# Journal of Plant Production

# Double Cross Hybrids Performance for Quality and Earliness Traits in some Egyptian Cotton Genotypes

El-Kadi, D. A.[1]; M. A. Abd El-Shafi[1]; T. A. El-Feki[2]; A. A. Abd El- Mohsen[1] and Eman S. Abdel aziz[2*]

**Cross Mark**

[1]Agronomy Department, Faculty of Agriculture, Cairo University, Egypt
[2]Cotton Research Institute, Agricultural Research Center, Egypt

## ABSTRACT

Genotypes used in present investigation consisted of five cotton varieties belong to (*Gossypium barbadense,* L.). Three of these varieties were long staple, BBB (big black boll) ($P_1$), Australian ($P_2$) and G97 ($P_3$) while the other two varieties were extra-long staple, Giza 92 ($P_4$) and G96 ($P_6$). Hybrids produced from these parents and evaluated with their parents in Sakha Agricultural Research Station, Egypt. Studied traits were; first fruiting node, days to first flower appearance, duration of the boll maturation, upper half mean (U.H.M), fiber strength and micronaire value. Highly significant differences among parents were detected for all traits, excluding days to opening first boll and upper half mean . Difference between single crosses was highly significant for all traits, except for days to first flower and upper half mean . Significant differences between double crosses were detected for all traits, excluding upper half mean . Alpha lattice analysis exhibited more efficiency than randomized complete block design at analyzing all of studied traits except for first fruiting node. Lowest values of (CV%) and SE were recorded for all traits excluding micronaire reading in Reml analysis which indicates high experimental precision

*Keywords*: *Gossypium barbadense, Single crosses, double crosses, alpha lattice design, ordinary Reml, mid-parent heterosis, earliness and quality traits*

## INTRODUCTION

The cotton is a strategic crop grown in different regions of the world (Mahdi *et al*., 2020). Egyptian cotton (*Gossypium barbadense* L.) is a favor as an extra-long staple and is excellent in the whole world for its good fiber properties. Improving fiber quality with increasing the yield potential is considered a big challenge.

Cotton breeders have a special interest in developing promising early varieties. The progress of any breeding program for earliness improvement depends on the available genetic variation to produce new early varieties that can replace the existing ones. Earliness measures of (such as days to first flower, first sympodium node) Egyptian cotton are very important in breeding programs to evaluate and select early varieties. Earliness traits in cotton are complicated to measure because the flowering in cotton plants and opening bolls done on over long periods.

(Randhawa and Singh, 1994) reported heterosis in cotton. Modern concept of heterosis has been formed by Shull1908. Improvement of yield and other quality traits over mid parents is known as hybrid vigor. (Ranganatha *et al*., 2013) mentioned that cotton is accessible to development of homozygous genotypes as varieties as well as amenable for commercial exploitation of heterosis by utilization of additive as well as non-additive genetic variance. (Naquibullah *et al*., 2000) reported that with the use of heterosis, seed cotton yield and quality traits can be developed significantly. Therefore, heterosis study is useful

in finding out high degree of heterotic response by hybrids and parents for yield and other yield contributing traits.

Loden and Richmond (1951) studied heterosis in cotton and pointed out findings ranging from zero heterosis in certain crosses to valuable amounts in other crosses. Today, higher lint yield and improved fiber properties exist in hybrids results from economically important heterosis. Thus, plant breeder's utilized heterosis for crop productivity improvement.

Balcha *et al.* (2019) studied heterosis for fiber traits among 16 parents, 32 hybrids and 4 check varieties and reported that 12 and 15 hybrids exhibited positive and negative mid and bp heterosis, respectively, and ranged from -22.08 (L3 x T2) to 17.16% (L11 x T2) for micronaire. Minimum negative mid parent heterosis was detected for hybrids L2 x T2, L1 x T1 and L3 x T for micronaire, while the top highly significant hybrids were L6 x T1 and L11 x T2 which is undesirable traits in cotton breeding.

Hamed and Said (2021) studied six Egyptian cotton varieties as lines i.e, Giza 80, Giza 86, Giza 90, Giza 93, Giza 94 and Giza 95 and results showed that the following crosses showed the best heterosis relative to mid- and better-parent, i.e, the crosses Giza 93 x Karashenky and Giza 93 x Ustraly 13 for most fiber quality traits. Soomro *et al*., (2021) evaluated 10 parents and 45 hybrids and found that MNH-886 x CIM-602 was the best for bolls open, and CRIS-129 x MNH-886 for days to 1st flower and uniformity index.

The main target of this study were evaluating mean performance and heterosis for five *Gossypium barbadense* L., genotypes, which were used to develop 10 $F_1$ populations following double cross breeding method of

hybridization in order to improve the populations for earliness and fiber quality traits.

# MATERIALS AND METHODS

Present study was performed during three seasons 2016, 2017 and 2018. The experiments were conducted at the Agricultural Experiments and Research Station, Faculty of Agriculture, Cairo University, Egypt (30.02°N 31.13°E, 118 m) at first and second season and conducted at Sakha Agricultural Research Station (31°W 31°N, 36 m), Agriculture Research Center, Egypt, in third season. Five *Gossypium barbadense* L., genotypes, were used. The description of these genotypes is presented in Table 1.

**First season:**

In first season 2016, the five parents were planted and mated in a diallel mating design excluding reciprocals to obtain 10 single crosses. Seeds from each parental genotype were sown in two rows for each parent. The row was 7 meters long and 60 cm apart and distance between hills 70 cm, the hills were thinned to one plant. Crossing process was made between the parents at flowering stage.

**Second season:**

In the second season 2017, $F_1$ single crosses were grown to mate in a diallel mating design to produce double cross seeds with the restriction that no parent should appear twice in the same double cross combination to obtain 15 double crosses (number of double crosses = P (P-1) (P-2) (P-3)/8 where, P: is equal to number of parental genotypes).

**Third season:**

In the third season 2018, the genetic material were used in these experiments consisted of 30 genotypes (the five parental genotypes, 10 F1`s single crosses and 15 double crosses). RCBD was used in first and second season while alpha lattice design (5 x 6) was used in third season. Each plot consisted of two rows. The rows were 4 meters long and 65 cm apart. Hills were spaced at 20 cm within rows and seedlings were thinned at two plants/hill. Throughout the growing season usual practices were followed as done with ordinary recommendations for cotton culture.

**Table 1. Names, pedigree, origins and Characteristics of the studied genotypes.**

| Genotypes | Pedigree | Origin | Characteristics * |
|---|---|---|---|
| Australian | Not available | Australian | It characterized by high yielding earliness and good fiber traits |
| BBB | BBB | Australian | The long staple characterized by big boll and black |
| G97 | ((G89 x G86 x Karshenky) xG94) | Egyptian | It characterized by high early maturity and leaves drop at the end of season. |
| G92 | G84 x (G74 x G68) | Egyptian | An extra long staple characterized by lint length (35.2 m) and Pressley (11.3) |
| G96 | G84 × PimaS6 | Egyptian | Long staple germplasm. It is characterized by earliness, high yield and outstanding component traits. |

**\* Source: Cotton Res. Dept., Agric. Res. Center (ARC), Egypt, G: Giza.**

## The studied traits:
### a. Earliness traits:
1. First fruiting node of first sympodium (F.F.N.): Estimated as number of nodes below first fruiting branch.
2. Days to first flower appearance (D.F.F.): Expressed as a number of days from planting date to first flower appearance.
3. Duration of the boll maturation (day) recorded on 10 plants as number of days from flower opening to the boll opening.

### b. Fiber properties:
The fiber properties were measured using HVI according to (ASTM D- 4605 - 86)
1. Upper half mean (U.H.M): Measured by HVI in (mm).
2. Fiber strength (F.S): Measured by HVI.
3. Micronaire value (Mic): Fiber fineness was expressed as micronaire reading. The characters were measured with micromat instrument. ASTM D-3818-98.

## Statistical analysis:
### a. Alpha lattice analysis of variance
Analysis of variance for alpha lattice design (ALD) were carried as outlined by Cochran and Cox (1957). The analysis of variance form is presented in Table 2.

**Table 2. Form of the analysis of variance for alpha lattice**

| S.V. | Df | SS | MS | F |
|---|---|---|---|---|
| Replications | r-1 | $SS_r$ | $MS_r$ | |
| Blocks (within replications) | rs-r | $SS_b$ | $MS_b$ | |
| Treatments (adjusted for blocks) | t-1 | $SS_t$ | $MS_t$ | $F_0$ |
| Error | rt-rs-t+1 | $SS_e$ | $MS_e$ | |

**Where t=treatment, r=replicates, s= blocks within replications, ignoring treatments, $F_0$= calculated F**

The relative efficiency of (ALD) compared with a randomized complete block design (RCBD) was done by using the MSe from each analysis according to the following equation:

$$\text{Relative efficiency} = \frac{\text{Error mean squares in RCBD}}{\text{Error mean square in alpha lattice design}}$$

The genotypes were partitioned to main effects parent, single crosses and double crosses and its interactions, P versus SCH (single cross hybrid), P versus DCH (double cross hybrid)

### b. single crosses analysis:
In this study, five parental varieties were utilized in a half diallel crosses mating design to produce 10 $F_1$ hybrids (single crosses) to estimate the different genotypic parameters in terms of additive and dominance genetic variances. The procedures of this analysis was described by Griffing (1956) based on method 2, model I (fixed model) as outlined by Singh and Chaudhary (1985).

### Estimates of heterosis:
Heterosis was estimated as increased percentage of means of the $F_1$ hybrids over parents average (M.P) according to Fehr (1987) as follows:

$$\text{H (F1, M.P) \%} = \frac{\overline{F_1} - \overline{M.P}}{\overline{M.P}} \times 100$$

### c- Double crosses analysis (qudriallel):
A double cross or a quadriallel is a product of four parents, for instance (A x B) (C x D). All possible double crosses would be equal P (P – 1) (P – 2) (P – 3) /8 where 'P' as the number of parents. The theoretical aspect of quadriallel analysis has been dealt. Analysis of double

cross data (Table 3) is carried out according to the procedure outlined by Singh and Chaudhary (1985).

**Estimates of heterosis:**

The heterotic effects were determined for double crosses hybrids (DCH) by comparing its value versus mid-parents (4P.). Also heterotic effect was estimated for DCH versus the average mean of 2 F$_1$ hybrids involved in each DCH. Therefore, heterosis values could be estimated as follows:

$$H \ (DCH, M.P) \ \% = \frac{\overline{DCH} - \overline{M.P}}{\overline{M.P}} \ x \ 100$$

The significance of heterosis was determined using (LSD) at 0.05 and 0.01 levels of probability, according to the following equation, which was calculated as suggested by Steel and Torrie (1980).

$$L.S.D. \ (5\%) = t_{(0.05, \ Ed.f)} \ x \ S_{\overline{d}} \qquad L.S.D. \ (1\%) = t_{(0.01, \ Ed.f)} \ x \ S_{\overline{d}}$$

$$S_{\overline{d}} \ for \ mid-parents \ heterosis = \sqrt{\frac{3MSe}{2r}}$$

**Where:** MSe = error mean square, E.d.f = Error degrees of freedom, r=number of replications.

**4- Ordinary Reml model analysis**

Several models of residual maximum likelihood (Reml) are described by Piepho *et al.*, (2012). Ordinary Reml model is designed to estimate the probability of errors, treatment effects and variance components in a linear mixed model with fixed and random effects. Reml model taking into account trend effect is presented below:

y = Bπ+ Tδ+RTβ + e

**Where,**
y: an n - vector of plot yields
π: b- vector of block effects within incidence matrix B.
T: corresponding design matrix
δ:T- vector o treatment effects
R: neibghour incidence matrix
β: T- vector o treatment effects
e: n vector whose elements represent local errors.

**Table 3. Form of the analysis of variance of the double crosses and expectation of mean squares**

| S.O.V. | d.F | S.S |
|---|---|---|
| Replications (R) | r-1 | $\left(\frac{8\sum Y^2_{....}}{p(p-1)(p-2)(p-3)}\right) - \left(\frac{8\sum Y^2_{....}}{r\,p(p-1)(p-2)(p-3)}\right)$ |
| Total (M) | $\left(3\,r\,C^p_4\right) - 1$ | $\sum Y^2_{(ij)(u)...} - \left(\frac{8\sum Y^2_{....}}{r\,p(p-1)(p-2)(p-3)}\right)$ |
| Hybrids (H) | $\left(3\,C^p_4\right) - 1$ | $\frac{\sum Y^2_{(ij)(u)}}{r} - \left(\frac{8\sum Y^2_{....}}{r\,p(p-1)(p-2)(p-3)}\right)$ |
| Error (E) | $(r-1)\left(3\,C^p_4 - 1\right)$ | M - R - H |
| 1-line general (G) | p-1 | $\left(\frac{2\sum Y^2_{i...}}{r(p-2)(p-3)(p-4)}\right) - \left(\frac{4(p-1)}{(p-4)}\frac{8\sum Y^2_{....}}{r\,p(p-1)(p-2)(p-3)}\right)$ |
| 2- line specific (S$_2$) | $\frac{p(p-3)}{2}$ | $\left(\frac{2\sum Y^2_{ij..}}{3r(p-4)(p-5)}\right) - \left(\frac{6(p-2)(p-3)}{(p-4)(p-5)}\frac{8\sum Y^2_{....}}{r\,p(p-1)(p-2)(p-3)}\right) - \left(\frac{3(p-3)}{(p-5)}G\right)$ |
| 2- line arrangement(T$_2$) | $\frac{p(p-3)}{2}$ | $\left(\frac{2\sum Y^2_{(ij)(..)}}{r(p-1)(p-2)}\right) + \left(\frac{\sum Y^2_{(i.)(j.).}}{r(p-1)(p-2)}\right) - \left(\frac{2\sum Y^2_{ij...}}{3r(p-1)(p-2)}\right)$ |
| 3- line arrangement (T$_3$) | $\frac{p(p-2)(p-4))}{3}$ | $\left(\frac{\sum Y^2_{(ij)(k.).}}{3(p-3)}\right) - \left(\frac{\sum Y^2_{ijk..}}{3r(p-3)(p-2)}\right) - \left(\frac{2(p-2)}{(p-3)}T_2\right)$ |

# RESULTS AND DISCUSSION

**a. Earliness traits**
**1- Analysis of variance**

Results in Table 4 showed highly significant differences between genotypes (*P≤0.01*), except for days to opening first boll which was significant only (*P≤0.05*). Genotypes variance was partitioned into basic effects of parents (P), single crosses (C), double crosses (D), P vs. C and P vs. D. Highly significant differences for mean squares of P, C, D, P vs. C and P vs. D (*P≤0.01*) for all earliness traits, except for days to opening first boll which was insignificant for P and C, also position of first fruiting node was insignificant for P vs. C and P vs. D. similar results found by many researchers. Variances due to genotypes, parents, crosses and parents vs crosses exhibited significant differences for fiber traits as recorded by Yehia and El-Hashash, (2019). Sultan *et al.,* (2018) found that the analysis of variance indicated that the mean squares of genotypes for all studied characters were significant and highly significant, indicating the present of considerable amount of genetic variability among genotypes, parents and hybrids.

Table 5 showed that highly significant differences *(P≤ 0.01)* among hybrids were for all earliness traits. Results also showed that line general was highly significant (*P≤ 0.01*) for all traits suggesting the presence of the additive variance in the inheritance of these traits subsequently

selection would be efficient in improvement these traits. Also result in Table 5 showed that 2- line arrangement was highly significant (*P≤ 0.01*) for all traits, excluding days to opening 1$^{st}$ boll which was significant only (*P≤ 0.05*) suggesting the presence of the non-additive variance in the inheritance of these traits. Also, 3- Line arrangement was highly significant (*P≤ 0.01*) for all traits excluding for days to opening first boll which was significant only (*P≤ 0.05*) indicating the contribution of the additive by dominance interaction including all three factors or higher order interaction except all dominance types.

**Table 4. Mean squares of analysis of variance for earliness traits.**

| S. V. | d.f. | Position of 1$^{st}$ fruiting node | Days to 1$^{st}$flower | Days to Opening 1$^{st}$ boll |
|---|---|---|---|---|
| | | MS | | |
| Replication | 2 | 0.60 | 0.576 | 0.30 |
| Block/rep | 12 | 0.52 | 21.57** | 0.84 |
| Genotypes (G) | 29 | 1.31** | 34.79** | 1.24* |
| Parents (P) | 4 | 1.57** | 33.99** | 1.1 |
| Single crosses C) | 9 | 1.79** | 38.30** | 0.87 |
| Double crosses (D) | 14 | 1.53** | 54.20** | 1.80** |
| P Vs C | 1 | 0.04 | 0.47** | 2.84** |
| P Vs D | 1 | 0.27 | 59.28 | 4.36** |
| Error | 46 | 0.701 | 2.03 | 0.86 |

\*, \*\* Significant at 5% and 1% level of probability, respectively

**Table 5. Analysis of variance of double cross hybrids for earliness traits**

| S.V. | d.f. | Position of 1st fruiting node | Days to 1st flower | Days to opening 1st boll |
|---|---|---|---|---|
| | | MS | | |
| Hybrid | 14 | 1.53** | 54.19** | 1.80** |
| 1- line g | 4 | 1.60** | 14.52** | 2.31** |
| 2- Line arra. | 5 | 0.74** | 62.23** | 1.58* |
| 3- Line arra. | 5 | 2.27** | 77.92** | 1.62* |
| Error | 28 | 0.26 | 0.37 | |

**\*, \*\* Significant at 5% and 1% level of probability, , respectively**

Similar trend of results was detected by El-Feki *et al.* (2012) who found highly significant 2- line arrangement and 3- Line arrangement for earliness traits and indicated that the order in which the parents were involved in double crosses was important.

**2. Mean performance and heterosis**

Results in Table 6 showed that the earliest parent for both traits position of first fruiting node and days to first flower was Australian ($P_1$), which exhibited significant different from G96 ($P_5$) for first fruiting node and from G97 ($P_3$), G92 ($P_4$) and G96 ($P_5$) for days to first flower. Regarding days to opening first boll, G96 ($P_5$) was the earliest, moreover, results in Table 6 revealed insignificant differences between G 96 ($P_5$) and parents Australian ($P_1$), BBB ($P_2$) and G92 ($P_4$) for days to opening first boll. Results also revealed that single hybrid (G97*G96) was the earliest for all earliness traits with significant difference from single hybrid (BBB* G96), which exhibited the latest for earliness traits. Conserning double crosses [(BBB*G97)*(G92*G96)] was the earliest for position of first fruiting node and days to first flower with significant different from [(Australian*G96)*(BBB*G97)].

Regarding days to opening first boll, three double crosses [(Australian*G97)*(BBB*G92)], [(Australian*G97)*(BBB*G96)] and [(Australian*G96) * (BBB*G97) ] were the earliest with significant differences from [(Australian*BBB) * (G97*G92)], [(Australian*G92)* (BBB*G97)], and [(Australian*G92)*(BBB*G96)].

Table 6 indicated that single cross G97* G96 showed negative and significant mid parent heterosis for first fruiting node with amount of heterosis -23.08 while in double crosses [ (Australian* G92)*( BBB* G96) ] and [ (BBB* G97)* (G92* G96) ] showed negative and significant mid parent heterosis for first fruiting node with amount of heterosis -12.33 and -15.79%, respectively. Also Table 6 showed that single crosses [Australian* G92], [G97* G96] and [G92* G96] showed negative and significant mid parent heterosis with amount of heterosis -4.92, -2.35 and -14.07%, respectively while in double crosses [ (Australian*BBB)*( G97* G92) ], [ (Australian* G97)*( G92* G96) ] and [ (BBB* G97)* (G92* G96) ] showed negative and significant mid parent heterosis with amount of heterosis -2.49, -3.16 and -4.20%, respectively. Regarding days to opening first boll, no hybrids showed negative and significant mid parent heterosis. These results agreed with El-Feki *et al.,* (2012) revealed that 1-general and 2-line specific and arrangement effects were significant indicating the importance of additive gene effects and all additive type of epistatic interaction.

**Table 6. Mean performance of parents, F₁ hybrids, double cross hybrids and its heterosis for earliness traits.**

| Genotypes | Position of 1st fruiting node | | Days to 1st flower | | Days to opening 1st boll | |
|---|---|---|---|---|---|---|
| | Mean | H% | Mean | H% | Mean | H% |
| Australian (P1) | 5.70 | | 65.10 | | 56.33 | |
| BBB (P2) | 6.30 | | 65.50 | | 56.00 | |
| G97 (P3) | 6.00 | | 67.70 | | 57.00 | |
| G92 (P4) | 6.00 | | 69.60 | | 56.33 | |
| G96 (P5) | 7.00 | | 67.40 | | 55.33 | |
| Mean | 6.10 | | 67.00 | | 56.20 | |
| Single crosses | | | | | | |
| P1 x P2 | 5.70 | 0.01 | 66.80 | 2.84** | 56.33 | 0.30 |
| P1 x P3 | 5.70 | 3.03 | 65.90 | -1.49 | 57.33 | 1.18 |
| P1 x P4 | 6.00 | 9.09 | 66.10 | -4.92** | 56.33 | 0.00 |
| P1 x P5 | 6.00 | 0.00 | 69.60 | 9.54** | 56.33 | 0.90 |
| P2 x P3 | 6.30 | 2.70 | 67.20 | 0.81 | 57.67 | 2.06* |
| P2 x P4 | 6.00 | -2.70 | 67.40 | 0.79 | 56.33 | 0.30 |
| P2 x P5 | 8.00 | 20.00** | 70.10 | 7.54** | 57.00 | 2.40** |
| P3 x P4 | 6.30 | 5.56 | 68.70 | -0.78 | 57.00 | 0.59 |
| P3 x P5 | 5.00 | -23.08** | 65.10 | -2.35* | 55.80 | 1.48 |
| P4 x P5 | 6.30 | -2.56 | 66.10 | -14.07** | 56.00 | 0.30 |
| Mean | 6.10 | | 67.50 | | 56.70 | |
| Double crosses | | | | | | |
| (P1xP2)(P3xP4) | 6.30 | 8.57 | 66.40 | -2.49* | 58.67 | 3.99** |
| (P1xP2)(P3xP5) | 6.00 | -1.37 | 68.70 | 2.49* | 57.00 | 1.48 |
| (P1xP2)(P4xP5) | 7.00 | 15.07* | 68.50 | 0.29 | 56.67 | 1.19 |
| (P1xP3)(P2xP4) | 5.80 | 0.00 | 69.00 | 1.43 | 56.00 | -0.74 |
| (P1xP3)(P2xP5) | 5.80 | -4.11 | 68.00 | 1.56 | 56.00 | -0.30 |
| (P1xP3)(P4xP5) | 6.20 | 2.78 | 66.90 | -3.16** | 56.33 | 0.15 |
| (P1xP4)(P2xP3) | 5.70 | -2.86 | 67.50 | -0.78 | 58.00 | 2.81** |
| (P1xP4)(P2xP5) | 5.30 | -12.33* | 68.80 | 0.78 | 57.67 | 2.98** |
| (P1xP4)(P3xP5) | 7.70 | 27.78** | 69.30 | 0.26 | 56.33 | 0.15 |
| (P1xP5)(P2xP3) | 7.50 | 23.29** | 69.70 | 4.00** | 56.00 | -0.30 |
| (P1xP5)(P2xP4) | 6.00 | -1.37 | 67.50 | -1.22 | 57.00 | 1.79* |
| (P1xP5)(P3xP4) | 6.70 | 11.11 | 69.30 | 0.36 | 56.67 | 0.74 |
| (P2xP3)(P4xP5) | 5.30 | -15.79** | 66.10 | -4.20** | 56.67 | 0.89 |
| (P2xP4)(P3xP5) | 5.70 | -10.53 | 67.90 | -1.59 | 57.00 | 1.48 |
| (P2xP5)(P3xP4) | 6.30 | 0.00 | 68.30 | -0.96 | 56.33 | 0.30 |
| Mean | 6.20 | | 68.10 | | 56.80 | |
| LSD 5% | 0.80 | 0.69 | 1.42 | 1.24 | 1.05 | 0.91 |
| LSD 1% | 1.15 | 1.00 | 2.07 | 1.8 | 1.52 | 1.32 |

**\*, \*\* Significant at 5% and 1% level of probability, , respectively**

**b. Quality traits**

**1- Analysis of variance**

Table 7 showed highly significant ($P \leq 0.01$) differences between genotypes, parents, single crosses and double crosses for all quality traits excluding for upper half mean which showed insignificance for all of them, except parents versus double crossess (P vs D) which was significant ($P \leq 0.05$). Parent versus single crosses (P vs C) was insignificant for fiber strength. Same trend of results were found by El-hoseiny (2009) who found that Parents vs F1 hybrids, F1,s vs double crosses and double crosses were highly significant.

Results in Table 8 showed highly significant differences among hybrids for all quality traits excluding upper half mean. Morover, mean square of hybrids were partitioned into line general, 2-line arrangement and 3- line arregements, all the parts exhibited highly significant difference upper half mean. El-Fesheikawy *et al.,* (2018) found highly significant mean squares of genotypes for all traits, the partition of crosses mean square to its

components showed that the mean square due to 1-line general, 2-line specific, 2-line arrangement, 3-line arrangement and 4-line arrangement were either significant or highly significant for all studied characters.This result suggesting the presence of the additive and non-additive genetic variance in the inheritance of these traits.

**Table 7. Mean squares of analysis of variance for quality traits**

| S.V. | d.f. | U.H.M. | F.S. | MIC |
|------|------|--------|------|-----|
| | | | MS | |
| Replication | 2 | 0.71 | 0.009 | 0.025 |
| Block/rep | 12 | 1.15 | 0.305** | 0.073** |
| Genotypes (G) | 29 | 0.63 | 1.017** | 0.294** |
| Parents (P) | 4 | 0.73 | 0.97** | 0.04** |
| Single crosses C) | 9 | 0.37 | 1.31** | 0.25** |
| Double crosses (D) | 14 | 0.42 | 1.35** | 0.46** |
| P Vs C | 1 | 0.11 | 0.01 | 0.03** |
| P Vs D | 1 | 1.98* | 0.43** | 0.03** |
| Error | 46 | 0.73 | 0.029 | 0.013 |

*, ** Significant at 5% and 1% level of probability, respectively, U.H.M = upper half mean, F.S = fiber strength,  Mic =micronaire value

**Table 8. Analysis of variance of double cross hybrids for quality traits**

| S.V. | d.f. | U.H.M. | F.S. | MIC |
|------|------|--------|------|-----|
| | | | MS | |
| Hybrids | 14 | 0.42 | 1.351** | 0.455** |
| 1-line g | 4 | 0.38 | 1.559** | 0.766** |
| 2- line arra | 5 | 0.48 | 0.386** | 0.570** |
| 3- line arr | 5 | 0.40 | 2.150** | 0.091** |
| Error | 28 | 0.92 | 0.008 | 0.004 |

** Significant at1% level of probability, respectively, U.H.M = upper half mean, F.S = fiber strength,  Mic =micronaire value

## 2. Mean performance and heterosis

Results in Table 9 showed that BBB ($P_2$) recorded the highest mean performance with significant difference from Australian ($P_1$) in upper half mean. Single crosses [BBB* G97] and [BBB* G96] showed the highest mean performance with significant difference from [Australian* G92]. Double cross [(Australian* G96)* (G97* G92)] recorded the highest mean performance with significant difference from [(BBB* G96)*(G97* G92)]. Regarding fiber strength, BBB and G97 recorded the highest mean performance with significant difference from other parents. Single cross [Australian* G92] showed the highest mean performance with significant difference from other crosses. Double cross [(Australian* G92)*(G97* G96)] showed the highest mean performance with significant difference from other crosses. With respect to fiber fineness (micronaire reading), values varied from 2.73 to 3.50 for $P_4$ and $P_5$ , respectively. In single crosses values varied from 2.6 to 3.6 for G92* G96 and G97* G92 , respectively. Double crosses values ranged from 2.47 (for two crosses [(Australian* G97)*(BBB* G96)] and [(Australian* G97)*(G92* G96)] to 3.60 for [(Australian* G97)*(BBB* G96)] and [(Australian* G97)*(G92* G96)], respectively. Also Table 9 showed that in fiber length, single crosses Australian*BBB and Australian* G96 showed positive and significant mid parent heterosis with amount of heterosis 1.14 and 1.68%, respectively while in double crosses eight crosses [ (Australian*BBB)*( G97* G92) ], [ (Australian*BBB)*( G97* G96) ], [ (Australian*BBB)*( G92* G96) ], [

(Australian* G97)*( BBB* G96) ] , [ (Australian* G97)*( G92* G96) ], [ (Australian* G96)*( BBB* G97) ], [ (Australian* G96)*( BBB* G92) ] and  [ (Australian* G96)* ( G97* G92) ] showed positive and significant mid parent heterosis with amount of heterosis 2.18, 1.47, 2.37, 1.85, 2.64,1.18, 2.27 and 2.73%, respectively. Similar results were detected by Hamed and Said (2021) found that the best heterosis relative to mid- and better-parent crosses for most fiber quality traits were, Giza 93 x Karashenky and Giza 93 x Ustraly 13.

**Table 9. Mean performance of parents, F1 hybrids and double cross hybrids and its heterosis for quality traits.**

| Genotypes | U.H.M. (mm) | | FS | | MIC. | |
|-----------|------|------|------|------|------|------|
| | Mean | H% | Mean | H% | Mean | H% |
| Australian (P1) | 34.43 | | 11.40 | | 2.80 | |
| BBB (P2) | 35.77 | | 12.40 | | 2.90 | |
| G97 (P3) | 35.40 | | 12.40 | | 3.13 | |
| G92 (P4) | 35.33 | | 11.60 | | 2.73 | |
| G96 (P5) | 35.13 | | 11.10 | | 3.50 | |
| Mean | 35.20 | | 11.80 | | 3.01 | |
| Single crosses | | | | | | |
| P1 x P2 | 35.50 | 1.14* | 11.9 | 0.42 | 3.20 | 12.28** |
| P1 x P3 | 35.10 | 0.53 | 10.9 | -8.56** | 2.83 | -4.49** |
| P1 x P4 | 34.37 | -0.91 | 12.6 | 9.43** | 3.00 | 8.43** |
| P1 x P5 | 35.37 | 1.68** | 12.0 | 6.80** | 3.17 | 0.53 |
| P2 x P3 | 35.70 | 0.33 | 12.5 | 1.35* | 2.93 | -2.76* |
| P2 x P4 | 35.47 | -0.23 | 11.3 | -5.57** | 2.83 | 0.59 |
| P2 x P5 | 35.70 | 0.71 | 11.6 | -1.28** | 3.40 | 6.25** |
| P3 x P4 | 35.00 | -1.04 | 11.2 | -6.13** | 3.60 | 22.73** |
| P3 x P5 | 35.23 | -0.09 | 12.4 | 5.53** | 2.63 | -20.60** |
| P4 x P5 | 35.53 | 0.85 | 10.8 | -4.55** | 2.60 | -1.60 |
| Mean | 35.30 | | 11.70 | | 3.02 | |
| Double crosses | | | | | | |
| (P1xP2)(P3xP4) | 36.00 | 2.18** | 12.1 | 1.22* | 2.93 | 1.44 |
| (P1xP2)(P3xP5) | 35.70 | 1.47* | 11.2 | -5.22** | 2.83 | -8.22** |
| (P1xP2)(P4xP5) | 36.00 | 2.37** | 11.4 | -1.58** | 3.43 | 14.97** |
| (P1xP3)(P2xP4) | 35.50 | 0.76 | 12.1 | 1.47* | 3.07 | 6.17** |
| (P1xP3)(P2xP5) | 35.83 | 1.85** | 12.1 | 2.65** | 2.47 | -19.89** |
| (P1xP3)(P4xP5) | 36.00 | 2.64** | 12.2 | 5.28** | 2.47 | -18.79** |
| (P1xP4)(P2xP3) | 35.50 | 0.76 | 11.6 | -2.47** | 3.27 | 13.08** |
| (P1xP4)(P2xP5) | 35.43 | 0.76 | 10.6 | -9.01** | 2.97 | -0.45 |
| (P1xP4)(P3xP5) | 35.10 | 0.07 | 12.7 | 9.58** | 3.03 | -0.38 |
| (P1xP5)(P2xP3) | 35.60 | 1.18* | 11.0 | -6.91** | 3.03 | -1.73 |
| (P1xP5)(P2xP4) | 35.97 | 2.27** | 12.0 | 3.30** | 3.60 | 20.67** |
| (P1xP5)(P3xP4) | 36.03 | 2.73** | 11.2 | -3.33** | 2.23 | -26.68** |
| (P2xP3)(P4xP5) | 35.50 | 0.26 | 11.3 | -4.71** | 3.10 | 1.09 |
| (P2xP4)(P3xP5) | 35.63 | 0.64 | 10.2 | -13.73** | 3.40 | 10.87** |
| (P2xP5)(P3xP4) | 34.70 | -2.00** | 11.7 | -1.34* | 3.07 | -15.22** |
| Mean | 35.60 | | 11.60 | | 2.99 | |
| LSD 5% | 1.24 | 1.07 | 0.14 | 0.12 | 0.088 | 0.08 |
| LSD 1% | 1.80 | 1.55 | 0.20 | 0.18 | 0.128 | 0.12 |

*, ** Significant at 5% and 1% level of probability, respectively, U.H.M = upper half mean, F.S = fiber strength,  Mic =micronaire value

In fiber strength four single crosses Australian* G92, Australian* G96, BBB* G97 and G97* G96 showed positive and significant mid parent heterosis with amount of heterosis 9.43, 6.80, 1.35 and 5.53%, respectively. While double crosses [ (Australian*BBB)*( G97* G92) ], [ (Australian* G97)*( BBB* G92) ], [ (Australian* G97)*( BBB* G96) ], [ (Australian* G97)*( G92* G96) ], [ (Australian* G92)*( G97* G96) ] and [ (Australian* G96)*( BBB* G92) ] showed positive and significant mid parent heterosis with amount of heterosis 1.22, 1.47, 265,

*El-Kadi, D. A. et al.*

5.28, 9.58, and 3.30, respectively. With respect to fiber fineness (Micronaire reading), three single crosses Australian* G97, BBB* G97 and G97* G96 showed negative and significant mid parent heterosis with amount of heterosis -4.49, -2.76 and -20.60%, respectively. While double crosses [ (Australian*BBB)*( G97* G96) ], [ (Australian* G97)*( BBB* G96) ] , [ (Australian* G97)*( G92* G96) ], [ (Australian* G96)*( G97* G92) ] and [ (BBB* G96)*( G97* G92) ] exhibited negative and significant mid parent heterosis with amount of heterosis 14.97, 6.17, 13.08, 20.67 and 10.87 , respectively. Similar results were detected by Hamed and Said (2021) who found that combinations : [(P1 x P3 ) x (P2 x P4 )], [(P1 x P3) x (P5 x P6 )] and [(P2 x P4 ) x (P5 x P6 )] appeared to be the best promising double crosses for breeding toward improvment most studied fiber quality traits .

**c. Efficiency of RCBD and Alpha Lattice Design**
**1- Earliness traits**

Results in Table 10 showed more efficiency for alpha lattice analysis compared with RCBD at analyzing all of the earliness traits except for first fruiting node. Smaller values of SE difference for alpha lattice design helps to detect smaller differences for the comparisons of mean. The effectiveness of the alpha lattice analysis at reducing experimental error was most evident in all traits. Moreover, the coefficients of variation (CV %) of alpha lattice design were low as compared to RCBD for all traits. Lowest values of the coefficients of variation (CV %) and standard error were recorded for all traits in reml analysis which indicates high experimental precision. .

**Table 10. Estimates of error mean squares (EMS), coefficient of variations (CV %) and standard errors (SE) of alpha lattice design, RCBD and REML analysis in earliness traits**

| Trait | EMS | | RE | CV% | | | | SE | |
|---|---|---|---|---|---|---|---|---|---|
| | RCBD | ALPHA | % | RCBD | RCBD | ALPHA | | RCBD | REML |
| Position of 1st fruiting node | 0.33 | 0.38 | 0.87 | 12.93 | 10.10 | 9.77 | 0.80 | 0.62 | 0.54 |
| Days to 1st flower | 3.08 | 2.02 | 1.52 | 5.75 | 2.12 | 2.08 | 3.86 | 1.42 | 1.14 |
| Days to Opening 1st boll | 0.97 | 0.86 | 0.66 | 3.01 | 1.46 | 1.36 | 0.76 | 0.83 | 0.63 |

**2- Quality traits**

Results in Table 11 showed that alpha lattice analysis was more efficient than the randomized complete block design at analyzing all of the fiber quality traits. Smaller values of SE difference for alpha lattice design helps to detect smaller differences for the comparisons of mean. The effectiveness of the alpha lattice analysis at reducing experimental error was most evident in fiber length and fiber fineness. Moreover, the coefficients of variation (CV%) of alpha lattice design were low as compared to RCBD for fiber length and fiber strength. Lowest values of the coefficients of variation (CV%) for all traits and lowest standard error were recorded for reml analysis in fiber length and fiber fineness which indicates high experimental precision. Carvalho *et al.* (2015) mentined that coefficient of experimental variation (CVe) was 3.20% which is lower than those of other studies carried out with the cotton crop.

**Table 11. Estimates of error mean squares (EMS), coefficient of variations (CV %) and standard errors (SE) of alpha lattice design, RCBD and REML analysis for fiber quality traits.**

| Trait | EMS | | RE% | CV% | | | SE | | |
|---|---|---|---|---|---|---|---|---|---|
| | RCBD | ALPHA | ALPHA | RCBD | ALPHA | REML | RCBD | ALPHA | REML |
| U.H.M. | 0.80 | 0.73 | 1.10 | 2.29 | 2.12 | 1.58 | 0.81 | 0.79 | 0.73 |
| F.S. | 0.04 | 0.03 | 1.38 | 3.06 | 1.47 | 1.50 | 0.09 | 0.17 | 0.14 |
| MIC. | 0.014 | 0.01 | 1.14 | 2.04 | 3.74 | 1.94 | 0.32 | 0.11 | 0.10 |

U.H.M = upper half mean, F.S = fiber strength, Mic =micronaire value

## CONCLUSION

Genotypes, single crosses, and double crosses under study showed Significant or highly significant differences. Mean square due to double crosses showed that line general, 2-line arrangement and 3-line arrangement were either significant or highly for most of studied traits excluding upper half mean which was insignificant. Lowest values for CV and SE for traits were calculated by ordinary REML reflecting the accuracy and precision of this method compared to ANOVA for estimating variance components.

## REFERENCES

Balcha, M., Mohammed, W., Desalegn Z. and Gudeta B. (2019). Heterosis Studies for Agro-morphological and Fiber Quality Traits in Cotton (Gossypium spp.) Hybrids at Werer, Ethiopia. International Journal of Plant Breeding and Crop Science (IJPBCS). 6(1): 498-507.

Carvalho, L.P., Farias, F.J.C., Morelo, C.L., Rodrigues, J.I.S and Teodoro, P.E. (2015) Agronomic and technical fibers traits in elite genotypes of cotton herbaceous. African Journal of Agricultural Research. 10: 4882-4887.

Cochran, W.C. and G.M. Cox (1957). Experimental design. 2nd ed., John Wiley and Sons Inc., New York. U.S.A.

El-Feki T.A., El- Agamy A.I., Yassien. H.E. And El-hoseiny H. A. (2012). Combining Ability and The Order Effect In Double Cross Hybrids Of Cotton. Egypt. J. Agric. Res., 90 (1), 173 – 190.

El-Fesheikawy, A.B.A.; Baker, Kh.M.A; El-Dahan; M.A.A. and Abd El-Rahman, Y.Sh. (2018). Double Crosses Analysis Of Some Economic Characters In Egyptian Cotton. Menoufia J. Plant Prod., (3) 147 – 164.

El-Hashash, E. F. (2017). Comparison of Variance Components Methods for One Way Random Effects Model in Cotton. Asian Journal of Advances in Agricultural Research, 3(1): 1-9.

Fehr, W.R. (1987). Principles of Cultivar Development. Theory and Technique. Macmillan Publishing Company, New York, U.S.A. 1: 115

Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing system. Aust. J. Biol. Sci., 9:463-493.

Hamed, H.H.E., Said, S.R.N. (2021). Estimation of heterosis and ability for yield and fiber quality traits by using line x tester analysis in cotton on (Gossypium barbadense L.). Menoufia Journal. (6): 35 – 51.

Loden HD, Richmond TR (1915) Hybrid vigor in cotton-cytogenetic aspects and practical applications. Econ Bot 5:387—408.

Mahdi, A.H.A.; R. S. Taha and S. M. Emam (2020). Foliar Applied Salicylic Acid Improves Water Deficit-Tolerance in Egyptian Cotton. J. Plant Production, Mansoura Univ., 11(5): 383-389.

Naquibullah, H., Abro, K., Kumbhar, M.B., Hassan, G. and Mahmood, G. 2000. Study of heterosis in upland cotton - II. Morphology and yield traits. Pak. Cottons. 44: 13-23.

Piepho, H-P., Mohring, J., Schulz-Streeck T and Ogutu, J. O. (2012). A stage-wise approach for the analysis of multi-environment trials. Biometrical Journal 54 (6), 844–860.

Randhawa, L.S. and Singh, T.H. 1994. Heterosis breeding for crossing parent yield barriers in cotton, In: G. A. Constable, and N. W. Forester (eds), Proc. World Cotton Res. Conf. 1, Challenging the Future, CSIRO, Brisbane, Australia.

Ranganatha, H.M., Patil, S., Shreekanth, S., Manjula, S.M. and Patil, B.C. 2013. Studies on heterosis in Cotton (Gossypium hirsutum L.) for seed cotton yield and its components. Asian J. Bio. Sci. 8(1): 82-55.

Singh, R.K. and B.D. Chaudhary (1985). Double cross hybrid analysis and order effects in barley. Advances in Cytogenetics and crop Improv. (Ed. Singh R.B., Singh, R.M. and Singh, B.D.) Kalyani Publishers, New Delhi, pp. 319-325.

Soomro, A., Shahzad, S. and Khan, S. (2021). Diallel analysis in upland cotton over the environments for yield, earliness, fiber quality traits and cotton leaf curl virus. Int. J. Biol. Biotech., 18 (1): 147-155.

Steel, R.G.D. and Torrie, J.H. (1980). Principles and procedures of statistics. Second Edition, McGraw Hill Book Company Inc., New York.

Sultan, M. S. ; Abdel-Moneam, M. A.; EL-Mansy, Y. M. and Huda S. El-Morshidy. (2018). Estimating of Heterosis and Combining Ability for some Egyptian Cotton Genotypes Using Line X Tester Mating Design. J. Plant Production, Mansoura Univ.,Vol 9 (12): 1121 – 1127.

Yehia, W.M.B. and E. F. EL-Hashash (2019). Combining Ability Effects and Heterosis Estimates through Line x Tester Analysis for Yield, Yield Components and Fiber Traits in Egyptian Cotton. Elixir Agriculture (3): 53238-53246.

El-hoseiny, H.A. (2009) Improving Egyptian Cotton Using Double Crossing Technique. PH. Fac. of Agri. Al-Azhar University.

أداء الهجن الزوجية في صفات التبكير في النضج وجودة الألياف في بعض التراكيب الوراثية للقطن المصري

ضياء احمد القاضى¹ ، محمد عبد المعبود عبد الشافى ¹، طلعت احمد الفقى ² ، اشرف عبد الاعلى عبد المحسن¹ و ايمان صلاح الدين عبدالعزيز ²
¹كلية الزراعة – جامعة القاهرة
²معهد بحوث القطن – مركز البحوث الزراعية

اشتملت التراكيب الوراثية المستخدمة في هذه الدراسة على خمسة آباء ثلاثة منها تابعة للنوع (.Gossypium barbadense L) التراكيب الوراثية المستخدمة في هذه الدراسة تم الحصول عليها من قسم التربية بمعهد بحوث القطن – مركز البحوث الزراعية بالجيزة. ثلاثة آباء تنتمي لطبقة الاقطان الطويلة واثنان منها من الاقطان الفائقة الطول. تم التهجين بين هذه الاباء وتم الحصول على ١٠ هجن فردية و١٥ هجين زوجي. تم تقييم هذه الآباء مع الهجن الفردية والزوجية في محطة بحوث سخا – مركز البحوث الزراعية. أظهرت النتائج وجود فروق معنوية بين كلا من الآباء والهجن الفردية والهجن الزوجية لمعظم الصفات تحت الدراسة. كما أظهرت النتائج أن المربع اللاتيني كان أكثر كفاءة في تحليل الصفات المدروسة مقارنة ب تصميم القطاعات كاملة العشوائية. اوضحت النتائج ان قيم كلا من cv و se كانت صغيرة بالنسبة لتحليل reml لصفات طول التيلة والنعومة مما يشير الى زيادة الدقة التجريبية. يوصى باستخدام المربع اللاتينى فى حالة زيادة عدد المعاملات لزيادة الدقة التجريبية. كما اظهرت النتائج ان الهجين الزوجى (BBB × جـ٩٧) * (جـ ٩٢ × جـ٩٦) كان افضل الهجن الزوجية في صفات التبكير اما بالنسبة لصفات التيلة الهجين الزوجى (استرالي × جـ٩٦) * (جـ ٩٧ × جـ٩٢) كان افضل الهجن.