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# EVALUATION OF SOME EGYPTIAN COTTON GENOTYPES OVER TWO STAGES

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## ABSTRACT

The present investigation deals with the variation among some Egyptian cotton (*Gossypium barbadense* L.) genotypes. They were evaluated within Giza 80 zone, Minya and Beni Souf (Upper Egypt) through two programs (breeding and regional) during 2009 and 2010 seasons. A randomized complete block design was used in the two programs to estimate the variance among the genotypes. The first analysis used one observation per experimental unit to evaluate the genotypes in the first stage (individual generations or locations). The second analysis used more than one observation per experimental unit to evaluate genotypes in the second stage (two generations or locations). The results of the breeding program exhibited significant variation due to genotypes and hybrids vs. G80 were observed for total yields (seed and lint) and earliness. Hybrids significantly surpassed G80 with respect to total yields (seed and lint) and earliness except G90 x Pima S 62 (24240), (G83 x Pima S 6) x Dandara, (G83 x (G75 x 5844)) x G85 and G91 x G80 for earliness in the two generations. The results of the analysis of two generations gave information with respect to variance between generations to be used in the breeding program. The results of the regional program showed that (G83 x (G75 x 5844)) x G80 gave the lowest values of variance between locations for boll weight and dry weight per boll in the first season, harvest index in the second season and number of seeds per boll in the two seasons. G90 x Australian gave similar results for seed cotton yield and boll weight in 2009 season. Thus hybrids were more stable than G80. Results exhibited showed that G80 was more stable than hybrids for lint cotton yield in the two seasons due to its lowest variance between locations. The present study was very important in the two programs, it selects the surpassed varieties in the breeding program, replace new varieties to cultivars in the regional program and enter the statistical measure to evaluate the genotypes.

***Key words:*** *cotton, genotypes , locations, randomized complete block design.*

## 1.INTRODUCTION

One of the objectives of the research stations is to develop high yielding cultivars and make them available to the growers. The productivity of cultivars, results to a large extent from how well it benefits from the environmental conditions. The attempt to adapt elements of production system used in Egypt brought about plant breeding efforts to develop cottons suited to wider range of environments in the Egyptian cotton belt. The Cotton Research Institute is the major player in cotton production policy in Egypt. It conducts fundamental and applied research on and undertakes development programs in a wide variety of areas as discussed below. Commercial cotton varieties are maintained through continuous release of new pure seed stock. Breeding materials for fiber properties are tested to select for high quality and best characteristics in cotton. Allocation of cotton varieties to different locations throughout the country is decided according to regional field trial results.

Sing and Narayanan (2000) mentioned the benefits of applying randomized complete block design in plant breeding The randomized complete block experiment is quite flexible. Since the variability between replications can be removed from the experimental error, it is unnecessary for the replications to be contiguous. An entire variable or replication may be omitted from the analysis when, for some reason, it is either lost or not comparable with the others.

Mohamed *et al. (*2003) evaluated twenty-four cotton genotypes in Upper Egypt using the randomized complete block design. The results showed that the cross ((G83 x G80) x G89) was a promising cross due to its performance for yield components and fiber quality. Idris (2005) studied five Egyptian cotton genotypes in two locations using two steps of analysis of randomized complete block design. Such steps considered each location as one replicate. Results showed no difference between the two methods of analysis with respect to location effects. Rahoumah *et al.* (2008) evaluated twenty-four cotton genotypes in five locations using randomized complete block design. They found that the mean squares for genotypes x locations was significant for yield (seed and lint) and boll weight.

Researchers need a statistical measure to evaluate genotypes from different generations and locations (breeding and regional programs). Thus, the objective of the present study was to evaluate some Egyptian cotton genotypes over two stages of analysis (breeding and regional programs) of randomized complete block design to estimate the variatice between genotypes and locations variance.

## 2.MATERIALS AND METHODS

Some Egyptian cotton (*Gossypium barbadense* L.) genotypes were evaluated within G80 zone (control) Minya and Beni Souf Governorates (Upper Egypt) through two programs of Cotton Research Institute (breeding and regional sections) during 2009 and 2010 seasons (Table 1). Planting was during the last week of March. All agricultural practices were done as usual.

### 2.1.Breeding program

One field experiment was carried out in Minya Governorate during 2009 and 2010 seasons. A randomized complete block design with six replications was used. Plot size was 7.2 $m^2$ (3 rows x 4 m long x 0.60 m apart). The first experiment evaluated the eleven genotypes with G80 for seed cotton yield, lint cotton yield, weight of (50 bolls) and earliness (expressed as yield percent of first pick relative to total seed cotton yield). One sample was obtained from each generation to estimate fiber properties, *viz.* fiber length, micronaire reading and yarn strength. The lint cotton samples were tested in the Cotton Research Laboratories, Cotton Research Institute.

### 2.2. Regional program

Two field experiments were carried out in two different locations (Minya and Beni Souf) during 2009 and 2010 seasons. A randomized complete block design with four replications was used. Plot size was 52 $m^2$ (20 rows x 4 m long x 0.65 m apart) and 62.4 $m^2$ (24 rows x 4 m long x 0.65 m apart) in the first and second seasons, respectively. The last three genotypes were evaluated for seed and lint cotton yield. One sample (50 bolls) was obtained from each plot to estimate boll components, *viz.* boll weight, dry weight per boll and the number of seeds per boll. In addition, harvest index per boll (seed cotton per boll / dry weight per boll) was measured. One sample was obtained from each location to estimate fiber properties, *viz.* fiber length, micronaire reading and yarn strength. The lint cotton samples were tested in the Cotton Research Laboratories, Cotton Research Institute.

### 2.3 Statistical analysis

Two analyses of randomized complete block design were used (Table 2). The first analysis was done using one observation per experimental unit to evaluate the genotypes in the first stage (individual generations or locations). The second analysis was using more than one observation per experimental unit to evaluate the genotypes in the second stage (two generations or locations). Analysis of fiber properties in the two generations or locations using one observation per experimental unit due to test one replicate in each generation or location.

Statistical analyses were straightforward according to Cochran and Cox (1950), Federer (1955), Little and Hills (1978), Gomez and Gomez (1984), Bailey (1994), Roger (1994) and Mcpherson (2001). The different genotype means were compared by L.S.D. test as given by Steel and Torrie (1980). All comparisons were done at 0.05 level of significance.

## 3. RESULTS AND DISCUSSION

### 3.1. Breeding program

The objective of the cotton breeding program is to develop long staple varieties for Upper Egypt to meet the domestic spinning industry needs for low count yarn, introduce early maturity to help produce short – season cotton varieties and enable farmers to grow a winter crop (especially wheat) before cotton.

#### 3.1.1.Analysis of individual generations (first stage)

The first stage of analysis was carried out with the data of individual generations to estimate genotype variance (Table 2). The analysis of variance of individual generations, with respect to total yields (seed and lint), weight of 50 bolls and earliness revealed the presence of significant difference among genotypes and hybrids vs. G80 (Table 3). In both seasons, significant variation due to genotypes and hybrids vs. G80 were

**Table (1): Pedigree of the Egyptian cotton genotypes.**

| No | Origin | 2009 season Families | 2010 season Families |
|---|---|---|---|
| **1** | G90 x Pima S 62 (24240) | $F_5$ 83 / 2007 | $F_6$ 146 / 2008 |
| **2** | (G83 x Pima S 6 ) x Karashinky | $F_5$ 102 / 2007 | $F_6$ 172 / 2008 |
| **3** | (G83 x Pima S 6) x Dandara | $F_5$ 111 / 2007 | $F_6$ 178 / 2008 |
| **4** | G91 x Pima S 62 (24202) | $F_5$ 116 / 2007 | $F_6$ 182 / 2008 |
| **5** | (G83 x (G75 x 5844)) x G85 | $F_6$ 126 / 2007 | $F_7$ 194 / 2008 |
| **6** | (G83 x (G75 x 5844)) x G91 | $F_6$ 139 / 2007 | $F_7$ 206 / 2008 |
| **7** | G 91 x G80 | $F_6$ 145 / 2007 | $F_7$ 212 / 2008 |
| **8** | (G83 x (G75 x 5844)) x G90 | $F_6$ 159 / 2007 | $F_7$ 215 / 2008 |
| **9** | (G83 x (G72 x Dandara)) x G91 | $F_7$ 173 / 2007 | $F_8$ 235 / 2008 |
| **10** | (G83 x (G72 x Dandara)) x G85 | $F_7$ 184 / 2007 | $F_8$ 240 / 2008 |
| **11** | (G83 x (G75 x 5844)) x (G83 x (G72 x Dandara)) | $F_8$ 208 / 2007 | $F_9$ 260 / 2008 |
| **12** | (G83 x (G75 x 5844)) x G80 | Bulk families | |
| **13** | G90 x Australian | Bulk families | |
| **14** | G 66 x G73 | G80 | |

**Table (2): Two analyses of randomized complete block design.**

| First stage (Individual generations or locations) | | Second stage (Two generations or locations) | |
|---|---|---|---|
| **Source of variation** | **df** | **Source of variation** | **df** |
| **Replications (r)** | (r-1) | **Replications (r)** | (r-1) |
| **Genotypes (g)** | (g-1) | **Genotypes (g)** | (g-1) |
| **Experimental error** | (g-1) (r-1) | **Experimental error** | (g-1) (r-1) |
| | | **Sampling (k) error** | r g (k – 1) |
| **Total** | r g - 1 | **Total** | r g k – 1 |

observed for total yields (seed and lint), bolls weight and earliness except bolls weight for hybrids vs. G80. This method of analysis gave detail for genotypes and hybrids vs. G80 variances to be used in the breeding program.

The hybrids significantly exceeded G80 with respect to total yields (seed and lint) for the two seasons except G90 x Pima S 62 (24240), (G83 x Pima S 6) x Dandara and G91 x G80 in the first season. The hybrid G90 x Pima S 62 (24240) was the best genotype for boll weight, significantly surpassing G80 in 2010 season. On the contrary, G80 significantly surpassed (G83 x Pima S 6) x Dandara and G91 x Pima S 62 (24202) for boll weight in the first season and (G83 x Pima S 6 ) x Karashinky in the second season. Selection of heavy boll weight genotypes could help the cotton breeder to improve yield since it is one of the main components of high seed cotton yield.

The hybrids significantly exceeded G80 with respect to earliness in the two seasons except G90 x Pima S 62 (24240), (G83 x Pima S 6) x Dandara and G91 x Pima S 62 (24202) in 2009 season, (G83 x (G75 x 5844)) x G85 , (G83 x (G72 x Dandara)) x G85 and (G83 x (G75 x 5844)) x (G83 x (G72 x Dandara)) in 2010 season and G 91 x G80 in the two seasons. Earliness is a very important character for the cotton breeder to produce early varieties, which can escape bollworm infection and can be harvested early enough before sowing winter crops (Table 4).

Total yields (seed and lint) in the two picks (Table 3) were partitioned. In both seasons, significant variation due to the genotypes and the hybrids vs. G80 were recorded for yields (seed and lint) in the first pick. The hybrids significantly exceeded G80 with respect to (seed and lint) yields except G90 x Pima S 62 (24240), (G83 x Pima S 6) x Dandara and G 91 x G80 in the 2009 season.

The results of analysis of the two picks showed that (G83 x (G72 x Dandara)) x G91, (G83 x (G72 x Dandara)) x G85 and (G83 x (G75 x 5844)) x (G83 x (G72 x Dandara)) gave the highest values of variance between picks for seed and lint yields in the 2009 season. Also, hybrids G91 x Pima S 62 (24202), (G83 x (G75 x 5844)) x G91 and (G83 x (G72 x Dandara)) x G91 gave the same results in the second season. This shows that these hybrids were earlier maturing than the other genotypes due to the presence of G83, G91 and Dandara in their pedigree. This analysis gave information for the behavior of genotypes needed for the breeding program.

**Table (3): Mean squares of traits for individual generations.**

| Breeding program | | | | | | | |
|---|---|---|---|---|---|---|---|
| **2009 Season** | | | | | | | |
| **Traits** | | **S. C. Y. (k/fed.)** | | **L. C. Y. (k/fed.)** | | **50 Bolls (g)** | **Earliness %** |
| **Source of variation** | **df** | **F. Pick** | **S. Pick** | **F. Pick** | **S. Pick** | | |
| **Replications** | 5 | 35.90** | 0.55 | 51.84** | 0.90 | 67.00 | 50.82** |
| **Genotypes** | 11 | 7.80** | 0.29 | 11.70** | 0.46 | 290.79* | 55.93** |
| **Hybrids vs. G80** | 1 | 31.71** | 0.13 | 43.16** | 0.16 | 295.74 | 122.33** |
| **Residual** | 10 | 5.41* | 0.31 | 8.55* | 0.49 | 290.30* | 49.28** |
| **Experimental error** | 55 | 2.19 | 0.36 | 3.17 | 0.49 | 108.10 | 14.66 |
| **Total** | 71 | | | | | | |
| **2010 Season** | | | | | | | |
| **Replications** | 5 | 8.37** | 1.13** | 13.19** | 1.83** | 152.20* | 34.13** |
| **Genotypes** | 11 | 6.46** | 0.26 | 10.76** | 0.48 | 175.46** | 21.84* |
| **Hybrids vs. G80** | 1 | 57.75** | 0.12 | 87.51** | 0.22 | 1.63 | 89.80** |
| **Residual** | 10 | 1.33 | 0.28 | 3.09 | 0.50 | 192.84** | 15.04 |
| **Experimental error** | 55 | 1.82 | 0.17 | 2.90 | 0.28 | 51.15 | 9.36 |
| **Total** | 71 | | | | | | |
| **Traits** | | **Total S. C. Y. (k/fed.)** | | **Total L. C. Y. (k/fed.)** | | | |
| **Source of variation** | **df** | **2009** | **2010** | **2009** | **2010** | | |
| **Replications** | 5 | 36.87** | 14.24** | 53.17** | 22.58** | | |
| **Genotypes** | 11 | 7.66** | 5.90** | 11.64** | 10.48** | | |
| **Hybrids vs. G80** | 1 | 35.92** | 52.57** | 48.14** | 78.95** | | |
| **Residual** | 10 | 4.84** | 1.24 | 7.99* | 3.64 | | |
| **Experimental error** | 55 | 2.30 | 1.94 | 3.35 | 3.08 | | |
| **Total** | 71 | | | | | | |
| **Traits** | | **S. C. Y. (k/fed.) Picks** | | **L. C. Y. (k/fed.) Picks** | | | |
| **Source of variation** | **df** | **2009** | **2010** | **2009** | **2010** | | |
| **Replications** | 5 | 18.42** | 7.12** | 26.34** | 11.30** | | |
| **Genotypes** | 11 | 3.83** | 2.95** | 5.69** | 5.24** | | |
| **Hybrids vs. G80** | 1 | 17.95** | 26.30** | 24.28** | 39.46** | | |
| **Residual** | 10 | 2.42* | 0.62 | 3.83* | 1.82 | | |
| **Experimental error** | 55 | 1.15 | 0.97 | 1.65 | 1.54 | | |
| **Between picks** | 72 | 24.00 | 55.96 | 34.63 | 89.26 | | |
| **1** | 6 | 12.59 | 58.70 | 19.08 | 97.23 | | |
| **2** | 6 | 26.36 | 54.16 | 36.38 | 79.83 | | |
| **3** | 6 | 16.03 | 61.24 | 21.07 | 91.72 | | |
| **4** | 6 | 25.37 | 66.31 | 34.84 | 100.23 | | |
| **5** | 6 | 27.85 | 48.49 | 39.89 | 79.65 | | |
| **6** | 6 | 26.10 | 66.99 | 38.20 | 111.99 | | |
| **7** | 6 | 17.68 | 52.77 | 25.58 | 84.99 | | |
| **8** | 6 | 26.06 | 56.29 | 37.56 | 87.28 | | |
| **9** | 6 | 32.30 | 66.83 | 46.53 | 107.65 | | |
| **10** | 6 | 33.25 | 55.33 | 50.15 | 92.35 | | |
| **11** | 6 | 32.62 | 57.01 | 48.93 | 93.78 | | |
| **G80** | 6 | 11.76 | 27.37 | 17.31 | 44.43 | | |
| **Total** | 143 | | | | | | |

*** , ** Significant at 0.05 and 0.01 levels, respectively.**
**S. C. Y. = Seed cotton yield    L. C. Y. = Lint cotton yield    k/fed = kentar / feddan**
**F. Pick = First pick    S. Pick = Second pick**

**Table (4): Means of traits for individual generations.**

| **Breeding program** | | | | | | |
|---|---|---|---|---|---|---|
| **2009 Season** | | | | | | |
| **Traits** | **S. C. Y. (k/fed.)** | | **L. C. Y. (k/fed.)** | | **50 Bolls (g)** | **Earliness %** |
| **Genotypes** | **F. Pick** | **S. Pick** | **F. Pick** | **S. Pick** | | |
| **1** | 7.66 | 3.05 | 9.43 | 3.76 | 153 | 71.06 |
| **2** | 9.80 √ | 2.91 | 11.52 √ | 3.43 | 155 | 76.67 √ |
| **3** | 8.18 | 2.79 | 9.56 | 3.43 | 138 x | 74.08 |
| **4** | 9.48 √ | 2.80 | 11.11 √ | 3.28 | 139 x | 76.35 |
| **5** | 9.62 √ | 2.72 | 11.52 √ | 3.26 | 155 | 77.05 √ |
| **6** | 9.44 √ | 2.35 | 11.42 √ | 2.84 | 148 | 79.89 √ |
| **7** | 8.31 | 2.77 | 10.00 | 3.34 | 158 | 74.00 |
| **8** | 9.57 √ | 2.48 | 11.49 √ | 2.98 | 150 | 79.21 √ |
| **9** | 10.23 √ | 2.48 | 12.28 √ | 2.98 | 154 | 79.98 √ |
| **10** | 10.65 √ | 2.98 | 13.08 √ | 3.66 | 157 | 77.42 √ |
| **11** | 10.31 √ | 2.54 | 12.62 √ | 3.11 | 155 | 79.61 √ |
| **Hybrids** | 9.39 √ | 2.72 | 11.28 √ | 3.28 | 151 | 76.85 √ |
| **G80** | 6.99 | 2.56 | 8.48 | 3.11 | 158 | 72.13 |
| **L.S.D.** | 1.73 | -- | 2.08 | -- | 12 | 4.47 |
| **2010 Season** | | | | | | |
| **1** | 12.00 √ | 1.22 | 15.44 √ | 1.57 | 152 √ | 91.09 √ |
| **2** | 11.29 √ | 0.90 | 13.71 √ | 1.09 | 130 x | 92.74 √ |
| **3** | 12.08 √ | 1.17 | 14.79 √ | 1.44 | 138 | 91.33 √ |
| **4** | 12.43 √ | 0.97 | 15.28 √ | 1.20 | 139 | 92.65 √ |
| **5** | 11.30 √ | 1.49 | 14.48 √ | 1.91 | 137 | 88.44 |
| **6** | 12.48 √ | 0.98 | 16.13 √ | 1.27 | 144 | 92.64 √ |
| **7** | 11.45 √ | 1.35 | 14.54 √ | 1.72 | 140 | 89.53 |
| **8** | 11.33 √ | 0.88 | 14.11 √ | 1.09 | 141 | 92.72 √ |
| **9** | 12.37 √ | 0.87 | 15.69 √ | 1.11 | 136 | 93.40 √ |
| **10** | 11.56 √ | 1.19 | 14.94 √ | 1.53 | 142 | 90.68 |
| **11** | 11.96 √ | 1.34 | 15.34 √ | 1.72 | 133 | 90.14 |
| **Hybrids** | 11.84 √ | 1.12 | 14.95 √ | 1.42 | 139 | 91.40 √ |
| **G80** | 8.60 | 1.27 | 10.96 | 1.62 | 139 | 87.36 |
| **L.S.D.** | 1.57 | -- | 1.99 | -- | 8 | 3.57 |
| **Traits** | **Total S. C. Y. (k/fed.)** | | **Total L. C. Y. (k/fed.)** | | | |
| **Genotypes** | **2009** | **2010** | **2009** | **2010** | | |
| **1** | 10.71 | 13.22 √ | 13.19 | 17.01 √ | | |
| **2** | 12.71 √ | 12.19 √ | 14.95 √ | 14.80 √ | | |
| **3** | 10.97 | 13.25 √ | 12.99 | 16.23 √ | | |
| **4** | 12.28 √ | 13.40 √ | 14.39 √ | 16.48 √ | | |
| **5** | 12.34 √ | 12.79 √ | 14.78 √ | 16.39 √ | | |
| **6** | 11.79 √ | 13.46 √ | 14.26 √ | 17.40 √ | | |
| **7** | 11.08 | 12.80 √ | 13.34 | 16.26 √ | | |
| **8** | 12.05 √ | 12.21 √ | 14.47 √ | 15.20 √ | | |
| **9** | 12.71 √ | 13.24 √ | 15.26 √ | 16.80 √ | | |
| **10** | 13.63 √ | 12.75 √ | 16.74 √ | 16.47 √ | | |
| **11** | 12.85 √ | 13.30 √ | 15.73 √ | 17.06 √ | | |
| **Hybrids** | 12.10 √ | 12.96 √ | 14.55 √ | 16.37 √ | | |
| **G80** | 9.55 | 9.87 | 11.59 | 12.58 | | |
| **L.S.D.** | 1.77 | 1.62 | 2.14 | 2.05 | | |

√, Hybrids significantly surpassed G80 (control). --: Not significant at 0.05 level.
x , G80 (control) significantly surpassed hybrids.

information for the behavior of genotypes needed for the breeding program.

**3.1.2. Analysis of generations (Second stage)**

In this proposal the data of the two generations were used together. Each cell contained two readings (k) one for each generation (Table 2). The analysis of variance in the two generations with respect to yields (seed and lint), weight of 50 bolls and earliness revealed significant differences among genotypes and between hybrids vs. G80 (Table 5). Significant variations due to genotypes and hybrids vs. G80 were also observed for total yields (seed and lint) and earliness. Hybrids significantly surpassed G80 with respect to total yields (seed and lint) and earliness, except G90 x Pima S 62 (24240), (G83 x Pima S 6) x Dandara, (G83 x (G75 x 5844)) x G85 and G 91 x G80 for earlines, (Table 6). Partitioning total seed and lint yields in the first and second picks was made (Table 5). Significant variations due to genotypes and hybrids vs. G80 were detected in the first pick. Hybrids significantly exceeded G80 with respect to seed and lint yields in the first pick (Table 6). This method of analysis of randomized complete block design gave information with respect to variation between generations and partitioning to individual genotypes to be used in the breeding program. In the fiber properties, the analysis considered each generation as one replicate due to test one sample (Table 5). Results of analysis showed that significance due to replications was observed for both fiber length and yarn strength. This method of analysis was very important in breeding program to estimate variation between generations when only one replicatation was tested.

**3.2.Regional program**

To establish the cotton varietal policy on sound scientific basis, promising and commercially – grown varieties are evaluated regionally to specify the most appropriate agroclimatic areas for each variety. This is also linked to the actual needs of each variety at the domestic and international markets.

**3.2.1. Analysis of individual locations**

The analysis of variance for individual locations during the two seasons, with respect to seed and lint yield, boll weight, dry weight per boll, harvest index and number of seeds / boll revealed the presence of significant differences among genotypes and hybrids vs. G80, (Table 7).

**3.2.1.1.Minya**

In 2009 season, significant variations due to genotypes and hybrids vs. G80 were observed for yields (seed and lint), boll weight, dry weight per boll, harvest index and number of seeds / boll in the two picks except for harvest index and number of seeds/ boll in the second pick. (G83 x (G75 x 5844)) x G80 gave the highest values for yields (seed and lint) in the first pick, it significantly surpassed G80. The hybrids significantly exceeded G80 with respect to harvest index in the first pick. In contrast, G80 significantly surpassed both hybrids for bolls weight and dry weight per boll in the two picks, and one hybrid (G83 x (G75 x 5844)) x G80 for number of seeds / boll in the first pick (Table 8).

In 2010 season, significant variations due to both genotypes and hybrids vs. G80 were recorded for seed cotton yield and dry weight per boll in the two picks, lint cotton yield, harvest index and number of seeds / boll in the first pick. Significant variation due to genotypes was observed for boll weight in the first pick. Hybrids significantly exceeded G80 with respect to yields (seed and lint) in the first pick. (G83 x (G75 x 5844)) x G80 had the highest values for boll weight and number of seeds / boll, significantly surpassed G80. On the contrary, G80 significantly surpassed both hybrids for dry weight per boll and seed cotton yield in the first and second picks, respectively and G90 x Australian for boll weight and dry weight per boll in the first and second picks, respectively.

In both seasons of the study, significant variation due to genotypes was detected for total yields (seed and lint) except for total seed cotton yield in the 2010 season. Significant variation due to hybrids vs. G80 was recorded for total lint cotton yield in 2010 season. (G83 x (G75 x 5844)) x G80 was the best genotype for seed and lint yield in the first season, significantly surpassing G80. Two hybrids significantly exceeded G80 with respect to total lint cotton yield in the second season. In contrast, G80 significantly surpassed G90 x Australian for seed cotton yield in the 2009 season (Table 8).

The results of analysis of two picks showed that the hybrids gave the highest values of variance between picks compared to G80 for (seed and lint yields) in both seasons. This is due to the faster maturity of these hybrids compared to G80.

**3.2.1.2.Beni Souf**

Significant variation due to genotypes was observed for dry weight per boll, harvest index and the number of seeds / boll in both seasons,

**Table (5): Mean squares of traits for two generations.**

| Breeding program | | | | | | | |
|---|---|---|---|---|---|---|---|
| **Traits** | | **S. C. Y. (k/fed.)** | | **L. C. Y. (k/fed.)** | | **50 Bolls (g)** | **Earliness %** |
| **Source of variation** | **df** | **F. Pick** | **S. Pick** | **F. Pick** | **S. Pick** | | |
| **Replications** | 5 | 23.11** | 1.48** | 33.92** | 2.46** | 70.89 | 55.73** |
| **Genotypes** | 11 | 10.85** | 0.343 | 17.19** | 0.609 | 210.07 | 56.63** |
| **Hybrids vs. G80** | 1 | 87.52** | 0.005 | 126.80** | 0.003 | 126.72 | 210.71** |
| **Residual** | 10 | 3.19 | 0.380 | 6.23* | 0.670* | 218.40* | 41.22** |
| **Experimental error** | 55 | 1.97 | 0.218 | 2.96 | 0.321 | 103.51 | 9.33 |
| **Between generations** | 72 | 6.39 | 1.51 | 11.72 | 2.07 | 169.44 | 123.19 |
| **1** | 6 | 12.57 | 1.84 | 23.01 | 2.64 | 46.33 | 206.45 |
| **2** | 6 | 3.26 | 2.39 | 5.40 | 3.24 | 339.83 | 143.39 |
| **3** | 6 | 12.86 | 1.61 | 21.20 | 2.15 | 66.42 | 150.53 |
| **4** | 6 | 6.15 | 1.81 | 11.15 | 2.37 | 69.58 | 136.73 |
| **5** | 6 | 5.09 | 1.25 | 9.78 | 1.65 | 234.17 | 106.17 |
| **6** | 6 | 5.47 | 1.09 | 12.42 | 1.49 | 46.67 | 95.54 |
| **7** | 6 | 6.02 | 1.17 | 11.98 | 1.56 | 214.17 | 131.90 |
| **8** | 6 | 4.62 | 1.33 | 8.08 | 1.84 | 58.08 | 99.74 |
| **9** | 6 | 4.16 | 1.39 | 8.61 | 1.89 | 271.00 | 102.61 |
| **10** | 6 | 7.46 | 2.09 | 12.68 | 3.03 | 215.50 | 117.10 |
| **11** | 6 | 5.86 | 0.910 | 10.61 | 1.28 | 255.08 | 65.56 |
| **G80** | 6 | 3.11 | 1.24 | 5.78 | 1.72 | 216.50 | 122.63 |
| **Total** | 143 | | | | | | |

| **Traits** | | **T. S.C.Y. (k/fed.)** | **T. L.C.Y (k/fed.)** |
|---|---|---|---|
| **Source of variation** | **df** | | |
| **Replications** | 5 | 28.86** | 42.89** |
| **Genotypes** | 11 | 10.19** | 16.67** |
| **Hybrids vs. G80** | 1 | 87.70** | 125.19** |
| **Residual** | 10 | 2.43 | 5.82 |
| **Experimental error** | 55 | 2.02 | 3.06 |
| **Between generations** | 72 | 4.09 | 7.24 |
| **1** | 6 | 7.57 | 14.28 |
| **2** | 6 | 1.79 | 2.31 |
| **3** | 6 | 10.13 | 16.61 |
| **4** | 6 | 2.89 | 5.24 |
| **5** | 6 | 3.36 | 6.11 |
| **6** | 6 | 1.72 | 5.45 |
| **7** | 6 | 2.80 | 6.37 |
| **8** | 6 | 2.66 | 4.30 |
| **9** | 6 | 1.97 | 3.91 |
| **10** | 6 | 6.15 | 8.97 |
| **11** | 6 | 4.86 | 8.21 |
| **G80** | 6 | 3.16 | 5.18 |
| **Total** | 143 | | |

| **Traits** | | **Fiber length (mm)** |
|---|---|---|
| **Source of variation** | **df** | |
| **Rep. (generations)** | 1 | 6.61* |
| **Genotypes** | 11 | 0.665 |
| **Hybrids vs. G80** | 1 | 0.970 |
| **Residual** | 10 | 0.634 |
| **Experimental error** | 11 | 0.744 |

| **Traits** | | **Micronaire reading** |
|---|---|---|
| **Rep. (generations)** | 1 | 0.135 |
| **Genotypes** | 11 | 0.014 |
| **Hybrids vs. G80** | 1 | 0.002 |
| **Residual** | 10 | 0.015 |
| **Experimental error** | 11 | 0.029 |

| **Traits** | | **Yarn strength** |
|---|---|---|
| **Rep. (generations)** | 1 | 44632* |
| **Genotypes** | 11 | 2681 |
| **Hybrids vs. G80** | 1 | 1678 |
| **Residual** | 10 | 2781 |
| **Experimental error** | 11 | 7196 |
| **Total** | 23 | |

*** , ** Significant at 0.05 and 0.01 levels, respectively.**

**Table (6): Means of traits of cotton genotypes for two generations.**

| Breeding program | | | | | | |
|---|---|---|---|---|---|---|
| **Traits** | **S. C. Y. (k/fed.)** | | **L. C. Y. (k/fed.)** | | **50 Bolls (g)** | **Earliness %** |
| **Genotypes** | **F. Pick** | **S. Pick** | **F. Pick** | **S. Pick** | | |
| **1** | 9.83 √ | 2.14 | 12.44 √ | 2.67 | 153 | 81.08 |
| **2** | 10.55 √ | 1.91 | 12.62 √ | 2.26 | 143 | 84.71 √ |
| **3** | 10.13 √ | 1.98 | 12.18 √ | 2.44 | 138 | 82.71 |
| **4** | 10.96 √ | 1.89 | 13.20 √ | 2.24 | 139 | 84.50 √ |
| **5** | 10.46 √ | 2.11 | 13.00 √ | 2.59 | 146 | 82.75 |
| **6** | 10.96 √ | 1.67 | 13.78 √ | 2.06 | 146 | 86.27 √ |
| **7** | 9.88 √ | 2.06 | 12.27 √ | 2.53 | 149 | 81.77 |
| **8** | 10.45 √ | 1.68 | 12.80 √ | 2.04 | 146 | 85.97 √ |
| **9** | 11.30 √ | 1.68 | 13.99 √ | 2.05 | 145 | 86.69 √ |
| **10** | 11.11 √ | 2.09 | 14.01 √ | 2.60 | 150 | 84.05 √ |
| **11** | 11.14 √ | 1.94 | 13.98 √ | 2.42 | 144 | 84.88 √ |
| **Hybrids** | 10.61 √ | 1.92 | 13.11 √ | 2.35 | 145 | 84.12 √ |
| **G80** | 7.80 | 1.92 | 9.72 | 2.37 | 149 | 79.75 |
| **L.S.D.** | 1.64 | -- | 2.01 | -- | -- | 3.56 |
| **Genotypes** | **T. S.C.Y. (k/fed.)** | **T. L.C.Y (k/fed.)** | **Fiber length mm** | **Micronaire reading** | **Yarn strength** | |
| **1** | 11.97 √ | 15.10 √ | 29.90 | 4.2 | 2318 | |
| **2** | 12.45 √ | 14.88 √ | 30.75 | 4.1 | 2328 | |
| **3** | 12.11 √ | 14.61 √ | 29.70 | 4.2 | 2328 | |
| **4** | 12.84 √ | 15.44 √ | 29.60 | 4.4 | 2305 | |
| **5** | 12.57 √ | 15.59 √ | 31.30 | 4.2 | 2343 | |
| **6** | 12.63 √ | 15.83 √ | 30.05 | 4.2 | 2290 | |
| **7** | 11.94 √ | 14.80 √ | 31.00 | 4.2 | 2355 | |
| **8** | 12.13 √ | 14.84 √ | 30.50 | 4.1 | 2265 | |
| **9** | 12.98 √ | 16.03 √ | 30.40 | 4.3 | 2357 | |
| **10** | 13.19 √ | 16.61 √ | 29.75 | 4.3 | 2275 | |
| **11** | 13.08 √ | 16.40 √ | 30.05 | 4.3 | 2245 | |
| **Hybrids** | 12.53 √ | 15.46 √ | 30.27 | 4.2 | 2310 | |
| **G80** | 9.71 | 12.09 | 31.00 | 4.2 | 2340 | |
| **L.S.D.** | 1.66 | 2.04 | -- | -- | -- | |

**√ , Hybrids significantly surpassed G80 (control). --: Not significant at 0.05 level.**

**Table (7): Mean squares of traits for individual locations.**

| Regional program | | | | | | | |
|---|---|---|---|---|---|---|---|
| **Minya 2009 Season** | | | | | | | |
| **Traits** | | **S. C. Y. (k/fed.)** | | **L. C. Y. (k/fed.)** | | **Boll weight (g)** | |
| **Source of variation** | **df** | **F. Pick** | **S. Pick** | **F. Pick** | **S. Pick** | **F. Pick** | **S. Pick** |
| **Replications** | 3 | 3.76** | 0.034 | 6.21** | 0.073 | 0.008* | 0.057** |
| **Genotypes** | 2 | 5.62** | 0.783* | 7.80** | 1.17* | 0.122** | 0.208** |
| **Hybrids vs. G80** | 1 | 3.08* | 1.57** | 5.78** | 2.33* | 0.218** | 0.224** |
| **Residual** | 1 | 8.16** | 0.011 | 9.81** | 0.005 | 0.025** | 0.192** |
| **Experimental error** | 6 | 0.310 | 0.113 | 0.309 | 0.185 | 0.002 | 0.005 |
| **Source of variation** | **df** | **Dry weight per boll (g)** | | **Harvest index (%)** | | **Number of seeds / boll** | |
| **Replications** | 3 | 0.003 | 0.004 | 0.013 | 0.087 | 0.476 | 2.05* |
| **Genotypes** | 2 | 0.069** | 0.033** | 0.122* | 0.053 | 4.22** | 1.05 |
| **Hybrids vs. G80** | 1 | 0.131** | 0.058** | 0.236* | 0.029 | 0.377 | 0.160 |
| **Residual** | 1 | 0.007 | 0.007 | 0.008 | 0.076 | 8.06** | 1.94* |
| **Experimental error** | 6 | 0.003 | 0.001 | 0.019 | 0.022 | 0.215 | 0.211 |
| **2010 Season** | | | | | | | |
| **Traits** | | **S. C. Y. (k/fed.)** | | **L. C. Y. (k/fed.)** | | **Boll weight (g)** | |
| **Source of variation** | **df** | **F. Pick** | **S. Pick** | **F. Pick** | **S. Pick** | **F. Pick** | **S. Pick** |
| **Replications** | 3 | 2.72** | 0.552** | 7.05** | 0.864** | 0.018** | 0.104** |
| **Genotypes** | 2 | 1.80** | 0.111** | 3.78** | 0.153 | 0.056** | 0.038 |
| **Hybrids vs. G80** | 1 | 3.57** | 0.167** | 7.44** | 0.265 | 0.001 | 0.043 |
| **Residual** | 1 | 0.038 | 0.054* | 0.115 | 0.042 | 0.110** | 0.033 |
| **Experimental error** | 6 | 0.082 | 0.007 | 0.114 | 0.081 | 0.001 | 0.014 |
| **Source of variation** | **df** | **Dry weight per boll (g)** | | **Harvest index (%)** | | **Number of seeds / boll** | |
| **Replications** | 3 | 0.019 | 0.003 | 0.097 | 0.141 | 2.11 | 2.17 |
| **Genotypes** | 2 | 0.078* | 0.070* | 0.267* | 0.160 | 6.96* | 6.85 |
| **Hybrids vs. G80** | 1 | 0.132** | 0.099* | 0.519** | 0.236 | 12.46* | 0.567 |
| **Residual** | 1 | 0.024 | 0.042 | 0.015 | 0.084 | 1.45 | 13.13* |
| **Experimental error** | 6 | 0.010 | 0.010 | 0.036 | 0.099 | 1.05 | 1.58 |
| **Total** | 11 | | | | | | |
| **Traits** | | **Total S. C. Y. (k/fed.)** | | **Total L. C. Y. (k/fed.)** | | | |
| **Source of variation** | **df** | **2009** | **2010** | **2009** | **2010** | | |
| **Replications** | 3 | 3.16** | 3.72 | 5.38** | 10.29** | | |
| **Genotypes** | 2 | 4.20** | 1.19 | 5.08** | 2.46* | | |
| **Hybrids vs. G80** | 1 | 0.254 | 2.19 | 0.767 | 4.90** | | |
| **Residual** | 1 | 8.14** | 0.183 | 9.40** | 0.018 | | |
| **Experimental error** | 6 | 0.162 | 0.450 | 0.158 | 0.338 | | |
| **Total** | 11 | | | | | | |
| **Two picks** | | | | | | | |
| **Traits** | | **S. C. Y. (k/fed.)** | | **L. C. Y. (k/fed.)** | | **Boll weight (g)** | |
| **Source of variation** | **df** | **2009** | **2010** | **2009** | **2010** | **2009** | **2010** |
| **Replications** | 3 | 1.89** | 2.77** | 3.10** | 5.76** | 0.051** | 0.102** |
| **Genotypes** | 2 | 2.10** | 0.593** | 2.54** | 1.23* | 0.311** | 0.080** |
| **Hybrids vs. G80** | 1 | 0.127 | 1.10** | 0.387* | 2.45** | 0.443** | 0.029 |
| **Residual** | 1 | 4.07 | 0.091 | 4.70* | 0.009 | 0.178** | 0.131** |
| **Experimental error** | 6 | 0.105 | 0.033 | 0.046 | 0.122 | 0.004 | 0.006 |
| **Between picks** | 12 | 27.69 | 44.70 | 43.19 | 76.28 | 0.282 | 0.320 |
| **12** | 4 | 39.85 | 49.18 | 61.07 | 86.68 | 0.211 | 0.408 |
| **13** | 4 | 23.86 | 48.81 | 38.73 | 81.87 | 0.353 | 0.296 |
| **G80** | 4 | 19.35 | 36.10 | 29.78 | 60.30 | 0.281 | 0.258 |

**Table (7): Cont.**

| **Traits** | | **Dry weight per boll (g)** | | **Harvest index (%)** | | **Number of seeds / boll** | |
|---|---|---|---|---|---|---|---|
| **Source of variation** | **df** | **2009** | **2010** | **2009** | **2010** | **2009** | **2010** |
| **Replications** | 3 | 0.006 | 0.014 | 0.067 | 0.033 | 1.84* | 1.86 |
| **Genotypes** | 2 | 0.098** | 0.147** | 0.116 | 0.407 | 0.780 | 10.41* |
| **Hybrids vs. G80** | 1 | 0.181** | 0.230** | 0.216* | 0.728* | 0.515 | 9.17 |
| **Residual** | 1 | 0.014 | 0.065* | 0.017 | 0.086 | 1.05 | 11.66 |
| **Experimental error** | 6 | 0.002 | 0.007 | 0.033 | 0.105 | 0.294 | 2.03 |
| **Between picks** | 12 | 0.025 | 0.028 | 0.037 | 0.124 | 6.05 | 3.62 |
| **12** | 4 | 0.019 | 0.020 | 0.012 | 0.210 | 1.55 | 2.92 |
| **13** | 4 | 0.020 | 0.034 | 0.086 | 0.112 | 11.17 | 6.98 |
| **G80** | 4 | 0.037 | 0.030 | 0.013 | 0.051 | 5.43 | 0.958 |
| **Total** | 23 | | | | | | |
| **Beni Souf (one pick)** | | | | | | | |
| **Traits** | | **Total S. C. Y. (k/fed.)** | | **Total L. C. Y. (k/fed.)** | | **Boll weight (g)** | |
| **Source of variation** | **df** | **2009** | **2010** | **2009** | **2010** | **2009** | **2010** |
| **Replications** | 3 | 1.04** | 4.57** | 1.52** | 7.64** | 0.087** | 0.127* |
| **Genotypes** | 2 | 0.408* | 0.270 | 0.684* | 0.237 | 0.033 | 0.124* |
| **Hybrids vs. G80** | 1 | 0.177 | 0.473 | 0.510 | 0.470 | 0.040 | 0.037 |
| **Residual** | 1 | 0.638* | 0.067 | 0.858* | 0.003 | 0.026 | 0.211* |
| **Experimental error** | 6 | 0.074 | 0.258 | 0.112 | 0.537 | 0.009 | 0.016 |
| **Source of variation** | **df** | **Dry weight per boll (g)** | | **Harvest index (%)** | | **Number of seeds / boll** | |
| **Replications** | 3 | 0.010 | 0.004 | 0.057 | 0.119 | 3.39 | 1.86 |
| **Genotypes** | 2 | 0.037* | 0.081* | 0.115* | 0.281* | 24.37** | 17.21** |
| **Hybrids vs. G80** | 1 | 0.074** | 0.158** | 0.198** | 0.468** | 14.25** | 0.760 |
| **Residual** | 1 | 0.006 | 0.003 | 0.031 | 0.095 | 34.49** | 33.66** |
| **Experimental error** | 6 | 0.004 | 0.008 | 0.013 | 0.029 | 0.871 | 1.11 |
| **Total** | 11 | | | | | | |

*** , ** Significant at 0.05 and 0.01 levels, respectively**

seed and lint yields in the first season and bollhybrids vs. G80 was recorded for dry weight per boll and harvest index in both seasons and the number of seeds / boll in the first season, (Table 7).

The hybrids significantly surpassed G80 in respect to harvest index in both seasons. G90 x Australian gave the highest value for number of seeds / boll, significantly exceeding G80 in both seasons. On the contrary G80 significantly surpassed both hybrids for dry weight per boll in both seasons, G90 x Australian for (seed and lint) yields in 2009 season and (G83 x (G75 x 5844)) x G80 for boll weight in 2010 season (Table 8).

**3.2.2 Analysis over locations (Second stage)**

The analysis of variance over the two locations (within G80 zone) in respect to seed and lint yields, boll weight, dry weight per boll, harvest index, number of seeds / boll and fiber properties revealed the presence of significant differences between genotypes and hybrids vs. G80 (Table 9).

Significant variation due to the genotypes was detected for seed and lint yields in the first season. Significant variation due to both genotypes and hybrids vs. G80 was observed for boll weight in the first season, dry weight per boll, harvest index and number of seeds / boll in both seasons. Hybrids significantly surpassed G80 with respect to harvest index in both seasons. (G83 x (G75 x 5844)) x G80 was the best genotypes for yields (seed and lint), it significantly exceeded G80 in 2009 season.

G90 x Australian gave the highest value for number of seeds / boll in both seasons, it significantly exceeded G80. On the contrary, G80 significantly surpassed two hybrids for dry weight per boll in both seasons, G90 x Australian for yields (seed and lint) and boll weight in the 2009 season (Table 10).

Results of analysis of variance over locations showed that (G83 x (G75 x 5844)) x G80 gave the lowest values of variance between locations for boll weight and dry weight per boll in the first season, harvest index in the second season, and number of seeds / boll in both seasons. G90 x Australian gave similar results for seed cotton yield and boll weight in the 2009 season. This explains that these hybrids were more stable than stable than the hybrids for lint cotton yield in both . G80. The results indicat that G 80 was more

**Table (8): Means of traits for individual locations.**

| Regional program | | | | | | |
|---|---|---|---|---|---|---|
| **Minya 2009 Season** | | | | | | |
| **Traits** | **S. C. Y. (k/fed.)** | | **L. C. Y. (k/fed.)** | | **Boll weight (g)** | |
| **Genotypes** | **F. Pick** | **S. Pick** | **F. Pick** | **S. Pick** | **F. Pick** | **S. Pick** |
| **12** | 10.13 √ | 1.24 x | 12.54 √ | 1.54 x | 2.90 x | 2.25 x |
| **13** | 8.09 | 1.25 x | 10.32 | 1.59 x | 2.78 x | 1.94 x |
| **Hybrids** | 9.11 √ | 1.25 x | 11.43 √ | 1.57 x | 2.84 x | 2.10 x |
| **G80** | 8.04 | 2.01 | 9.96 | 2.50 | 3.13 | 2.39 |
| **L.S.D.** | 0.96 | 0.58 | 0.96 | 0.74 | 0.07 | 0.13 |
| **Genotypes** | **Dry weight per boll (g)** | | **Harvest index (%)** | | **Number of seeds / boll** | |
| **12** | 1.00 x | 0.81 x | 2.90 √ | 2.78 | 16.11 x | 14.47 |
| **13** | 0.94 x | 0.75 x | 2.95 √ | 2.58 | 18.12 | 13.49 |
| **Hybrids** | 0.97 x | 0.78 x | 2.93 √ | 2.68 | 17.12 | 13.98 |
| **G80** | 1.20 | 0.93 | 2.61 | 2.58 | 17.49 | 14.23 |
| **L.S.D.** | 0.09 | 0.06 | 0.24 | -- | 0.80 | -- |
| **2010 Season** | | | | | | |
| **Genotypes** | **S. C. Y. (k/fed.)** | | **L. C. Y. (k/fed.)** | | **Boll weight (g)** | |
| **12** | 11.50 √ | 1.60 x | 15.25 √ | 2.13 | 2.87 √ | 1.99 |
| **13** | 11.64 √ | 1.77 x | 15.01 √ | 2.28 | 2.63 x | 1.86 |
| **Hybrids** | 11.57 √ | 1.69 x | 15.13 √ | 2.21 | 2.75 | 1.93 |
| **G80** | 10.41 | 1.93 | 13.46 | 2.52 | 2.77 | 2.05 |
| **L.S.D.** | 0.50 | 0.14 | 0.58 | -- | 0.05 | -- |
| **Genotypes** | **Dry weight per boll (g)** | | **Harvest index (%)** | | **Number of seeds / boll** | |
| **12** | 1.12 x | 0.96 | 2.54 √ | 2.10 | 18.92 √ | 17.13 |
| **13** | 1.02 x | 0.82 x | 2.62 √ | 2.30 | 18.07 | 14.57 |
| **Hybrids** | 1.07 x | 0.89 x | 2.58 √ | 2.20 | 18.50 √ | 15.85 |
| **G80** | 1.30 | 1.08 | 2.14 | 1.90 | 16.33 | 15.39 |
| **L.S.D.** | 0.17 | 0.18 | 0.33 | -- | 1.77 | -- |
| **Traits** | **Total S. C. Y. (k/fed.)** | | **Total L. C. Y. (k/fed.)** | | | |
| **Genotypes** | **2009** | **2010** | **2009** | **2010** | | |
| **12** | 11.37 √ | 13.10 | 14.08 √ | 17.38 √ | | |
| **13** | 9.34 x | 13.41 | 11.91 | 17.29 √ | | |
| **Hybrids** | 10.36 | 13.26 | 13.00 | 17.34 √ | | |
| **G80** | 10.05 | 12.34 | 12.46 | 15.98 | | |
| **L.S.D.** | 0.70 | -- | 0.69 | 1.01 | | |
| **Beni Souf (one pick)** | | | | | | |
| **Traits** | **Total S. C. Y. (k/fed.)** | | **Total L. C. Y. (k/fed.)** | | **Boll weight (g)** | |
| **Genotypes** | **2009** | **2010** | **2009** | **2010** | **2009** | **2010** |
| **12** | 7.04 | 9.21 | 9.16 | 12.01 | 2.47 | 2.57 x |
| **13** | 6.47 x | 9.39 | 8.51 x | 11.97 | 2.58 | 2.89 |
| **Hybrids** | 6.76 | 9.30 | 8.84 | 11.99 | 2.53 | 2.73 |
| **G80** | 7.01 | 8.88 | 9.27 | 11.57 | 2.65 | 2.85 |
| **L.S.D.** | 0.47 | -- | 0.58 | -- | -- | 0.22 |
| **Genotypes** | **Dry weight per boll (g)** | | **Harvest index (%)** | | **Number of seeds / boll** | |
| **12** | 0.97 x | 0.99 x | 2.55 √ | 2.59 √ | 16.38 | 16.79 |
| **13** | 0.97 x | 1.03 x | 2.68 √ | 2.81 √ | 20.53 √ | 20.90 √ |
| **Hybrids** | 0.97 x | 1.01 x | 2.62 √ | 2.70 √ | 18.46 √ | 18.85 |
| **G80** | 1.13 | 1.26 | 2.34 | 2.28 | 16.15 | 18.31 |
| **L.S.D.** | 0.11 | 0.15 | 0.20 | 0.30 | 1.61 | 1.82 |

**√,Hybrids significantly surpassed the control (G80).--: Not significant at 0.05 level.**
**x , G80 (control) significantly surpassed hybrids.**

**Table (9) : Mean squares of traits for two locations.**

| Regional program | | | | | | | |
|---|---|---|---|---|---|---|---|
| **Traits** | | **Total S. C. Y. (k/fed.)** | | **Total L. C. Y. (k/fed.)** | | **Boll weight (g)** | |
| **Source of variation** | **df** | **2009** | **2010** | **2009** | **2010** | **2009** | **2010** |
| **Replications** | 3 | 3.87** | 6.76** | 6.27** | 14.27** | 0.074** | 0.117** |
| **Genotypes** | 2 | 3.34** | 1.29 | 3.99** | 2.11 | 0.111** | 0.017 |
| **Hybrids vs. G80** | 1 | 0.004 | 2.35 | 0.013 | 4.20 | 0.223** | 0.025 |
| **Residual** | 1 | 6.67** | 0.235 | 7.97** | 0.018 | 0.006 | 0.008 |
| **Experimental error** | 6 | 0.089 | 0.615 | 0.066 | 1.12 | 0.004 | 0.008 |
| **Between locations** | 12 | 6.20 | 7.63 | 7.90 | 13.55 | 0.084 | 0.038 |
| **12** | 4 | 9.44 | 7.88 | 12.14 | 15.38 | 0.112 | 0.048 |
| **13** | 4 | 4.27 | 8.58 | 6.08 | 15.04 | 0.021 | 0.035 |
| **G80** | 4 | 4.88 | 6.45 | 5.48 | 10.22 | 0.118 | 0.032 |
| **Total** | 23 | | | | | | |
| **Source of variation** | **df** | **Dry weight per boll (g)** | | **Harvest index (%)** | | **Number of seeds / boll** | |
| **Replications** | 3 | 0.009 | 0.018 | 0.020 | 0.029 | 4.27** | 3.18* |
| **Genotypes** | 2 | 0.102** | 0.148** | 0.235** | 0.540** | 21.47** | 10.12** |
| **Hybrids vs. G80** | 1 | 0.200** | 0.290** | 0.433** | 0.986** | 4.99** | 9.68** |
| **Residual** | 1 | 0.003 | 0.005 | 0.036* | 0.093 | 37.95** | 10.56** |
| **Experimental error** | 6 | 0.002 | 0.012 | 0.006 | 0.042 | 0.236 | 0.505 |
| **Between locations** | 12 | 0.005 | 0.008 | 0.070 | 0.068 | 1.61 | 3.76 |
| **12** | 4 | 0.003 | 0.012 | 0.060 | 0.032 | 0.279 | 3.03 |
| **13** | 4 | 0.006 | 0.008 | 0.100 | 0.125 | 3.38 | 4.83 |
| **G80** | 4 | 0.005 | 0.003 | 0.049 | 0.047 | 1.17 | 3.44 |
| **Total** | 23 | | | | | | |
| | | **Fiber length (mm)** | | **Micronaire reading** | | **Yarn strength** | |
| **Rep. (locations)** | 1 | 0.202 | 0.042 | 0.027 | 0.002 | 12604 | 10004 |
| **Genotypes** | 2 | 1.20 | 1.42 | 0.072* | 0.052 | 44663 | 27630 |
| **Hybrids vs. G80** | 1 | 1.76 | 2.80 | 0.053* | 0.013 | 24303 | 40252 |
| **Residual** | 1 | 0.640 | 0.040 | 0.090* | 0.090 | 65024 | 15008 |
| **Experimental error** | 2 | 0.352 | 0.412 | 0.002 | 0.012 | 9653 | 3179 |
| **Total** | 5 | | | | | | |

***, ** Significant at 0.05 and 0.01 levels, respectively.**

**Table (10) : Means of traits of cotton genotypes for two locations.**

| Regional program | | | | | | |
|---|---|---|---|---|---|---|
| **Traits** | **Total S. C. Y. (k/fed.)** | | **Total L. C. Y. (k/fed.)** | | **Boll weight (g)** | |
| **Genotypes** | **2009** | **2010** | **2009** | **2010** | **2009** | **2010** |
| **12** | 9.21 √ | 11.16 | 11.62 √ | 14.70 | 2.69 x | 2.72 |
| **13** | 7.91 x | 11.40 | 10.21 x | 14.63 | 2.68 x | 2.76 |
| **Hybrids** | 8.56 | 11.28 | 10.92 | 14.67 | 2.69 x | 2.74 |
| **G80** | 8.53 | 10.61 | 10.87 | 13.78 | 2.89 | 2.81 |
| **L.S.D.** | 0.52 | -- | 0.44 | -- | 0.11 | -- |
| **Genotypes** | **Dry weight per boll g** | | **Harvest index (%)** | | **Number of seeds / boll** | |
| **12** | 0.99 x | 1.06 x | 2.72 √ | 2.57 √ | 16.25 | 17.86 |
| **13** | 0.96 x | 1.03 x | 2.82 √ | 2.72 √ | 19.33 √ | 19.49 √ |
| **Hybrids** | 0.98 x | 1.05 x | 2.77 √ | 2.65 √ | 17.79 √ | 18.68 √ |
| **G80** | 1.17 | 1.28 | 2.48 | 2.21 | 16.82 | 17.32 |
| **L.S.D.** | 0.07 | 0.19 | 0.13 | 0.35 | 0.84 | 1.23 |
| **Genotypes** | **Fiber length (mm)** | | **Micronaire reading** | | **Yarn strength** | |
| **12** | 30.60 | 29.90 | 4.2 | 3.9 | 2325 | 2243 |
| **13** | 29.80 | 30.10 | 4.5 √ | 4.2 | 2070 | 2120 |
| **Hybrids** | 30.20 | 30.00 | 4.4 √ | 4.1 | 2198 | 2182 |
| **G80** | 31.35 | 31.45 | 4.1 | 4.0 | 2333 | 2355 |
| **L.S.D.** | -- | -- | 0.2 | -- | -- | -- |

**√, Hybrids significantly surpassed G80 (control). -: Not significant at 0.05 level.- x , G80 (control) significantly surpassed hybrids.**

In respect to fiber properties, the analysis considered each location as one replicate due to test one sample (Table 9). Results of analysis fiber properties showed that no significant differences due to replications for fiber properties in indicating that these traits were more stable in different locations. This way of analysis was very important in regional program to estimate variation between locations when test one replicate. Significant variation due to both genotypes and hybrids vs. G80 were detected for micronair reading in the first season. G90 x Australian gave the highest value for micronaire reading, and significantly exceeded G80. Also, this way of analysis could be calculated genotypes variance under different locations when test one replicate

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## تقييم بعض التراكيب الوراثية من القطن المصري على مرحلتين


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**ملخص**

تم تقييم المحصول ومكوناته (صفات اللوزة) والصفات التكنولوجية لثلاثة عشر تركيب وراثي من القطن المصري داخل المنطقة المخصصة لزراعة الصنف التجاري جيزة 80 (المنيا - بنى سويف) موسمي 2009 ، 2010 طبقا للقرار الوزاري بتحديد مناطق زراعة أصناف القطن من خلال برنامجي التربية والتقييم الإقليمي بمعهد بحوث القطن بهدف التعاون والربط بين القسمين فى تقييم التراكيب الوراثية الجديدة من القطن المصري. تم استخدام تصميم القطاعات الكاملة العشوائية.

**أولا : قسم بحوث التربية**

تم تقييم 11 تركيب وراثي (هجن مبشرة في أجيال مختلفة) مع الصنف جيزة 80 في 6 مكررات (مساحة القطعة التجريبية 7.2 م$^2$) بالمنيا بهدف تحديد التراكيب الوراثية المتفوقة على الصنف المنزرع فى منطقة زراعة الصنف لاستمرارها فى البرنامج واستبعاد التراكيب الوراثية غير المتفوقة. تم إجراء تحليل إحصائي فى المرحلة الأولى بتقييم كل جيل على حده (مشاهدة واحدة فى الخلية) لتقدير تباين التراكيب الوراثية مع تقدير الاختلاف بين الهجن والصنف جيزة 80. ثم إجراء تحليل إحصائي فى المرحلة الثانية بتقييم للجيلين (أكثر من مشاهدة في الخلية) لتقدير التباين بين الجيلين لكل تركيب وراثي على حده للاستفادة به فى برنامج التربية. و أظهرت النتائج تفوق الهجن معنويا على الصنف جيزة 80 في المحصول الزهر والشعر والتبكير ماعدا جـ 90 x بيما س 62 (24240) ، (جـ 83 x بيما س 6) x دندرة ، (جـ 83 x (جـ 75 x 5844)) x جـ85 ، جـ 91 x جـ 80 بالنسبة للتبكير.

**ثانيا : قسم التقييم الإقليمي**

تم تقييم (2) تركيب وراثي في المراحل النهائية من برنامج التربية (مخلوط عائلات) مع الصنف جيزة 80 في 4 مكررات (مساحة القطعة التجريبية كبيرة 52 م$^2$ ، 62.4م$^2$ في الموسم الأول و الثاني على التوالي) بالمنيا وبنى سويف بهدف تحديد التركيب الوراثي المتفوق على الصنف المنزرع ومدى نجاحه في التفاعل فى منطقة زراعة الصنف تمهيدا لزراعته بدلا منه. تم إجراء تحليل إحصائي في المرحلة الأولى لكل موقع على حده (مشاهدة واحدة فى الخلية) لتقدير تفاعل التراكيب الوراثية في الموقع لتحديد المتفوق منها. ثم تحليل إحصائي فى المرحلة الثانية للموقعين (أكثر من مشاهدة في الخلية) لتقدير التباين بين المواقع لكل تركيب وراثى على حده لتحديد المتفوق منها فى منطقة زراعة الصنف. وأوضحت النتائج أن (جـ 83 x (جـ 75 x 5844)) x جـ80 أظهر تباينا بين المواقع من حيث أقل من الصنف جيزة جـ 80 بالنسبة إلى وزن اللوزة ، الوزن الجاف للوزة فى الموسم الأول ، دليل الحصاد فى الموسم الثاني ، عدد البذور باللوزة في الموسمين. وكذلك أظهر جـ 90 x أسترالي نفس النتائج بالنسبة إلى المحصول الزهر ، وزن اللوزة في الموسم الأول ، بينما أظهر الصنف جـ 80 تباين بين المواقع أقل من الهجن بالنسبة إلى محصول القطن الشعر في الموسمين.

و**يستفاد من هذه الدراسة فى برامج قسمي التربية والتقييم بالآتي:**

1 – تحديد التراكيب الوراثية المبشرة التي تتفوق على الأصناف المنزرعة.

2 – تقدير التباين بين جيلين أو موقعين لكل تركيب وراثي على حده .

3- إدخال طرق تحليل إحصائي في برامج التربية و التقييم لتقدير التباين بين التراكيب الوراثية.

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