf} + \sigma^2_{ml} + \sigma^2_{fl} + \sigma^2_{mfl} + \sigma^2 e}$$

Heritaiblity in narrow sense ($h^2 n$):

$$(h^2_n) = \frac{\sigma^2_m + \sigma^2_f}{\sigma^2_m + \sigma^2_f + \sigma^2_{mf} + \sigma^2_{ml} + \sigma^2_{fl} + \sigma^2_{mfl} + \sigma^2 e}$$

RESULTS AND DISCUSSION

An analysis of variance of the eight parental varieties and their 15 F_1's hybrids were made from the data combined over the two locations and the obtained results for studied earliness and vegetative traits are presented in Table 2. The mean squares of genotypes were highly significant for all studied earliness and vegetative traits; first fruiting node (FFN), days to first flower (DFF), days to first opening boll (DFOB), earliness index (EI), number of fruiting branches per plant (NFB/P) and plant height (PH). In addition, the locations and genotypes by locations interaction mean square were highly significant for these traits. These results indicated the presence of real differences between these genotypes for all earliness and vegetative traits. Therefore, comparison tests between genotypic means could be made. Furthermore, these genotypes gave different performance at different environments.

Table 2: Combined analysis of variance and mean squares for earliness and vegetative traits for the parents and F_1's hybrids obtained from the combined data over the two locations.

S.O.V.	d.F.	FFN	DFF	DOFB	EI	NFB/P	PH
Locations	1	1.800**	28.883**	75.546**	3590.191**	995.333**	106036.807**
Reps/lac.	6	0.023	0.574	0.503	7.321	1.896	0.484
Genotypes	22	3.882**	18.611**	44.636**	463.740**	16.626**	712.266**
Geno. X Loca.	22	0.210**	2.459**	18.460**	137.956**	4.544**	111.984**
Error	132	0.026	0.249	0.433	7.438	0.285	0.587

**** Significant at 1% level.**

The means of eight parents and their 15 F_1 hybrids at the two locations of Sakha (L_1), El-Serw (L_2) and the combined data over two locations were determined for the previous traits and the results are presented in Table 3. The means showed that there was no specific parent, which was superior or inferior for all studied traits. However, the variety Giza-89 (P_6) was the earlier parent with respect to first fruiting node (FFN) at the two locations and from combined data over both locations. The creamy type [Bahteem 105 x Giza-67] x [Giza-72 x Delsero] (P_8) was the earlier parent for days to first flower (DFF), days to first opening boll (DFOB.) and earliness index (EI) with the means of (71.95, 73.15 and 72.55 days), (122.33, 122.05 and 122.19 days) and (80.05, 87.16 and 83.61days) at first, second locations and combined data over both locations, respectively. In contrast, the variety

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Giza-45 (P_3) was the latest parent for most of earliness traits at the two locations and from the combined data over both locations. Concerning vegetative traits the variety Giza-45 (P_3) was the tallest parent at the first location (Sakha) and from the combined data over both locations with the mean of 161.50 and 137.20 c.m, respectively. Also, it was the best parent for number of fruiting branches per plant (NFB/P) at the first, second location and their combined data with the means of 24.6, 18.95 and 21.78, respectively. The means of the most F_1's hybrids were fluctuated between their parental varieties for most of earliness and vegetative traits at each location. These F_1 hybrids gave different performance over different locations. Therefore, the means from the combined data would present precise information concerning the F_1 hybrids. Generally, the means showed that most of F_1 hybrids exceeded their parents, which were involved in the hybridization in most of earliness and vegetative traits. It also appeared that the best F_1 hybrids was resulted from crosses involving the best parents. Similarly, the poorest F_1 hybrid for most of earliness and vegetative traits was also resulted from crosses combining the inferior two parents. The earliest F_1 hybrid for first fruiting node (FFN) was (P_1 x P_6) with the mean of 5.75 node. While, the earliest F_1 hybrids for days to first flower (DFF), days to first opening boll (DFOB) and earliness index (EI) were (P_1 x P_7), (P_3 x P_8) and (P_1 x P_4), respectively. The tallest F_1 hybrid was (P_3 x P_5) with the mean of 132.70 cm. Whereas, the shortest F_1 hybrid was (P_1 x P_7) with the mean of 114.15 cm. However, the higher number of fruiting branches was observed in the F_1 hybrid (P_3 x P_4) with the mean of 20.18.

The amounts of heterosis over the mid-parents (M.P) and better parent (B.P) for studied traits were obtained from the data at Sakha (L_1) and El-Serw (L_2) locations as well as from the combined data over them and the results are presented in Table 4. Regarding earliness traits, the results showed that the means of F_1 hybrids were decreased towards earliness over the mid-parents (M.P) for the first fruiting node, days to first flower and days to first opening boll. Therefore, there were significant negative heterosis values over mid-parents (M.P) for first fruiting node (FFN) and days to first flower (DFF) at Sakha (L_1) location, while it was undesirable positive and significant for these two traits at El-Serw (L_2) location. In the case of days to first opening boll (DFOB) the same trend was observed at both locations, which the heterosis estimates were desirable negative and highly significant with values of -0.492 and -1.102 at Sakha (L_1) and El-Serw (L_2), respectively. It was undesirable negative for earliness index (E.I) at both locations. Concerning vegetative traits the means of F_1 hybrid were significantly exceeded their mid-parents for number of fruiting branches per plant (NFB/P) at the first location (L_1). Thus, the amount of heterosis over mid-parents was highly significant with value of (4.291). However, the results indicated the amount of heterosis over mid-parents was positive and highly significant at both location for plant height (P.H) with values of 3.17 and 2.53 at Sakha (L_1) and El-Serw (L_2), respectively. On the other hand, the calculated values of heterosis versus the better parent (B.P) were highly significant and not of economical importance for all studied earliness and vegetative traits at two locations and from combined data. The absence of heterosis over the better-

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parent (B.P) was expected, since the varieties used in this investigation are closely related cotton varieties. These results are in agreement with many authors, such as El-Kilany and Mazar (1985); El-Harony (1988), Hendawy *et al* (1989), Kosba *et al* (1991), Gomma and Shaheen (1995), Khalil and Khattab (1997), Amer (1998) and Kosba *et al* (1999).

Mating design were generally developed to partition genetic variance into its components. In factorial mating design, the total genetic variance is divided into males, females and males by females interaction components. The first two portions of variance, i.e., male and female are an estimation of additive genetic variance while the latter portion males by females component is an estimation of non-additive genetic variance including dominance. The magnitudes of additive genetic variance relatively to non-additive genetic variances have an important implication to determine the breeding program which could be followed. Generally, when additive genetic variance is significant and higher in magnitude than those of non-additive genetic variance would indicate its importance in the inheritance of studied traits. Therefore, the breeding program should be directed to develop elite lines through selection from the segregation of the promising F_1 hybrids. Later on, these new lines would be utilized in the production of superior hybrids.

Combined analysis of variance of 3 x 5 factorial mating design from the combined data over both locations was made for the studied earliness and vegetative traits. The mean squares were obtained and the results are presented in Table 5. The results showed that mean squares of males and females were highly significant and larger in magnitude than the corresponding values of males by females interaction for all studied earliness and vegetative traits. This results indicates the predominance of additive genetic variance in the inheritance of these traits. Furthermore, locations, males by locations, females by locations and males by females by locations interactions mean squares were highly significant in most of traits. This finding cleared that the behavior of this genetic materials varied with different environmental conditions.

Table 5: Combined analysis of variance and mean squares of 3 x 5 factorial mating design for earliness and vegetative traits from the combined data over the two locations.

S.O.V.	d.F.	M.S.					
		FFN	DFF	DFOB	EI	NFB/P	PH
Locations (L)	1	0.507**	15.123**	30.000**	2465.499**	790.533**	71282.250**
Rep/Loca.	6	0.011	0.403	0.381	13.303	1.076**	0.486
Crosses (C)	14	2.678**	9.118**	22.960**	341.42**	6.407**	317.862**
Males (M)	2	5.324**	7.706**	12.112**	462.373**	30.441**	691.246**
Females (F)	4	5.412**	24.773**	64.339**	802.716**	2.126**	412.802**
M x F	8	0.651**	1.645**	4.984**	80.536**	2.541**	177.048**
C x L	14	0.1899**	1.777**	9.432**	141.027**	2.515	80.236**
M x L	2	0.462**	0.647*	6.357**	136.357**	0.421	2.032
F x L	4	0.247**	2.300**	11.211**	183.140**	3.723**	145.493**
M x F x L	8	0.093**	1.798**	9.312**	121.138**	2.435**	67.159**
Error	84	0.029	0.171	0.458	10.129	0.289	0.706

*** Significant at 5% level ** Significant at 1% level.**

To understand the nature of gene action, the estimates of genetic parameters were calculated from the combined data over both locations. The obtained results are shown in Table 6. Calculation of genetic parameters from combined analysis over both locations would present more accurate results after the elimination of the confounded effects on genetic parameters by location interactions. The results showed that the additive genetic variance (σ^2_A) were positive and larger in magnitude than those of non-additive genetic variance for all studied earliness and vegetative traits. Furthermore, non-additive genetic variance (σ^2_D) was negative in cases of days to first flower (DFF), days to first opening boll (DFOB) and earliness index (EI), which considered equal zero. These results indicated that additive effects play a major role in the expression of these traits, while dominance effects had a minor role, especially, in the cases of first fruiting node (FFN), number of fruiting branches per plant (NFB/P) and plant height (PH). In addition, this finding may explain the absence of heterosis in most of these traits, especially over better parent. Genetic parameters by locations interactions also revealed that the magnitude of non-additive by locations interaction (σ^2_{DL}) were positive and larger than the corresponding values of additive by locations interaction (σ^2_{AL}) for all earliness and vegetative traits except for first fruiting node (FFN). These results suggests the additive effects are more stable over the environments than non-additive effects with respect to all studied earliness and vegetative traits except first fruiting node (FFN).

Table 6:Estimation of genetic parameters and their standard error from the combined data over both locations for earliness and vegetative traits.

Genetic parameters	FFN	DFF	DFOB	EI	NF B/P	pH
$\sigma^2M \pm$ S.E.	0.147 ±0.0947	0.204 ±0.139	0.1205 ±0.264	8.250 ±8.675	0.897 ±0.539	19.09 ±12.40
$\sigma^2F \pm$ S.E.	0.199 ±0.131	0.984 ±0.0600	2.361 ±1.582	25.181 ±19.98	0.0173 ±0.122	13.851 ±11.106
$\sigma^2A = \sigma^2\ M + \sigma^2\ F$	0.346	1.188	2.480	33.431	0.910	32.941
$\sigma^2D = \sigma^2$ M.F $\pm$ S.E.	0.069 ±0.0367	0.00 ±0.136	0.00 ±0.590	0.00 ±8.138	0.0133 ±0.196	13.736 ±10.593
σ^2_{AL}	0.031	0.0418	0.158	5.926	0.107	6.528
σ^2_{DL}	0.016	0.406	2.213	27.752	0.536	16.613
σ^2e	0.00725	0.042	0.1145	2.532	0.0722	0.176
D.d = $\sqrt{\frac{\sigma^2 D}{\sigma^2 A}}$	0.446	0.00	0.00	0.00	0.121	0.645
$h^2{}_b$ % $\pm$ S.E	88.42 ±1.372	70.84 ±0.649	49.845 ±0.368	48.00 ±0.083	59.31 ±0.546	69.94 ±0.1023
(h^2_n) % $\pm$ S.E.	73.71 ±1.250	70.84 ±0.649	49.84 ±0.368	48.00 ±0.083	51.74 ±0.542	49.35 ±0.0859

The estimated value of heritability also confirmed the previously mentioned results. Broad sense heritability (h^2_b) estimates were close or equal to narrow sense heritability (h^2_n) for all studied earliness and vegetative traits. These results were obtained because some traits showed negative estimates of dominance effects (σ^2_D), which represented by zero. The highest narrow sense heritability estimates were observed in the cases of first fruiting node and days to first flower with values of 73.71% and 70.84%, respectively. Other traits showed low estimates of heritability either in broad or in narrow sense. It should be indicated that these traits were highly influenced by ecological conditions. Therefore, the low estimates of heritability in narrow sense were ranged from 48% to 51.74% for earliness index (EI) and number of fruiting branches per plant (NFB/P), respectively.

The importance of additive genetic variance (σ^2_A) over the dominance genetic variance (σ^2_D) was verified once again by the dominance degree ratio (D.d), which was less than one for first fruiting node (FFN), number of fruiting branches per plant (NFB/P) and plant height (PH) or equal zero for days to first flower (DFF), days to first opening boll (DFOB.) and earliness index. These results were in accordance with Zaitoon *et al*(1982), Rady and Gomma (1983), Kosba *et al* (1991), Tomar and Singh (1992), Hendawy (1994-b), Gomma and Shaheen (1995), Khalil and Khattab (1997), Hassan and Awaad (1997), El-Feki *et al* (1998) and Kosba *et al* (1999).
Depending on the above results, it could be concluded that the investigated traits are mainly controlled by additive genetic variance, while non-additive and its interactions with epigenetic factors play a minor role in the inheritance of these traits. Thus, the selection program is a proper to produce superior genotypes with respect to earliness and vegetative traits.

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الفعل الجينى للتبكير وبعض الصفات المورفولوجية فى القطن تحت الظروف البيئية المختلفة

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هذه الدراسة تهدف الى معرفة الفعل الجينى وتقسيم كل من التباين الوراثى والتباين الراجع للتداخل بين التراكيب الوراثية والظروف البيئية الى مكوناتة لمعظم الصفات المتعلقة بالتبكير وبعض الصفات الخضرية وذلك بإستخدام ثمانية أصناف من القطن المصرى وهى الأشمونى (جيزه 19) – جيزه 70 – جيزه 45 – جيزه 85 – جيزه 86 - جيزه 89 – بيما س 6 والطراز الكريمى. هذه الأصناف بالإضافة الى 15 هجين ناتجة بينهما بإستخدام نظام التزاوج العاملى تم تقيمها فى منطقتين مختلفتين على أساس صفات التبكير وبعض الصفات الخضرية وكانت أهم النتائج المتحصل عليها من هذه الدراسة هى كما يلى:

متوسط مربعات التراكيب الوراثية كانت عالية المعنوية لكل من الصفات التالية: أول عقدة تحمل فرع ثمرى، عدد الأيام لظهور أول زهرة، عدد الأيام لتفتح أول لوزة، دليل التبكير، عدد الأفرع الثمرية لكل نبات وطول النبات. بالإضافة الى ذلك كانت متوسط المربعات لكل من المواقع والتداخل بينها وبين التراكيب الوراثية المدروسة عالى المعنوية لهذه الصفات مما يشير الى أن هناك إختلافات معنوية بين هذه التراكيب الوراثية وأيضا هذه التراكيب تعطى تعبيرا مختلفا مع الظروف البيئية المختلفة فيما يتعلق بالتبكير والصفات الخضرية.

وأوضحت النتائج أيضا أن الهجن كانت أكثر تبكيرا مقارنة بمتوسط الآباء التى دخلت فى تكوينها، خاصة فى حالة أول عقدة تحمل فرع ثمرى ، عدد الأيام لتفتح أول زهرة و عدد الأيام لتفتح أول لوزة. ولذلك كانت قيم قوة الهجين سالبة.

وأشارت النتائج أن الفعل الجينى المضيف يلعب الدور الرئيسى فى تعبير هذه الصفات، بينما الفعل الجينى السيادى له دور ثانوى. وتبين أيضا أن تداخل المواقع مع الفعل السيادى كان موجبا وأكثر قيمة من القيم المقابلة من التداخل بين الفعل الجينى الإضافى والمواقع مما يشير الى أن الأثر المضيف أكثر ثباتا مع الظروف البيئية المختلفة عنه من الفعل الجينى السيادى فى صفات التبكير والصفات الخضرية المدروسة. وأمكن تأكيد هذه الحقيقة بتقدير قيم درجة السيادة للصفات المختلفة والتى كانت أقل من الواحد الصحيح فى حالة أول عقدة ثمرية، عدد ألأفرع الثمرية لكل نبات و طول النبات بينما كانت مساوية للصفر فى حالة عدد الأيام لتفتح أول زهرة وعدد الأيام لتفتح أول لوزة بالإضافة الى صفة معامل التبكير مما يؤكد أهمية الفعل المضيف عن الفعل السيادى فى هذه الصفات.

ومن هذه النتائج التى سبق الإشارة إليها يمكن أن نستخلص أن هذه الصفات محكومة رئيسيابالعوامل الجينية ذات الأثر المضيف بينما العوامل ذات الأثر الجينى السيادى والتداخل بينه وبين العوامل البيئية يلعب الدور الثانوى فى توريث مثل هذه الصفات، ولذلك يكون برنامج الإنتخاب هو المفضل لإنتاج تراكيب وراثية أكثر تبكيرا.

Table 3: The mean performances of parents and F_1's hybrids generations for studied traits at each locations and from combined data over both locations.

Genotypes	FFN			DFF			DOFB			EI			NFB/P			PH		
	L_1	L_2	Comb	L_1	L_2	Comb	L_1	L_2	Comb	L_1	L_2	Comb	L_1	L_2	Comb.	L_1	L_2	Comb
Ashmouni (M) (1)	6.35	6.100	6.23	73.95	75.38	74.66	125.15	125.70	125.43	59.21	66.89	63.05	20.73	17.05	18.89	151.30	106.7	129.03
Giza (70) (M) (2)	6.50	6.48	6.94	75.53	76.55	76.04	124.70	126.30	125.50	53.52	80.93	67.22	21.65	15.90	18.78	144.75	88.0	116.38
Giza (45) (M) (3)	8.50	7.80	8.15	77.70	78.70	78.20	126.45	136.00	131.23	52.07	57.61	54.84	24.60	18.95	21.78	161.50	112.90	137.20
Giza (85) (F) (4)	5.97	5.55	5.76	74.00	73.55	73.78	124.95	123.25	124.10	64.66	73.56	69.11	20.20	17.00	18.60	130.65	99.75	115.20
Giza (86) (F) (5)	7.20	7.40	7.30	76.45	79.90	78.18	127.53	134.80	131.16	54.41	63.10	58.75	18.78	16.05	17.541	149.45	114.90	132.18
Giza (89) (F) (6)	5.47	5.36	5.43	75.33	73.90	74.62	126.28	123.65	124.96	70.84	76.53	73.69	20.35	16.35	18.35	142.25	94.60	118.43
Pima S_6 (F) (7)	6.13	5.80	5.96	72.68	74.03	73.35	124.48	124.37	124.43	80.71	77.04	78.88	13.85	13.60	13.73	119.85	64.50	92.18
Cr. Ty. (Baht. 105 x G.67) x (G.72 x Dels.) (F) (8)	6.20	5.38	5.79	71.95	73.15	72.55	122.33	122.05	122.19	80.05	87.16	83.61	20.50	15.75	18.13	147.05	92.3	119.68
1 x 4	6.43	6.03	6.23	73.08	73.30	73.19	124.00	125.05	124.53	71.98	83.54	77.76	21.05	14.90	17.97	145.60	101.00	123.30
1 x 5	6.73	6.10	9.41	74.38	76.68	75.53	124.90	130.50	127.70	65.83	61.54	63.69	20.40	15.70	18.05	149.40	102.15	125.78
1 x 6	5.98	5.53	5.75	75.00	74.15	74.58	127.10	125.70	126.40	62.18	79.23	70.70	20.50	17.60	19.05	152.63	104.65	128.64
F_1 1 x 7	6.13	6.30	6.21	73.15	72.63	72.89	122.75	125.15	123.95	59.81	69.88	64.84	20.75	15.05	17.90	143.10	85.20	114.15
1 x 8	6.10	5.68	5.89	72.70	73.93	73.32	123.20	123.00	123.10	71.02	82.43	76.72	20.58	15.23	17.90	153.05	104.5	128.78
2 x 4	6.13	6.08	6.10	73.93	76.35	75.14	124.03	128.15	126.09	66.69	81.07	73.89	21.30	14.90	18.10	134.55	95.7	115.13
2 x 5	7.13	7.10	7.11	75.88	76.10	75.99	128.55	128.60	128.58	51.52	89.73	55.62	20.40	14.75	17.58	142.35	93.5	117.95
2 x 6	6.03	6.03	6.03	75.43	75.20	75.31	127.78	125.45	126.61	57.02	63.88	60.45	19.95	14.60	17.28	146.65	105.4	126.03
2 x 7	6.10	6.48	6.29	73.60	74.80	74.20	124.18	123.68	123.93	65.88	52.75	59.32	20.10	14.70	17.40	147.45	94.8	121.13
2 x 8	6.00	6.13	6.06	72.60	73.88	73.24	123.55	122.60	123.08	66.06	76.39	71.22	19.75	15.75	17.75	146.00	84.6	115.33
3 x 4	6.90	6.35	6.63	74.38	75.40	74.89	124.20	125.05	124.63	58.11	80.55	69.33	23.55	16.80	20.18	149.60	100.8	125.20
3 x 5	7.98	7.88	7.93	75.45	75.60	75.53	124.45	126.25	125.35	59.01	69.89	64.45	20.15	17.15	18.65	151.95	113.5	132.70
3 x 6	6.13	5.90	6.01	74.80	75.00	74.90	124.00	126.85	125.43	62.74	69.98	66.36	21.70	15.90	18.80	155.25	104.3	129.78
3 x 7	7.18	7.10	7.14	72.85	73.85	73.35	123.25	125.45	124.35	63.80	73.57	68.69	21.30	16.55	18.93	143.55	91.40	117.48
3 x 8	6.20	6.50	6.35	72.63	73.63	73.13	123.30	122.75	123.03	67.91	81.13	74.52	22.65	17.55	20.10	157.45	105.8	131.65
L.S.D. 0.05	0.066	0.074	0.225	0.241	0.192	0.641	0.283	0.297	0.923	0.499	1.60	1.194	0.261	0.202	0.796	0.397	0.259	1.065
0.01	0.088	0.099	0.298	0.321	0.256	0.914	0.376	0.395	1.220	0.655	2.145	1.588	0.348	0.268	1.053	0.528	0.345	1.408

Table 4: Amount of heterosis (H%) versus mid-parents (M.P) and better parent (B.P.) for earliness and vegetative traits at each location and from the combined data over both locations.

Traits	FFN			DFF			DFOB			EI			NFB/P			pH		
Locations	L_1	L_2	Comb.	L_1	L_2	Comb.	L_1	L_2	Comb.	L_1	L_2	Comb.	L_1	L_2	Comb.	L_1	L_2	Comb.
M.P.	6.541	6.24	6.387	74.697	75.64	75.170	125.23	127.02	126.13	64.43	72.85	68.642	20.08	16.33	18.193	143.35	96.72	120.031
B.P.	5.475	5.38	5.425	71.950	73.15	72.550	122.33	122.05	122.19	80.71	87.16	83.602	24.60	18.95	21.775	161.50	114.90	137.20
F_1	6.473	6.34	6.408	73.988	74.69	74.343	124.62	125.62	125.12	63.31	72.37	67.836	20.94	15.81	18.375	147.90	99.16	123.532
H% (M.P)	-1.039*	1.748**	0.328	-0.949**	1.322**	-1.100*	-0.492**	-1.102**	-0.800*	-1.74**	-0.659	-1.173	4.291**	-3.202**	1.000	3.177**	2.531**	2.916**
H% (B.P)	18.228**	18.009**	18.110**	2.833**	2.105**	2.471**	1.872**	2.920**	2.395**	-21.57**	-16.96**	-18.857**	-14.87**	-16.58**	-15.614**	-8.417**	-13.69**	-9.962**
L.S.D.0.01	0.06	0.0745	0.225	0.241	0.192	0.691	0.283	0.292	0.923	0.499	1.60	1.194	0.261	0.202	0.796	0.397	0.259	1.065
0.05	0.088	0.0992	0.298	0.321	0.256	0.914	0.376	0.395	1.220	0.665	2.45	1.588	0.348	0.268	1.052	0.528	0.345	1.408

*** Significant at 0.05 level. ** Significant at 0.01 level.**