

## **USING BIPARENTAL MATING DESIGN TO BREAKUP UNDESIRABLE LINKAGE GROUPS AND OBTAIN NEW RECOMBINATIONS IN COTTON (*G. barbadense* L.)**

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### **ABSTRACT**

*The present experiment was carried out at Sakha Agricultural Research Station, Kafr EL-Sheikh Governorate, Cotton Research Institute, Agricultural Research Center, Egypt, during 2021 and 2022 growing seasons. The aim of study was to breakup undesirable linkage groups and obtain new recombinations in cotton. The genetic materials included the cross combination belong to *Gossypium barbadense* L. (Giza 68 x CB58). The data indicated significant or highly significant mean squares for all studied traits, except seed index. Significant and highly significant variances among biparental families for all studied traits were found, except for seed index and uniformity ratio, indicating presence a lot of genetic variation among families. Results showed that desirable means values of the BIP for all studied characters, indicating possible accumulation of favourable genes due to breakage of undesirable linkage by intermating. The results indicated higher values for PCV as compared with GCV for most studied traits due to involvement of high genotypic x environmental interaction effect in the expression of these characters. High broad sense heritability was observed for most studied characters, indicating high magnitude of genetic variability and that environmental influence was low on this studied traits except, seed index and uniformity ratio which are influence with environmental factor ranged from 0.133 and 0.464 respectively. In general, genotypic correlations were higher than corresponding phenotypic correlations indicated that genetic effects were greater than the environmental effects in the expression of the traits. The observed gain in seed cotton yield of best five families ranged from 9.66% to 32.68% for seed cotton yield and from 1.82% to 3.34% for lint percentage while, ranged from 0.59% to 8.34% for seed index. Also, some hybrids gave simile in fiber strength compare with mid-parent. The positive direct effect of lint yield / plant was (1.1035) followed by lint index (0.2433), 2.5% SL (0.1383), fiber strength (0.0949) and boll weight (0.0124). However, the indirect effects of lint yield on seed cotton yield via lint index was the highest one (0.1947). Hence selection for these characters would be useful effective for improving seed cotton yield.*

**Key words:** *Gossypium barbadense* L., Biparental mating design, Genetic variance, North Carolina design II, Recombination and Path analysis.

### **INTRODUCTION**

Traditional breeding procedures, such as pedigree, bulk, and back crossing methods with minor changes, limit the chances of better recombination because of larger linkage blocks associated with the weakness of creating rapid homozygosity and low genetic variability (Rudra *et al* 2009). The genetic information about diverse polygenic characteristics may help the breeder to improve the genetic makeup of the plant in a certain direction. The use of existing genetic variability in breeding material, as well as the development of new variability, is critical in breeding programmes for this reason. Biparental mating among segregants in the F<sub>2</sub> of a cross may increase the chance of recombination, mopping up desirable

genes and releasing concealed variability (Pradeep and Sumalini 2003). Biparental mating, is an effective mating system for increasing diversity and may be used where desired variation for traits of interest is lacking (Guddadamath *et al* 2010) and (2011). Many studies utilising biparental mating in cotton found that biparental intermated was more receptive to improvement through selection than F<sub>3</sub> selfed and more effective in breaking down undesirable linkages. On the other hand, several cycles intermittent population may be effective for exploiting both additive and non-additive gene effects, leading to increasing the frequency of favourable alleles (El-Mansy *et al* 2010, El-Shazly, 2013 and Hamoud *et al* 2013).

In biparental mating design, Plants are picked at random from an F<sub>2</sub> or later generation of a cross and crossed (intermated). Biparental mating refers to random intercross mating between F<sub>2</sub> individuals or later generations, and the offspring created from that as a result are referred to as biparental progenies (BIPs). Biparental offspring are based on the core premise that rare recombinants that are limited due to linkage disequilibrium are rapidly created by forced recombination and become available for selection in early segregating generations (F<sub>3</sub>/F<sub>4</sub>). BIPs can accurately estimate the additive (A) and dominance (D) components of genetic variance, as well as the average dominance level.

The following assumptions are made when biparental crossings result in full-sibling and half-sibling offspring. The genotype distribution is a random distribution, the mated plants are collected at random, lack of effect maternal impact, linkage and epistasis and the absence of several alleles.

Constructing genetic superiority can be judged based on progeny performance, which represents the breakup of unfavourable linkage groups and encourages desirable recombination of fixable epistasis (Singh and Dwevidi 1978).

The objectives of this study were to breakup undesirable linkage groups and obtain new recombinations in cotton (*G. barbadense* L.)

## **MATERIALS AND METHODS**

The present experiment was done at Sakha Agricultural Research Station, Kafr EL-Sheikh Governorate, Cotton Research Institute,

Agricultural Research Center, Egypt, during 2021 and 2022 growing seasons. The genetic materials for the present investigation included the cross combination (Giza 68 x CB58) belonging to *Gossypium barbadense* L. which comprised of F<sub>2</sub> generation. North Carolina Design II according to Singh and Naryanan (1993) was used in this study. In F<sub>2</sub> population, some plants were chosen on the basis of their vigour for selective intermating. The F<sub>2</sub> plants were divided into (7 male plants and 28 female plants), one male was crossed with 4 female. Thus 28 biparental progenies were developed.

Twenty eight biparental progenies as well as original parents (Giza 68 and CB58) were evaluated in a randomized complete blocks design with three replicates. Experimental plot was a single row of 4.0 meter in length and 70 cm in width. Seeds were planted in hills spaced 30 cm apart and one plant was left per hill at thinning time. During the growing seasons, all recommended package practices were implemented.

The following data were collected on six guarded plants in BIP: seed cotton yield per plant in grams (SCY/P), lint yield per plant in grams (LY/P), boll weight in grams (BW), lint percentage (L%), seed index in grams (SI), lint index in grams (LI), fiber length at 2.5% span length (2.5%SL), uniformity ratio (UR), fiber strength (FS) as g/tex, and fiber fineness as micronaire reading (MR).

#### **Statistical analysis**

Data were subjected to statistically analysis of variance proposed by Comstock and Robinson (1952) and developed by Kearsey and Pooni (1996) and Singh and Pawar (2002). The analysis of variance would be as in Table (1). The mean, range, phenotypic (PCV) and genotypic (GCV) coefficients of variation for each trait were calculated in the biparental progenies. Heritability in broad sense was estimated according to Kersey and Pooni (1996). Genotypic correlation coefficients were calculated using the analysis of variance and covariance procedures proposed by Falconer and Muckey (1996). The data was statistically analyzed to estimate genotypic and phenotypic correlation coefficients Falconer, (1964) and path coefficient analysis Dewey and Lu (1959).

**Table 1. Analysis of variance for North Carolina Design II.**

SOV	df	MS	EMS
Replications	r-1		
Males	m-1	MS <sub>m</sub>	$\sigma^2e + r\sigma^2mxf + fr\sigma^2m$
Females	f-1	MS <sub>f</sub>	$\sigma^2e + r\sigma^2mxf + rm\sigma^2f$
Males x Females	(m-1)(f-1)	MS <sub>mxf</sub>	$\sigma^2e + r\sigma^2mxf$
Error	(r-1)(mf-1)	MS <sub>e</sub>	$\sigma^2e$
Total	rmf-1		

Where, m = males      f = females      r = replications

$$\sigma^2_m = (MS_m - MS_{mxf})/fr = (1/4) \sigma^2A$$

$$\sigma^2_f = (MS_f - MS_{mxf})/mr = (1/4) \sigma^2A$$

$$\sigma^2_{mxf} = (MS_{mxf} - MS_e)/r = (1/4) \sigma^2D$$

### RESULTS AND DISCUSSION

Performance and variability in segregating generations are very important for plant breeder to relationship with the efficiency of breeding programs. Analyses of variance of biparental progenies for studied characters are presented in Table (2). The data indicated significant or highly significant in both male and female mean squares for SCY/P, LY/P, BW, FS and MR. This indicated that there was a sufficient additive variability for further exploitation. On the other hand, male x female mean squares showed significant for all studied traits, except SI and UR, suggesting the presence of dominance or epstatic genetic variance. Non-significant mean squares due to this interaction revealed that the male or female had a degree of similarity for remaining traits. Table (2) showed significant and highly significant variances among biparental families for all studied traits, except, seed index and uniformity ratio indicating presence a lot of genetic variation among biparental families. Similar results were obtained by Abo-Arab (2000), El-Mansy (2005) and El-Shazly (2013).

**Table 2. Analysis of variance for studied characters in biparental progenies.**

SOV	df	Mean squares				
		SCY/P (g)	LY/P (g)	BW (g)	LP (%)	SI (g)
Replication	2	48.2301	10.2658	0.0090	0.1037	0.1162
Male	6	282.3729**	48.1704**	0.0966**	2.3779**	0.2372
Female	3	181.3052*	28.5509*	0.1122*	0.4004	0.0598
Male x Female	18	143.0384*	24.2749**	0.1050*	1.6641**	0.1474
Error	54	68.5542	10.5825	0.0273	0.2067	0.1327
SOV	df	Mean squares				
		LI (g)	2.5% SL	UR	FS	MIC
Replication	2	0.0775	0.0801	0.2843	0.0882	0.0523
Male	6	0.4686**	2.5405**	1.2536*	0.5476**	0.6613**
Female	3	0.0290	0.1825	0.1300	1.8783**	0.5087**
Male x Female	18	0.2580**	0.6752*	0.6003	0.9320**	0.2648**
Error	54	0.0728	0.3280	0.4643	0.0693	0.0774

\*, \*\*: Significant at 0.05 and 0.01 levels of probability, respectively.

In the present study a comparison of mean and range of expression of different traits are presented in Table (3). Results showed that desirable means of the BIP's for SCY/P, L%, SI and 2.5% SL. Also, performances of BIP gave relatively acceptable value than those of M.P. for remaining characters, indicating attributed to possible accumulation of favourable genes due to breakage of undesirable linkage by intermating. Similar results were reported by Sharma and Kalia (2003) and Selvam (2012), who found that intermating in F<sub>2</sub> generation increased the mean performance in biparental progenies. All studied characters exhibited wide range of variation for intermating biparental progenies. The traits recorded a wide range from 37.9 to 77.8 for seed cotton yield and from 14.1 to 30 for lint yield. In respect to uniformity ratio it ranged from 86.2 to 90.4 suggesting that intermating has helped in releasing more variability. Similar results were reported by Vinayan and Govindarasu (2010).

**Table 3. Mean, range, PCV and GCV for all studied characters in biparental progenies.**

Characters	Mean $\pm$ Std. Error	Mid-parent	Range	PCV%	GCV%
SCY/P (g)	54.051 $\pm$ 1.1114	48.50	37.9 - 77.8	25.82	20.78
LY/P (g)	20.599 $\pm$ 0.4487	20.78	14.1 - 30.0	27.98	23.10
BW (g)	3.1625 $\pm$ 0.0246	3.28	2.5 - 3.82	11.41	10.14
LP (%)	38.116 $\pm$ 0.0903	37.93	36.3 - 39.8	3.85	3.66
SI (g)	9.2833 $\pm$ 0.0409	9.03	8.4 - 10.0	4.31	1.75
LI (g)	5.7036 $\pm$ 0.0408	6.22	5.0 - 6.5	10.11	8.93
2.5% SL	34.562 $\pm$ 0.0811	34.43	33.0 - 35.9	2.97	2.47
UR	88.975 $\pm$ 0.0798	89.50	86.2 - 90.4	0.95	0.56
FS	42.907 $\pm$ 0.0652	43.02	42.0 - 44.9	2.60	2.53
MIC	3.8452 $\pm$ 0.0457	3.75	2.9 - 4.9	16.79	15.15

The PCV was generally higher than the GCV for all the characters. High PCV and GCV values were observed for SCY/P, LY/P, BW, LI and MR. This indicated that materials used in this study were sufficient for providing rather substantial amount of improvement through selection of superior progenies (Table 3). However, L%, SI, 2.5% SL, UR and FS indicated low PCV and GCV. Slight discrepancy between PCV and GCV

for most studied traits reflected less effect of environmental factors and the presence of dominance or epistatic genetic variances Table (2). Similar results were reported by Kaushik *et al* (1996), Gooda (2001), El-Lawendy (2003) and El-Shazly (2013).

Concerning to biparental progenies, additive (VA), dominance (VD), genetic (VG), environmental (VE) variances, degree of dominance for all studied characters are presented in Table (4). The data indicated that dominance components were larger in magnitude than additive ones for all studied characters which is reflected in the increase of dominance degree ratio than unity, indicating importance of over dominance in the inheritance of the studied traits. In this situation, recurrent selection is suggested in biparental progenies and next generations. Similar results were reported by Mohamed *et al* (2009).

**Table 4. Additive (VA), dominance (VD), genetic (VG), environmental (VE) variances, degree of dominance (D/A)<sup>1/2</sup> and heritability (H) for all studied characters in biparental.**

Characters	VA.	V D.	V G.	V E.	V Ph.	(D/A) <sup>1/2</sup>	H <sup>2</sup> <sub>b</sub> %	H <sup>2</sup> <sub>n</sub> %
SCY/P (g)	26.867	99.312	126.179	68.554	194.733	1.923	64.796	13.797
LY/P (g)	4.390	18.257	22.646	10.583	33.229	2.039	68.153	13.211
BW (g)	0.001	0.104	0.103	0.027	0.130	10.198	79.032	0.77
LP (%)	0.001	1.943	1.942	0.207	2.149	44.079	90.380	0.05
SI (g)	0.007	0.020	0.026	0.133	0.159	1.723	16.488	4.154
LI (g)	0.013	0.247	0.260	0.073	0.333	4.309	78.138	3.994
2.5% SL	0.264	0.463	0.727	0.328	1.055	1.324	68.907	25.026
UR	0.064	0.181	0.246	0.464	0.710	1.682	34.587	9.031
FS	0.026	1.150	1.176	0.069	1.246	6.638	94.436	2.095
MIC	0.089	0.250	0.339	0.077	0.417	1.673	81.421	21.435

On the other side, high broad sense heritability was observed for most characters, indicating high magnitude of genetic variability and environmental influence was low on studied traits, except, seed index and uniformity ratio, where are influence with environmental factor ranged from 0.133 and 0.464, respectively, (Table 4). Hence, heritability with genetic variability gave a good picture for genetic advance. These results are in agreement with Agdem *et al* 2014 and El-Shazly (2018).

A strong correlation and heritability of economically-important traits are highly desirable in breeding and interpretation program work. Coefficient of genotypic correlations among different character combinations are given in Table 5. The coefficient of genotypic correlations revealed that LY/P, BW, L%, SI, LI, 2.5%SL and UR had positive and significant correlation with SCY/P. Also, yield components were positively correlated between them in most cases. The same nature of association occurred between 2.5% SL and each of UR, FS and MR, but yield components showed a weak relationship (-/+) with fiber properties. Similar results reported by Desalegn *et al* (2009) and Karademir *et al* (2009).

Concerning phenotypic correlation (Table 5), the relationships among studied traits exhibited insignificant with some exceptions SCY/P with LY/P, LY/P with each of L% and LI, L% with each of SI and LI, SI with LI, and FS with MR which exhibited positive association.

**Table 5. Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficients among all studied traits of BIP.**

Characters	SCY/P (g)	LY/P (g)	BW (g)	LP (%)	SI (g)	LI (g)	2.5% SL	UR	FS	MIC
SCY/P (g)		0.999**	0.456*	0.658**	1.191**	0.744**	0.682**	0.530**	0.075	-0.083
LY/P (g)	0.989**		0.455*	0.752**	1.175**	0.799**	0.000	0.451*	0.061	-0.077
BW (g)	0.296	0.297		0.206	0.721**	0.323	0.333	0.168	0.222	0.194
LP (%)	0.297	0.386*	0.317		1.486**	1.038**	-0.103	-0.368*	0.001	-0.076
SI (g)	0.226	0.313	0.167	0.477*		1.236**	0.316	-0.006	0.430*	-0.004
LI (g)	0.300	0.403*	0.274	0.840**	0.877**		0.025	-0.241	0.114	-0.049
2.5% SL	0.207	0.189	0.086	-0.090	0.017	-0.034		0.768**	0.470*	0.504**
UR	0.273	0.252	0.149	-0.113	0.054	-0.030	0.335		0.161	0.073
FS	-0.034	-0.042	0.134	0.047	0.021	0.042	0.217	0.028		0.716**
MIC	-0.098	-0.111	0.186	-0.045	0.006	-0.023	0.168	0.008	0.450*	

\*, \*\*: Significant at 0.05 and 0.01 levels of probability, respectively.

In general, genotypic correlations were higher in magnitude than corresponding phenotypic correlations, indicating that genetic effects were greater than the environmental effects in expression of the traits. Similar results were found by Miller and Rawlings (1967), who reported that a



decrease in the magnitude of genotypic correlation in populations showed coupling linkages and an increase in genotypic correlation in those showing repulsion phase linkages in cotton. Koli and Punia (2012) exhibited that intermating in F<sub>2</sub> was quite effective to break undesirable linkage. Thus, it could be reshuffling of genes responsible for correlation among some traits, resulting in new combinations which, presumably were due to changes from a coupling phase to repulsion phase.

Results in Table (6) exhibited that grand mean of the five families out yielded the mid- parent. The observed gain in seed cotton yield/plant of the best five families ranged from 9.66% to 32.68% for seed cotton yield and from 1.82% to 3.34% for lint percentage while, ranged from 0.59% to 8.34% for seed index. Also, some hybrids gave simile in fiber strength compare with mid-parent.

**Table 6. Observed direct and correlated response for seed cotton yield and lint percentage measured in percentage of the mid-parent of BIP.**

Hybrids	SCY/P (g)	LY/P (g)	BW (g)	LP (%)	SI (g)	LI (g)	2.5% SL	UR	FS	MIC
Hybrid 23	32.68*	23.90	-1.12	1.82	6.50	-2.65	1.22	0.02	-0.23	-4.89
Hybrid 4	30.89*	26.56	-2.95	2.83*	5.94*	-1.58	1.70	0.19	1.79*	8.44
Hybrid 14	28.66*	33.16	-0.71	2.42*	8.34*	0.03	1.46	-0.52	-0.85	4.00
Hybrid 13	23.51	19.06	-1.02	3.34**	4.47	-2.12	1.90	0.55	1.01*	12.00
Hybrid 24	9.656	15.19	-1.626	2.575*	0.591	-6.946	0.687	-0.814	-1.12	-8.445
Grand mean	54.03	21.87	3.16	38.11	9.26	5.71	34.53	89.05	42.89	3.85
Mid-parent	48.50	20.78	3.28	37.93	9.03	6.22	34.43	89.50	43.02	3.75
LSD 0.05	13.66	5.37	0.27	0.75	0.60	0.45	0.95	1.12	0.43	0.46
LSD 0.01	18.28	7.18	0.36	1.00	0.80	0.60	1.26	1.50	0.58	0.61

\*, \*\*: Significant at 0.05 and 0.01 levels of probability, respectively.

The superior mean of intermating progenies as a result of increased genetic variability was caused by the breakage of both coupling and repulsion phase linkage. The results are in agreement with Abdel-Moneam *et al* (2015), who reported that increase mean performance of BIP families would generally be expected when major portion is additive and additive x

additive type, as well as even dominance and epistasis components could play some role towards increase in the BIP. Thus, using these hybrids in breeding programs would a chance to isolate more superior genotypes compared with the best original parents. Similar results reported by Chandel *et al* (2015).

Path-coefficient analysis is an effective method to study direct and indirect effects of characters on the dependent variable, seed cotton yield / plant. The genotypic correlation coefficients of seed cotton yield through all the studied traits were partitioned to direct and indirect effects, and shown in Table (7).

**Table 7. The direct (in brackets) and indirect effects on seed cotton yield/plant through all the studied traits based on genotypic correlations.**

Characters	LY (g)	BW (g)	L%	SI (g)	LI (g)	2.5%SL	UR	FS	MR	r
LY (g)	(1.1035)	0.0056	-0.1745	-0.1816	0.1947	0.0834	-0.0485	0.0058	0.0105	0.9990**
BW (g)	0.5036	(0.0124)	-0.0475	-0.1115	0.0784	0.0462	-0.0188	0.0212	-0.0263	0.4577*
L%	0.8299	0.0025	(-0.2320)	-0.2299	0.2526	-0.0143	0.0394	0.0003	0.0103	0.6588**
SI (g)	1.2950	0.0089	-0.3448	(-0.1547)	0.3009	0.0437	0.0002	0.0410	0.0006	1.1909**
LI (g)	0.8833	0.0040	-0.2410	-0.1914	(0.2433)	0.0038	0.0259	0.0108	0.0067	0.7455**
2.5%SL	0.6653	0.0041	0.0240	-0.0489	0.0067	(0.1383)	-0.0833	0.0447	-0.0687	0.6821**
UR	0.4972	0.0022	0.0850	0.0003	-0.0586	0.1070	(-0.1077)	0.0157	-0.0098	0.5313**
FS	0.0671	0.0028	-0.0008	-0.0669	0.0278	0.0651	-0.0179	(0.0949)	-0.0974	0.0747
MR	-0.0853	0.0024	0.0174	0.0006	-0.0119	0.0697	-0.0077	0.0678	(-0.1364)	-0.0834

The correlation coefficient of lint yield/plant with seed cotton yield/plant was (0.999). The positive direct effect of lint yield/plant was (1.1035) followed by lint index (0.2433), 2.5% SL (0.1383), fiber strength(0.0949) and boll weight (0.0124). However, the indirect effects of lint yield on seed cotton yield via lint index was the highest one (0.1947). Also, the indirect effects of this trait via remaining traits were (-/+) very low. Hence selection for these characters would be useful effective for improving seed cotton yield. Similar reported were cleared by Kaushik and Kapoor (2006) and Sunayana and Nimbale (2017).

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## إستخدام تصميم نظام التزاوج ثنائي الأباء لكسر الإرتباطات غير المرغوبة

### والحصول على تراكيب وراثية جديدة فى أقطان الباربادنس

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أجريت هذه الدراسة في محطة البحوث الزراعية بسخا خلال موسمي الزراعة 2021 و 2022 و تهدف الدراسة لكسر الإرتباطات غير المرغوبة والحصول على تراكيب وراثية جديدة فى أقطان الباربادنس حيث تم تقييم عشيرة الهجن ثنائية الأباء و الناتج داخل عشيرة الجيل الثانى (تم تقسيم نباتات الجيل الثانى إلى 7 نباتات ذكور و 28 نباتات إناث ، حيث تم تهجين ذكر واحد مع 4 إناث. وهكذا تم الحصول على 28 تركيب وراثى) مع الأباء الأصلية للهجين جيزة 28 × سي بي 58 في تجربة القطاعات الكاملة العشوائية فى ثلاثة مكررات بإستخدام *North Carolina Design II*. أظهرت النتائج التالى: أظهر تحليل التباين و جود إختلافات عالية المعنوية لجميع الصفات المدروسة مما يدل على وجود إختلافات بين الأباء و أن الأباء كانت متباعدة وراثيا و هذا التباعد إنتقل إلى النسل الهجن. كما أظهر تحليل التباين أن متوسط مربعات الإنحرافات الراجع للأباء كان على المعنوية مقارنة بمتوسط مربعات الإنحرافات الراجع للأمهات داخل الأباء مما يعكس إختلافات بين نباتات الأباء بالجيل الثانى. لوحظ فروق معنوية وعالية المعنوية بين أنسال الهجن ثنائية الأباء لجميع الصفات المدروسة بإستثناء معامل البذرة و الإنتظام مما يدل على وجود الكثير من التباين الوراثي بين العائلات و الذى أثر على هذه الصفات. أظهرت النتائج قيم متوسطات مرغوبة لجميع الصفات المدروسة مما يشير إلى التراكم المحتمل للجينات المفضلة بسبب كسر الإرتباط غير المرغوب فيه عن طريق التزاوج. أشارت النتائج إلى قيم أعلى لمعامل الإختلاف المظهري مقارنة بمعامل

الإختلاف الوراثي لجميع الصفات المدروسة و الذي يرجع إلى تأثير هذه الصفات بالتفاعل بين التركيب الوراثي X البيئة في التعبير الوراثي. أظهرت النتائج قيم عالية لكفاءة التوريث بالمعنى الواسع لمعظم الصفات مما يشير إلى الحجم الكبير للتنوع الوراثي كما كان التأثير البيئي منخفضاً على مثل هذه الصفات المدروسة باستثناء معامل البذرة ونسبة الإنتظام التي تأثرت بالعوامل البيئية والتي تراوحت بين ٠,١٣٣ و ٠,٤٦٤ على التوالي. كانت الإرتباطات الوراثية أعلى من الإرتباطات المظهرية المقابلة التي تشير إلى أن التأثيرات الوراثية كانت أكبر من التأثيرات البيئية في التعبير عن هذه الصفات. تراوحت الزيادة الملحوظة في محصول القطن الزهر/نبات لأفضل خمس عائلات من ٩,٦٦ إلى \* ٣٢,٦٨ بينما تراوحت من ١,٨٢ إلى \*\* ٣,٣٤ لصفة معدل الحليج بينما تراوحت من ٠,٥٩ إلى ٨,٣٤ لمعامل البذرة و من ناحية أخرى، أعطت بعض الهجن تشابهاً في متانة التيلة مقارنة مع متوسط الأباء. لوحظ تأثير إيجابي مباشر لمحصول الشعر/نبات (١,١٠٣٥) متبوعاً بمعامل الشعر (٠,٢٤٣٣)، طول التيلة (0.1383)، النعومة (٠,٠٩٤٩) ووزن اللوزة (٠,٠١٢٤) في حين كانت التأثيرات غير المباشرة لمحصول القطن الشعر على محصول القطن الزهر هي الأعلى (٠,١٩٤٧) ومن ثم فإن الإنتخاب لمثل هذه الصفات سيكون مفيداً وفعالاً في تحسين محصول القطن الزهر.

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