

GENETIC BASIS FOR VARIABILITY OF SEED PROPERTIES AND SOME ASSOCIATED TRAITS AMONG EXTRA-LONG STAPLE COTTON GENOTYPES IN EGYPT

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Abstract

The expression of seed characteristics would facilitate further improvement of cotton seed properties in breeding programme. Thus, this research aimed to estimate genotypic and phenotypic coefficients of variation, heritability, correlation coefficient and genetic diversity of extra long staple Egyptian cotton genotypes. All genotypes were grown at two locations, El-Behera and Domietta governorates during 2002 and 2003 seasons. The results revealed that the differences among the genotypes were highly significant for all studied traits. Significant interactions between genotypes and locations were found for most studied characters.

Highly significant positive correlations were recorded between both seed cotton yield and embryo index, seed index, seed density, seed protein %, seed protein index and seed oil index. Also, significant positive correlation between seed cotton yield with germination %, embryo % and seed oil %, while significant negative correlation was obtained with earliness % and seed coat %. Significant positive correlations between chemical seed qualities, seed oil %, seed oil index, seed protein %, embryo protein % and physical seed properties, embryo index, seed index, 100-seed volume and embryo %.

The heritability estimates were high for seed coat protein %, moisture content %, seed oil %, seed free fatty acid, embryo acid value and embryo index and 100- seed volume. Moderate h^2 were recorded for seed index, seed density and embryo oil index, while it was low for the other seven traits. Very close estimates of genotypic and phenotypic coefficients of variation are used for assessment of variability for boll weight, embryo free fatty acid and embryo acid value.

The studied genotypes were divided into two clusters with similarity index (36.99%) and distance level (8.98). The first cluster group hybrid (G.68×G.45) × ((G.84 ×G.45) × G.45). The two-cluster group divided into two subgroups, the first of them represented the genotype (G.84 × F. 108) × ((G. 84 ×G.45) × G.45) and the commercial variety G. 70, While the second included the other genotypes with a similarity index of (71.52%) and distance level of (4.06).

INTRODUCTION

The basic genetic principles have in fact systematized the science of plant breeding. In Egypt, the breeding programme to improve cotton seed quality required three prerequisites. 1) a variability of sufficient genetic materials (germplasm or local

varieties. 2) appropriate breeding methods. 3) effective testing and evaluation facilitates to produce desirable new combinations for breeding high seed quality.

A few previous researches studied variability and genetic estimates for cotton seed quality and associated traits. Abo El-Zahab *et al.* (1992) found high broad sense heritability estimates for seed oil percentage and seed oil index. In addition, they reported significant negative correlation among embryo oil percentage and embryo index. Abo El-Zahab *et al.* (2003) stated that negative significant values for phenotypic and genotypic correlation of oil and protein in seed. However, seed oil index was significantly positively correlated with protein percentage and index. The correlation coefficient of seed protein index with each of seed oil percentages in seed and embryo were insignificant. Badr and Soad (2004) in five Extra Long Staple cottons found that seed oil and crude protein % ranged from 21.5-26.80 and 20.74-27.19%. Hence this study was initiated to determine the following aspects. 1) genotypic and phenotypic coefficient of variations. 2) assessment of 19 cotton genotypes for their seed quality traits to determine the best potential as source material for breeding high seed quality genotypes. 3) estimation of variance components. 4) estimation of correlation coefficient between studied traits. 5) determination of the genetic diversity between these genotypes.

MATERIALS AND METHODS

Genetic materials and experimental procedures

Nineteen extra long cotton genotypes of the breeding programme in Egypt were evaluated at two locations (El-Behera and Domeitta governorates) in 2002 and 2003 seasons, four of them only were commercial releases developed for north Delta, the other fifteen genotypes represent advanced promising hybrids. These genotypes are partially described in Table (1) Seeds of the parental genotypes were grown in a randomized complete block design experiment with four replications in each location. Each replication included five row 4m long and 60cm. apart. The distance between hills was 25 cm. At seedling stage, were thinned to two plants per hill. All agricultural practices were as recommended by Cotton Research Institute for the two locations.

Table 1. Code numbers, genotypes and origin.

| Code | Genotypes | Origin |
|------|---|---------------------------|
| 1 | (G .68×G. 45) × ((G.84 ×G. 45) × G.45) | C ₅ 1122/2001 |
| 2 | (G.84 × F. 108)×((G. 84 ×G.45) × G.45) | C ₅ 1143/2001 |
| 3 | (G.84 × F. 108)×((G. 84 ×G.45) × G.45) | C ₅ 1153/2001 |
| 4 | (G.84 × G .70) × (G .45 × Sea Island) | C ₆ 1157/2001 |
| 5 | (G.76 × G. 77) × G.87 | C ₆ 1176/2001 |
| 6 | (G.76 × G .77) × G.87 | C ₆ 1189/2001 |
| 7 | G.87 × (G. 71 × G. 74) | C ₇ 1198/2001 |
| 8 | G .70 × Pima S ₆ | C ₁₀ 1222/2001 |
| 9 | (G. 77 × Pima S ₆) × (G. 87 × (G.77 × G. 70)) | C ₁₀ 1238/2001 |
| 10 | G .77 × Pima S ₆ | C ₁₁ 1261/2001 |
| 11 | G .77 × Pima S ₆ | C ₁₁ 1262/2001 |
| 12 | G .77 × Pima S ₆ | C ₁₁ 1266/2001 |
| 13 | G .87 × (G.77 × G. 70) | C ₁₁ 1284/2001 |
| 14 | G.77 × (G.84 × (G.70× G.51 B)) | C ₃ 1293/2001 |
| 15 | G.84 × (G.74 × G. 68) | G.84 × (G.74 × G. 68) |
| 16 | G.87 | G .77 × G .45 A |
| 17 | G .88 | G .77 × G. 45 B |
| 18 | G .45 | G. 28 × G. 7 |
| 19 | G .70 | G .59 A × G. 51 B |

The three central rows of each plot were hand harvested to determine seed cotton yield (K/F). Random sample of 50 open bolls harvested from outer two rows was used to obtain boll weight. Earliness % was estimated according to the following formula.

$$\text{Earliness \%} = \text{weight of first harvesting} / (\text{total weight of the two harvesting}) \times 100$$

Physical properties of cotton seed

- Seed index and seed volume: One hundred seeds were counted and weighted. Then their volume was measured by the absolute displacement method (Kramer and Twigg, 1962).
- Seed density: was calculated according to Kramer and Twigg, (1962) as follows:

Seed density = Ratio of seed index to 100- seed volume

$$.g/cm^3 = \frac{100 - seeds(g.)}{100 - seeds(mm^3)} = gm/mm^3$$

- Seed coat: One hundred-gram of seeds of both samples was decorticated. The decorticated seeds and seed coats were weighed separately (Shehata et al., 1985). Percentage of seed coat was calculated as follows:

$$- \text{Seed coat \%} = \frac{\text{Wt. of seed coats (g.)}}{\text{Wt. of seed coat + wt. of decorticated seeds}} \times 100$$

- Embryo percentage: 100 seeds were separated into seed coat and embryo to determine embryo percentage
- Embryo index (weight of embryo in 100 seeds)
- Standard germination: test was carried out under optimum conditions according to International rules for Seed Testing Association (ISTA, 1999).
- Seed vigor, the standard germination test outlined by the International rules for Seed Testing Association (ISTA, 1999) was used.

Chemical composition properties of cotton seed:

Seed samples were taken at random from each plot and ground to fine powder to pass through two mm mesh for chemical analysis, i.e. moisture content, seed oil percentage, embryo oil percentage, seed protein percentage, embryo protein percentage, seed coat protein percentage, seed free fatty acid (F.F.A) percentage, embryo free fatty acid, seed acid value (A.V), embryo acid value were determined according to procedures outlined in AOAC (1990)

- Seed- oil index = seed oil % × seed index /100
- Seed- protein index = seed protein % × seed index /100

Statistical procedures:

Analysis of variance was carried out as a combined analysis for the two locations and two years according to Senedcor and Cochran. (1982). Least significant difference test (L.S.D) was used to detect differences between genotypes means. The variance components were calculated according to Miller *et al.* (1959). The form of analysis of variance and the composition of the mean square of interest by the following formula.

$$\text{Genotypes } (\sigma^2_g) = \frac{(M_5 + M_2 - M_4 - M_3)}{rly}$$

$$\text{Genotypes } \times \text{ locations } (\sigma^2_{gl}) = (M_4 - M_2) / r y$$

$$\text{Genotypes } \times \text{ years } (\sigma^2_{gy}) = (M_3 - M_2) / r e$$

$$\text{Genotypes } \times \text{ locations } \times \text{ years } = (\sigma^2_{gly}) = (M_2 - M_1) / r$$

$$\text{Plot error } \sigma^2_e = M_1$$

Where M_1, \dots, M_5 are the values of the appropriate mean squares as indicated in Table 2, and r , e and y are the number of replications, locations and years, respectively.

Table 2. Form of the combined analysis of variance and expectations of mean square for all genotypes over years and locations.

| S.O.V. | d.F | M.S | EMS |
|--------------------|-----------------|-------|--|
| Years | Y-1 | | |
| Locations | L-1 | | |
| Reps/yea.and loca. | YL (R-1) | | |
| Genotypes | (G-1) | M_5 | $\sigma^2e + r\gamma\sigma^2g + r\gamma\sigma^2gy + r\gamma\sigma^2g + r\gamma\sigma^2g$ |
| Genotypes x years | (Y-1) (G-1) | M_4 | $\sigma^2e + r\gamma\sigma^2gy + r\gamma\sigma^2g$ |
| Genotypes x loca. | (L-1) (G-1) | M_3 | $\sigma^2e + r\gamma\sigma^2g + r\gamma\sigma^2g$ |
| Gen. x yea.x loca. | (Y-1)(L-1)(G-1) | M_2 | $\sigma^2e + r\gamma\sigma^2g$ |
| Error | YL (R-1) (G-1) | M_1 | σ^2e |

Where: G is number of genotypes in number of environments, M_5, M_4, M_3, M_2 and M_1 are the mean squares of genotypes gen.x yea., gen. x loca., gen. x yea. x loca. and error respectively.

The phenotypic variance were estimated by the following formula as outlined by Miller *et al* (1959) and Comstock and Mull (1963)

$$\sigma^2 p = \sigma^2 g + \frac{\sigma^2 gl}{l} + \frac{\sigma^2 gy}{Y} + \frac{\sigma^2 gly}{lY} + \frac{\sigma^2 e}{rly}$$

Heritability (H^2) were calculated as: $H^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$

$$\text{Genotypic coefficient of variation \% (GCV \%)} = \frac{\sigma^2 g}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variation \% (PCV \%)} = \frac{\sigma^2 p}{\bar{X}} \times 100$$

Correlations coefficients were estimated while, similarity and taxonomic distance were calculated by hierarchical clustering analysis, (Anderberg1973)

RESULTS AND DISCUSSION

I. Analysis of variance

The combined analysis of variance over environments indicated that the differences among the nineteen Extra Long genotypes studied and the mean square of location were highly significant for all characters Table 3, indicating broad spectrum of genetic variability for all 23 characters. Such variability in physical properties in

Egyptian cotton germplasm was detected by Abo El-Zahab *et al* (2003). The genotypes \times locations interaction was highly significant for all studied characters but was insignificant for seed cotton yield and earliness %, indicating that differences between means were unstable under two locations. On the other hand, the mean squares of years, the two first order interactions between years with genotypes and locations, In addition, the second order interaction of genotypes \times locations \times years were insignificant for most studied characters, indicating, that although environment influences were high the genotypes differed and maintained their rank across environments.

Table 3. Mean squares for 23 characteristics of 19 genotypes combined over 2 years& 2 locations

| S. O.V. | D. F. | Boll weight | S.C.Yk/F | Earliness% | Germination % | Storability% | Embryo Index | Weight 100 seed | Volume 100 seed | Relative density | Embryo % | Seed coat % | Seed protein % | Seed coat protein % | Embryo protein % | Seed protein Index | Moisture % | Seed oil % | Embryo oil % | Seed oil Index | Seed F.F.A | Embryo F.F.A | Seed A.V | Embryo A.V |
|---------------|-------|-------------|-----------|-------------|---------------|--------------|--------------|-----------------|-----------------|------------------|------------|-------------|----------------|---------------------|------------------|--------------------|------------|------------|--------------|----------------|------------|--------------|------------|------------|
| Location (L) | 1 | ** 0.095 | ** 9.127 | ** 20643.51 | ** 84.211 | ** 531.592 | ** 190.106 | ** 376.759 | ** 480.013 | ** 0.017 | ** 288.308 | ** 282.61 | ** 5.925 | ** 2.732 | ** 1278.872 | ** 24.664 | ** 0.949 | ** 268.088 | ** 162.601 | ** 46.16 | ** 0.062 | ** 0.001 | ** 0.193 | ** 0.034 |
| R(L.Y) | 12 | N.S 0.003 | ** 0.625 | N.S 137.68 | ** 25.219 | N.S 21.022 | N.S 0.034 | N.S 0.156 | N.S 0.296 | N.S 0.0001 | N.S 0.293 | N.S 0.491 | N.S 0.259 | N.S 0.187 | N.S 1.174 | N.S 0.004 | N.S 0.029 | N.S 0.388 | N.S 0.276 | N.S 0.001 | N.S 0.0001 | N.S 0.0001 | N.S 0.0001 | N.S 0.0001 |
| Year (Y) | 1 | ** 0.914 | ** 8.608 | ** 12417.05 | N.S 0.329 | N.S 0.474 | N.S 0.004 | ** 0.579 | ** 2.293 | N.S 0.001 | N.S 0.306 | N.S 0.681 | N.S 0.507 | N.S 0.0001 | N.S 0.001 | N.S 0.001 | * | N.S 0.658 | N.S 0.177 | N.S 0.004 | N.S 0.0001 | N.S 0.0001 | N.S 0.002 | N.S 0.002 |
| LxY | 1 | N.S 0.0001 | ** 38.287 | ** 38598.40 | N.S 0.329 | N.S 25.474 | * | 0.492 | N.S 0.200 | N.S 0.0001 | N.S 2.168 | N.S 3.066 | N.S 0.114 | N.S 0.80 | N.S 0.980 | N.S 0.001 | N.S 0.0001 | N.S 0.056 | N.S 0.036 | N.S 0.001 | N.S 0.0001 | N.S 0.0001 | N.S 0.0001 | N.S 0.001 |
| Genotypes (G) | 18 | ** 0.020 | ** 1.030 | ** 260.81 | ** 166.054 | ** 482.84 | ** 1.151 | ** 2.467 | ** 12.461 | ** 0.042 | ** 13.777 | ** 40.759 | ** 17.226 | ** 164.199 | ** 0.377 | ** 2.178 | ** 36.576 | ** 14.024 | ** 0.494 | ** 0.028 | ** 0.033 | ** 0.118 | ** 0.132 | ** 0.009 |
| LxG | 18 | * 0.018 | N.S 0.257 | N.S 74.36 | ** 105.912 | N.S 239.543 | N.S 0.454 | ** 1.101 | ** 4.857 | ** 0.025 | ** 10.726 | ** 9.943 | ** 31.074 | ** 4.976 | ** 107.992 | ** 0.563 | ** 0.773 | ** 14.051 | ** 16.391 | ** 0.230 | ** 0.015 | ** 0.002 | ** 0.051 | ** 0.009 |
| YxG | 18 | N.S 0.012 | ** 0.479 | ** 254.59 | N.S 4.669 | N.S 4.883 | N.S 0.032 | ** 0.297 | * | * | N.S 0.588 | N.S 0.662 | N.S 0.303 | N.S 0.070 | N.S 0.802 | N.S 0.001 | N.S 0.035 | N.S 0.089 | N.S 0.161 | N.S 0.002 | N.S 0.0001 | N.S 0.001 | N.S 0.0001 | |
| LxYxG | 18 | ** 0.026 | N.S 0.249 | N.S 102.86 | N.S 2.933 | N.S 2.939 | N.S 0.029 | ** 0.228 | ** 0.834 | ** 0.002 | N.S 0.827 | N.S 0.787 | N.S 0.307 | N.S 0.066 | N.S 0.836 | N.S 0.001 | N.S 0.038 | N.S 0.121 | N.S 0.265 | N.S 0.002 | N.S 0.0001 | N.S 0.001 | N.S 0.001 | |
| Error | 216 | 0.010 | 0.193 | 67.462 | 7.877 | 12.531 | 0.021 | 0.097 | 0.290 | 0.001 | 0.727 | 0.765 | 0.368 | 0.132 | 2.071 | 0.005 | 0.031 | 0.152 | 0.164 | 0.002 | 0.0001 | 0.0001 | 0.001 | 0.001 |

*: Significant at 0.05 level of probability.
 **: Significant at 0.01 level of probability
 n.s : Not significant.

Table 4. Mean values of 19 genotypes for yield, its components, physiological and physical traits.

| Genotypes | Boll weight | S.C.Y. k/f | Earliness % | Germination % | Storability% | Embryo index | Seed Index | Volume-100 seeds | Seed density | Embryo % | Seed coat % |
|-----------|-------------|---------------|----------------|------------------|--------------|-----------------|------------|---------------------|--------------|-------------|-------------|
| 1 | 2.94 | 6.06 | 50.51 | 94.70 | 85.00 | 5.67 | 9.37 | 11.84 | 0.79 | 60.97 | 39.03 |
| 2 | 2.97 | 5.75 | 52.59 | 93.40 | 77.50 | 6.02 | 10.16 | 13.91 | 0.73 | 59.35 | 40.65 |
| 3 | 3.00 | 7.61 | 49.80 | 96.30 | 87.80 | 6.16 | 10.13 | 12.25 | 0.84 | 60.77 | 39.23 |
| 4 | 2.97 | 7.26 | 57.47 | 95.60 | 84.40 | 6.67 | 10.70 | 12.99 | 0.83 | 62.03 | 37.99 |
| 5 | 2.98 | 7.60 | 57.62 | 92.80 | 82.80 | 6.49 | 10.54 | 12.80 | 0.83 | 61.72 | 38.28 |
| 6 | 2.99 | 6.85 | 60.01 | 96.90 | 86.90 | 6.23 | 10.13 | 12.26 | 0.83 | 61.09 | 38.91 |
| 7 | 2.97 | 8.81 | 57.84 | 96.60 | 86.60 | 6.53 | 10.35 | 13.15 | 0.79 | 62.87 | 37.21 |
| 8 | 2.99 | 6.82 | 62.84 | 95.60 | 81.90 | 6.53 | 10.67 | 14.01 | 0.75 | 61.70 | 38.30 |
| 9 | 2.96 | 8.06 | 65.26 | 99.40 | 93.80 | 5.87 | 9.43 | 10.71 | 0.89 | 61.72 | 38.47 |
| 10 | 3.04 | 7.85 | 57.55 | 90.60 | 78.80 | 6.16 | 10.11 | 10.91 | 0.93 | 60.71 | 39.29 |
| 11 | 3.01 | 7.87 | 56.74 | 93.10 | 76.60 | 6.06 | 9.98 | 11.39 | 0.88 | 60.46 | 39.54 |
| 12 | 3.04 | 7.77 | 59.42 | 88.10 | 74.40 | 6.14 | 10.15 | 11.82 | 0.85 | 60.91 | 39.09 |
| 13 | 3.04 | 7.53 | 56.64 | 96.90 | 89.40 | 6.12 | 9.81 | 11.84 | 0.83 | 62.20 | 37.80 |
| 14 | 3.04 | 8.73 | 53.89 | 94.40 | 77.80 | 6.14 | 9.96 | 12.09 | 0.82 | 61.61 | 38.39 |
| 15 | 2.96 | 7.85 | 61.70 | 98.10 | 77.50 | 6.33 | 10.19 | 12.96 | 0.79 | 62.16 | 37.84 |
| 16 | 2.98 | 7.88 | 59.92 | 98.10 | 89.10 | 5.96 | 9.52 | 12.48 | 0.76 | 61.88 | 38.12 |
| 17 | 2.98 | 8.41 | 56.43 | 91.90 | 80.60 | 6.13 | 9.95 | 12.11 | 0.82 | 61.10 | 38.90 |
| 18 | 3.03 | 5.76 | 59.04 | 88.40 | 74.90 | 6.09 | 9.71 | 13.09 | 0.74 | 62.79 | 37.11 |
| 19 | 3.08 | 6.84 | 58.08 | 97.80 | 84.40 | 5.70 | 9.54 | 12.17 | 0.78 | 59.75 | 40.25 |
| F | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** |
| LSD | 0.07 | 0.31 | 5.72 | 1.96 | 2.47 | 0.10 | 0.22 | 0.38 | 0.02 | 0.59 | 0.61 |

(**P < 0.01)

II. Mean performance

The data in Tables 4 and 5 indicated the mean performances of 23 traits affected by cotton genotypes in two locations and two seasons. For yield and its components, Giza 88 expressed the highest mean value for boll weight followed by the four hybrids G.84 × (G.74 × G.68), G.77 × (G.84 × (G.70 × G.51B)), G.87 × (G.77 × G.70) and G.77 × Pima S₆, while the hybrid (G.68 × G.45) × ((G.84 × G.45) × G.45) recorded the lowest mean value. The highest mean values for seed cotton yield and earliness % were recorded by the promising hybrid G.77 × Pima S₆ followed by the promising hybrid G.84 × (G.74 × G.68), while the lowest mean value for these traits were recorded by the hybrid (G.68 × G.45) × ((G.84 × G.45) × G.45) for seed cotton yield and by (G.84 × F.108) × ((G.84 × G.45) × G.45) for earliness %.

Concerning physiological characters, the highest mean values for germination % and storability were attained by the promising hybrid G.77 × Pima S₆ while, the lowest mean value were recorded by the hybrid G.87 × (G.77 × G.70).

Regarding physical properties of cotton seed, the highest mean values for seed and embryo indices were reached by the genotype G.76 × (G.77 × G.87), meanwhile the lowest mean values were possessed by the genotype (G.68 × G.45) × ((G.84 × G.45) × G.45). The highest mean values for 100-seeds volume were obtained by the genotype G.70 × Pima S₆ followed by the genotype (G.84 × F.108) × ((G.84 × G.45) × G.45). The highest mean values for seed density and embryo % were recorded by the promising hybrid G.77 × Pima S₆ and the old variety G.45, respectively.

For chemical composition properties, the commercial variety G.70 and the genotype (G.84 × F.108) × ((G.84 × G.45) × G.45) surpassed all genotypes for seed protein % whereas the genotype G.87 × (G.71 × G.74) recorded the lowest mean value. The highest mean values for oil index was recorded by the genotype G.70 × Pima S₆. The genotype G.87 × (G.77 × G.70) was the best for embryo and seed oil %, meanwhile, the lowest mean value for these traits was recorded by (G.77 × Pima S₆) × (G.87 × (G.77 × G.70)). The genotype G.77 × (G.84 × (G.70 × G.51 B)) recorded the highest value for embryo protein %, seed and embryo free fatty acid % and embryo A.V. The genotypes (G.84 × G.70) × (G.45 × Sea Island), (G.77 × Pima S₆) × (G.87 × (G.77 × G.70)) and G.84 × (G.74 × G.68) attained the highest values for seed coat protein %, moisture % and seed acid value, respectively.

III. Correlations

Correlation coefficient among various traits is shown in Table 6. For yield and its components, seed cotton yield had a highly significant positive correlation with embryo index, seed index, seed density, embryo protein %, seed protein index and seed oil index. Significant positive correlations of seed cotton yield with germination %, embryo % and seed oil % were also observed. Significant negative correlations were recorded between seed cotton yield and seed coat %, embryo oil % and earliness %

which indicated that with an increase in seed cotton yield there would be a considering decline in these traits. The magnitude of correlation coefficients between seed cotton yield and embryo index, seed index and seed oil index were found to be very high. Thus, these traits appeared to be the most important components of seed cotton yield. Earliness % showed highly significant positive correlations with physical seed properties (embryo index, seed index, 100- seed volume, embryo %) and seed quality traits (embryo protein %, seed protein index, seed oil % and seed oil index, this suggests that selection for increased earliness % will result in substantial increases for these traits.

The results showed that the physiological traits, germination % and storability which were positively associated with seed physical properties (embryo index, seed index, seed density and embryo %, in addition to seed quality traits (seed protein and oil index). Among physical cotton seed properties, seed index, seed volume, seed density and embryo % were positively correlated with them, but was negatively correlated with seed coat %, indicating that all associations among physical property measurements were in the desired direction from the point of view of cotton breeder, yet at the expense of decreased seed coat %. Similar associations were reported among embryo % and embryo index by Abo El-Zahab *et al.* (1992).

As for seed quality properties, the results in Table (6) showed highly significant positive correlation between seed oil %, seed oil index, seed protein % and embryo protein % with physical seed traits, embryo index, seed index, seed volume, embryo %. Very high magnitudes of genotypic correlations of seed protein index with embryo index, seed index and seed volume were observed. Also seed oil % with seed volume and seed protein index suggested that the genes governing these traits were linked. These results were in harmony with those obtained by Abo El-Zahab *et al.*(1992) and Abo El-Zahab *et al.* (2003). Moisture % was negatively associated with seed coat %, embryo index, seed index, seed volume and seed density. Also embryo oil % showed negative relationship with embryo index, seed index, seed volume, embryo %, seed protein % and seed protein index. Significant negative correlations between embryo oil % and these traits revealed that on increase in embryo oil % would result in declines for these traits. Seed free fatty acid % and acid value were positively correlated with embryo index, seed index, seed volume, seed oil index and seed oil %, positive correlations were observed between seed index and seed oil % by Singh and Singh (1985). However, it had inverse correlation with seed density and embryo oil %. Embryo free fatty acid failed to register significant positive correlations with any of the attributes except seed density, embryo protein and seed free fatty acid. In general, seed and embryo acid value, seed and embryo free fatty acid had low correlation with most traits. The characters association may be attributed to both linkage and pleiotropic effects, hence the hybridization procedures could be successful in breaking this linkage.

Table 5. Mean values of 19 genotypes for chemical characters oil quality.

| | Seed protein % | Seed coat protein % | Embryo protein% | Seed protein index | Moisture% | Seed oil% | Embryo oil % | Seed oil index | Seed FFA% | Embryo FFA% | Seed A V | Embryo A V |
|-----|----------------|---------------------|-----------------|--------------------|-----------|-----------|--------------|----------------|-----------|-------------|----------|------------|
| 1 | 25.65 | 4.12 | 50.35 | 2.41 | 9.90 | 25.69 | 39.04 | 2.42 | 0.4033 | 0.3308 | 0.8131 | 0.6608 |
| 2 | 26.95 | 4.14 | 53.68 | 2.71 | 9.82 | 24.15 | 37.20 | 2.51 | 0.4103 | 0.2647 | 0.8182 | 0.5324 |
| 3 | 24.05 | 5.05 | 53.55 | 2.55 | 9.91 | 26.13 | 39.08 | 2.65 | 0.4135 | 0.3513 | 0.8185 | 0.7048 |
| 4 | 24.11 | 7.33 | 51.83 | 2.57 | 9.64 | 26.66 | 38.19 | 2.88 | 0.4057 | 0.2771 | 0.8141 | 0.5550 |
| 5 | 24.46 | 6.58 | 58.28 | 2.51 | 9.95 | 26.18 | 38.57 | 2.78 | 0.4115 | 0.2914 | 0.8339 | 0.5817 |
| 6 | 23.51 | 4.73 | 57.79 | 2.38 | 9.08 | 24.34 | 38.00 | 2.50 | 0.2820 | 0.2665 | 0.5644 | 0.5316 |
| 7 | 21.96 | 5.08 | 56.83 | 2.31 | 8.97 | 26.18 | 39.67 | 2.75 | 0.4151 | 0.3865 | 0.8315 | 0.7734 |
| 8 | 25.52 | 5.92 | 57.56 | 2.69 | 9.52 | 27.76 | 37.54 | 2.96 | 0.3804 | 0.2785 | 0.7702 | 0.5599 |
| 9 | 22.76 | 4.81 | 55.52 | 2.21 | 10.43 | 23.21 | 36.36 | 2.30 | 0.3852 | 0.2735 | 0.7785 | 0.5407 |
| 10 | 22.64 | 4.95 | 55.12 | 2.32 | 10.14 | 24.73 | 38.42 | 2.52 | 0.3397 | 0.3067 | 0.6781 | 0.5731 |
| 11 | 24.67 | 5.29 | 58.76 | 2.49 | 10.05 | 25.60 | 37.52 | 2.59 | 0.3924 | 0.3422 | 0.7934 | 0.6075 |
| 12 | 22.46 | 4.43 | 58.54 | 2.35 | 9.99 | 24.55 | 37.49 | 2.51 | 0.3864 | 0.3210 | 0.8087 | 0.6671 |
| 13 | 25.36 | 3.90 | 60.46 | 2.53 | 9.51 | 29.36 | 39.84 | 2.90 | 0.3394 | 0.2596 | 0.6796 | 0.5182 |
| 14 | 26.27 | 4.65 | 61.54 | 2.58 | 9.52 | 26.52 | 37.28 | 2.64 | 0.4382 | 0.3677 | 0.8888 | 0.7762 |
| 15 | 23.60 | 4.68 | 52.20 | 2.44 | 9.44 | 28.29 | 37.54 | 2.71 | 0.4290 | 0.2365 | 0.8458 | 0.4619 |
| 16 | 22.03 | 2.95 | 51.09 | 2.13 | 9.67 | 25.67 | 38.78 | 2.46 | 0.3924 | 0.2315 | 0.7914 | 0.4591 |
| 17 | 25.76 | 4.91 | 55.87 | 2.56 | 9.93 | 25.90 | 38.00 | 2.59 | 0.2970 | 0.2641 | 0.5881 | 0.5217 |
| 18 | 24.30 | 4.48 | 56.17 | 2.34 | 9.44 | 25.39 | 37.16 | 2.48 | 0.3734 | 0.3014 | 0.7527 | 0.5680 |
| 19 | 27.13 | 4.51 | 52.81 | 2.55 | 9.33 | 27.53 | 37.12 | 2.63 | 0.4056 | 0.2798 | 0.8127 | 0.5693 |
| F | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** |
| LSD | 0.42 | 0.25 | 1.0 | 0.05 | 0.12 | 0.27 | 0.28 | 0.03 | 0.0069 | 0.0069 | 0.0220 | 0.0220 |

(**P < 0.01)

Table 6. Correlation coefficients between studied characters of nineteen extra-long Egyptian cotton genotypes combined over two years and two locations.

| Variable | X2 | X3 | X4 | X5 | X6 | X7 | X8 | X9 | X10 | X11 | X12 | X13 | X14 | X15 | X16 | X17 | X18 | X19 | X20 | X21 | X22 | X23 |
|--------------------------------|--------|--------|--------|--------|--------|--------|---------|---------|--------|---------|---------|---------|---------|---------|---------|---------|---------|---------|--------|---------|---------|---------|
| Germination % (X1) | 0.54** | 0.14* | 0.10 | -0.02 | 0.18** | 0.20** | -0.18** | 0.06 | -0.06 | -0.06 | 0.15** | -0.16** | 0.13* | -0.03 | 0.14* | 0.03 | -0.16** | -0.01 | -0.11 | -0.10 | 0.12* | 0.10 |
| Storability (X2) | 1.00 | 0.19** | 0.15** | -0.02 | 0.27** | 0.16** | -0.15** | -0.05 | -0.11 | 0.05 | 0.14* | -0.08 | 0.06 | 0.10 | 0.16** | -0.01 | -0.13* | -0.05 | -0.03 | -0.14* | 0.06 | 0.10 |
| Embryo index (X3) | | 1.00 | 0.94** | 0.75** | 0.15** | 0.65** | -0.65** | 0.02 | 0.12* | 0.50** | 0.77** | -0.18** | 0.49** | -0.38** | 0.91** | 0.24** | 0.04 | 0.21 | 0.11* | -0.18** | 0.25** | 0.44** |
| W-100 seed (X4) | | | 1.00 | 0.80** | 0.15** | 0.53** | -0.54** | 0.07 | 0.15** | 0.49** | 0.79** | -0.16** | 0.48** | -0.35** | 0.90** | 0.26** | 0.04 | 0.01** | 0.12* | -0.13* | 0.24** | 0.42** |
| V-100 seed (X5) | | | | 1.00 | -0.45 | 0.45** | -0.45** | 0.20** | 0.08 | 0.29** | 0.69** | -0.30** | 0.51** | -0.36** | 0.77** | 0.32** | -0.05 | 0.29** | 0.03 | -0.06 | 0.10 | 0.34** |
| Relative density (X6) | | | | | 1.00 | 0.02 | -0.02 | -0.25** | 0.10 | 0.26** | 0.02 | 0.29** | -0.13* | 0.11 | 0.06 | -0.14 | 0.15 | -0.14* | 0.13* | -0.12* | 0.17** | 0.04 |
| Embryo % (X7) | | | | | | 1.00 | -0.98** | -0.13* | -0.02 | 0.29** | 0.34** | -0.14* | 0.32** | -0.32** | 0.53** | 0.10 | 0.02 | 0.09 | 0.06 | -0.11 | 0.12* | 0.35** |
| Seed coat % (X8) | | | | | | | 1.00 | 0.13* | 0.02 | -0.29** | -0.34** | 0.15** | -0.32** | 0.30** | -0.53** | -0.09 | -0.01 | -0.09 | -0.06 | 0.09 | -0.12* | -0.36** |
| Seed protein % (X9) | | | | | | | | 1.00 | 0.10 | 0.16** | 0.58** | 0.01 | 0.29** | -0.25** | 0.16** | 0.04 | 0.06 | 0.02 | 0.06 | 0.02 | -0.03 | -0.03 |
| Seed coat protein % (X10) | | | | | | | | | 1.00 | 0.07 | 0.17** | 0.12* | 0.12* | -0.04 | 0.18** | -0.05 | 0.10 | -0.03 | 0.09 | -0.02 | 0.02 | -0.01 |
| Embryo protein % (X11) | | | | | | | | | | 1.00 | 0.48** | -0.07 | 0.25** | -0.09 | 0.47** | 0.06 | 0.29** | 0.04 | 0.25** | -0.04 | 0.18** | 0.21** |
| Seed protein index (X12) | | | | | | | | | | | 1.00 | -0.10 | 0.55** | -0.44** | 0.82** | 0.20** | 0.09 | 0.17** | 0.16** | -0.13* | 0.22** | 0.30** |
| Moisture % (X13) | | | | | | | | | | | | 1.00 | -0.29** | -0.07 | -0.22** | -0.09 | -0.04 | -0.06 | -0.08 | -0.01 | -0.04 | -0.04 |
| Seed oil % (X14) | | | | | | | | | | | | | 1.00 | 0.07 | 0.74** | 0.13* | -0.05 | 0.11 | -0.01 | -0.03 | 0.13* | 0.17** |
| Embryo oil % (X15) | | | | | | | | | | | | | | 1.00 | -0.26** | -0.21** | 0.07 | -0.21** | 0.02 | -0.004 | -0.17** | -0.29** |
| Seed oil index (X16) | | | | | | | | | | | | | | | 1.00 | 0.22** | 0.03 | 0.19** | 0.09 | -0.13* | 0.23** | 0.38** |
| Seed F.F.A % (X17) | | | | | | | | | | | | | | | | 1.00 | 0.29** | 0.96** | 0.31** | -0.05 | 0.11 | 0.09 |
| Embryo F.F.A % (X18) | | | | | | | | | | | | | | | | | 1.00 | 0.32** | 0.91** | 0.03 | 0.04 | -0.06 |
| Seed A.V. (X19) | | | | | | | | | | | | | | | | | | 1.00 | 0.34** | -0.03 | 0.10 | 0.09 |
| Embryo A.V (X20) | | | | | | | | | | | | | | | | | | | 1.00 | 0.01 | 0.06 | -0.04 |
| Boll weight (X21) | | | | | | | | | | | | | | | | | | | | 1.00 | 0.09 | -0.16** |
| Seed cotton yield (t/ha) (X22) | | | | | | | | | | | | | | | | | | | | | 1.00 | -0.30** |
| Earliness % (X23) | | | | | | | | | | | | | | | | | | | | | | 1.00 |

* = Significant ** = highly significant r at 5 % = 0.113 r at 1 % = 0.148

IV. Genetic estimates and heritability

The efficiency of breeding programme for improvement of seed properties depends on the extent of genetic variability present in population and the heritability of the concerned characters. In cotton the heritability estimate in broad sense can be used as an approximation of narrow sense heritability because these genotypes are essentially homozygous and most of gene actions are of an additive effect (Brim1973). The results in Table (7) showed variance components, heritability estimate, genotypic and phenotypic coefficients of variability.

For yield and its components, the data indicated the heritabilities for seed cotton yield, boll weight and earliness % were 52.72 %, 80.00 % and 13.31 % respectively. The heritabilities for seed protein index and embryo oil % were considered as zero and not calculated due to the minus values for genetic variance. High genetic coefficients of variation in addition to high heritabilities reflect the importance for heritable components. The GCV % values ranged from 0.033 % for boll weight to 3.76 for earliness %.

As for physiological cotton seed characters, the results indicated the presence of some amounts of genetic coefficient of variability. The GCV % values were 18.63 % for storability and 1.17 % for germination %. The heritabilities were low for germination % (35.17) and moderate (49.99 %) for storability.

Concerning physical cotton seed properties, the data showed the presence of a large amount of genetic coefficient of variability. The heritabilities were 60.30 %, 52.37 %, 63.45 %, 40.48 %, 23.88 % and 28.36 % for embryo index, seed index, volume 100- seed, seed density, embryo % and seed coat %, respectively. The GCV % values ranged from 0.63 % for seed coat % to 3.99 % for 100- seed volume.

Regarding chemical cotton seed properties, the results indicated high heritability for seed coat protein %, moisture %, seed oil %, embryo free fatty acid, and embryo acid value. Whereas, it was moderate for seed oil index, seed free fatty acid and seed acid value, while it was low for seed protein % and embryo protein %. The heritabilities for seed protein index and embryo oil % were considered as zero and were not calculated due to the minus values for genetic variance. The GCV % values ranged from 0.21 % for seed free fatty acid to 15.91% for seed coat protein %. Burton (1952) suggested that a genetic coefficient of variation together with heritability would give the best indication of the genetic advance to be expected from selection. Thus, improvement of seed properties depends on three prerequisite: low estimates of interactions between genotypes and environments (years and locations), very close estimates of genotypic and phenotypic coefficients of variation used for assessment of variability and high heritability.

GENETIC BASIS FOR VARIABILITY IN COTTON

Table 7. Variance components, heritability, genotypic and phenotypic coefficient of variations for the studied characters.

| S.O.V. | Boll weight (g.) | Seed cotton yield (kg) | Earliness% | Germination % | Storability% | Embryo index | Weight 100 seed | Volume 100 seed | Relative density | Embryo % | Seed coat % | Seed protein % | Seed coat protein % | Embryo protein % | Seed protein index | Moisture % | Seed oil % | Embryo oil % | Seed oil index | Seed F.F.A | Embryo F.F.A | Seed A.V | Embryo A.V |
|--------------------------------|------------------|------------------------|------------|---------------|--------------|--------------|-----------------|-----------------|------------------|----------|-------------|----------------|---------------------|------------------|--------------------|------------|------------|--------------|----------------|------------|--------------|----------|------------|
| $\sigma^2 G$ | 0.001 | 0.034 | 2.17 | 3.65 | 15.09 | 0.04 | 0.081 | 0.49 | 0.001 | 0.21 | 0.24 | 0.61 | 0.77 | 3.51 | - | 0.090 | 1.41 | - | 0.017 | 0.001 | 0.002 | 0.004 | 0.008 |
| $\sigma^2 G \times L$ | 0.001 | 0.001 | -3.56 | 12.87 | 29.58 | 0.05 | 0.109 | 0.50 | 0.003 | 1.24 | 1.15 | 3.85 | 0.614 | 13.39 | 0.070 | 0.090 | 1.74 | 2.02 | 0.028 | 0.002 | 0.0002 | 0.006 | 0.001 |
| $\sigma^2 G \times Y$ | -0.002 | 0.028 | 18.96 | 0.217 | 0.24 | 0.001 | 0.009 | -0.04 | 0.00 | -0.03 | -0.02 | -0.001 | 0.001 | -0.004 | 0.000 | -0.001 | -0.004 | -0.01 | 0.000 | 0.000 | 0.000 | 0.000 | -0.001 |
| $\sigma^2 G \times L \times Y$ | 0.004 | 0.014 | 8.85 | -0.24 | -2.39 | 0.002 | 0.033 | 0.14 | 0.0003 | 0.03 | 0.01 | -0.015 | -0.02 | -0.31 | -0.001 | 0.002 | -0.008 | 0.03 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| $\sigma^2 P$ | 0.0013 | 0.06 | 16.30 | 10.38 | 30.18 | 0.072 | 0.15 | 0.78 | 0.003 | 0.87 | 0.86 | 2.55 | 1.08 | 10.26 | 0.002 | 0.140 | 0.88 | 0.03 | 0.03 | 0.002 | 0.002 | 0.007 | 0.008 |
| H^2 | 80.00 | 52.72 | 13.31 | 35.17 | 49.99 | 60.30 | 52.57 | 63.45 | 40.48 | 23.88 | 28.4 | 23.77 | 71.09 | 34.25 | 49.34 | 64.65 | 16.14 | 53.44 | 46.43 | 93.94 | 56.78 | 93.86 | |
| G.C.V % | 0.033 | 1.37 | 3.757 | 3.856 | 18.26 | 0.705 | 0.81 | 3.99 | 0.135 | 0.34 | 0.63 | 2.48 | 15.91 | 6.31 | - | 1.313 | 5.424 | - | 0.63 | 0.21 | 0.64 | 0.54 | 1.312 |
| P.C.V % | 0.043 | 2.60 | 28.22 | 10.96 | 36.52 | 1.17 | 1.54 | 6.30 | 0.32 | 1.40 | 2.22 | 10.45 | 22.38 | 18.43 | 0.096 | 2.03 | 8.80 | 2.30 | 1.18 | 0.47 | 0.71 | 0.96 | 1.41 |

Table 8. Euclidean methods for 19 extra long cotton genotypes groups including genotypes distance and similarity

| Nod | Cluster joint | | Similarity | Distance | No. of genotypes |
|-----|---------------|----|------------|----------|------------------|
| | C1 | C2 | | | |
| 18 | 6 | 12 | 87.51 | 1.87 | 2 |
| 17 | 6 | 11 | 81.44 | 2.65 | 3 |
| 16 | 5 | 8 | 80.95 | 2.72 | 2 |
| 15 | 3 | 10 | 79.19 | 2.97 | 2 |
| 14 | 5 | 6 | 78.85 | 3.02 | 5 |
| 13 | 3 | 9 | 78.75 | 3.03 | 3 |
| 12 | 3 | 17 | 77.99 | 3.14 | 4 |
| 11 | 3 | 18 | 76.98 | 3.28 | 5 |
| 10 | 4 | 15 | 76.73 | 3.32 | 2 |
| 9 | 3 | 5 | 76.33 | 3.37 | 10 |
| 8 | 3 | 4 | 74.11 | 3.69 | 12 |
| 7 | 3 | 7 | 73.63 | 3.76 | 13 |
| 6 | 3 | 14 | 72.74 | 3.88 | 14 |
| 5 | 3 | 16 | 71.69 | 4.04 | 15 |
| 4 | 2 | 19 | 71.52 | 4.06 | 2 |
| 3 | 3 | 13 | 70.19 | 4.25 | 16 |
| 2 | 2 | 3 | 69.32 | 4.37 | 18 |
| 1 | 1 | 2 | 36.99 | 8.98 | 19 |

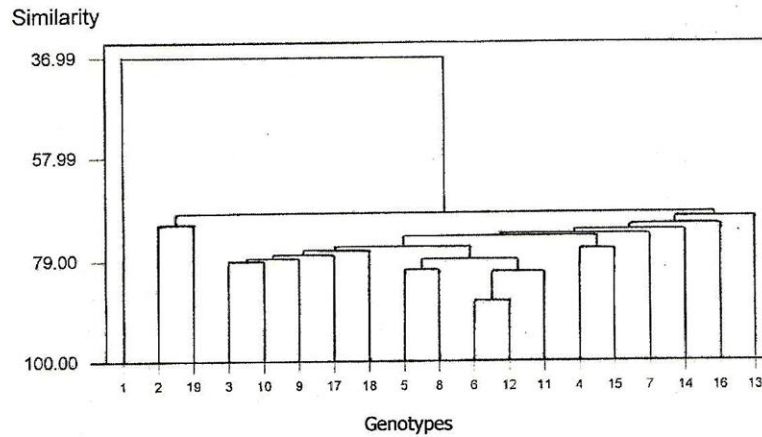


Fig. 1. Dendrograms of similarity of nineteen extra-long cotton genotypes.

V. Genetic diversity for physical and chemical properties.

Hierarchical clustering was applied to provide information about the relationships between various clusters. The distances between two clusters are the measure of the degree of diversification. The data in Table 8 and Fig.1, showed that 19 extra long cotton genotypes were divided into two clusters which were joined at the distance level 8.98 % with a similarity index of 36.19 %. The first cluster group included only the genotype $(G.68 \times G.45) \times ((G.84 \times G.45) \times G.45)$. The second group was divided into two subgroups at distance level 4.37% with similarity index of 69.32 %. The first subgroup consisted of the genotype $(G.84 \times F.108) \times ((G.84 \times G.45) \times G.45)$ and the commercial variety G.70 with distance level 4.06 % and similarity index of 71.52 %. The second subgroup was represented by other races of the genotype $(G.84 \times F.108) \times ((G.84 \times G.45) \times G.45)$ and the genotype $G.87 \times (G.77 \times G.70)$ with similarity index of 70.14 % and distance level of 4.25 and it was divided into a number of sub-subgroups. The first of them included the hybrid $(G.76 \times G.77) \times G.87$ with the two races of the promising hybrid $G.77 \times Pima S_6$ by similarity indices of 87.51 % and 81.44 % with distance levels 1.78 and 2.65 respectively. The second cluster included the two hybrids $(G.84 \times G.70) \times (G.45 \times Sea\ Island)$ and $G.70 \times Pima S_6$ with similarity index 80.95 % and distance level 2.72. The third of them included the genotype $(G.84 \times G.70) \times (G.45 \times Sea\ Island)$, and the promising hybrid $G.84 \times (G.74 \times G.68)$ with similarity index of 76.73 % and distance level of 3.32. The latter group was represented by the hybrid $(G.84 \times F.108) \times ((G.84 \times G.45) \times G.45)$ with the genotypes numbers. 13, 16, 14, 7, 4, 5, 18, 17, 9 and 10. The similarity index ranged between 70.19 % for the genotype $G.87 \times (G.77 \times G.70)$ and 79.19 % for the promising hybrid $G.77 \times Pima S_6$.

Breeding potential of the materials.

The genotypes differed in their genetic potential for physical and chemical properties. The commercial variety G.70 and the genotype $(G.84 \times F.108) \times ((G.84 \times G.45) \times G.45)$ surpassed all other genotypes for seed protein%. The genotypes $G.87 \times (G.77 \times G.70)$ was the best for embryo and seed oil %. The highly significant positive correlations between earliness % with physical seed properties and seed quality traits (embryo protein %, seed protein index, seed oil % and seed oil index. indicated that selection for increased earliness % will result in substantial increase for these traits. Generally the low estimates of genotype \times environments interaction variance, the high estimates of heritability and the very close estimates of genotypic and phenotypic coefficient of variations support our findings. Thus further breeding experiments are needed to improve oil and protein contents in the cotton seed.

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الأساس الوراثي لتباينات صفات جودة البذور و بعض الصفات المرتبطة بها للتراكيب الوراثية للقطن فائق الطول في مصر

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يهدف هذا البحث إلى تقدير معالم الاختلاف المظهري والوراثي، مكونات التباين، معالم الارتباط لصفات جودة البذور والتباين الوراثي في ١٩ مادة وراثية للقطن فائق الطول، اشتملت على أربعة أصناف تجارية وخمس عشرة سلالة مبشرة من برنامج تربية القطن لهذه الطبقة، وزرعت المواد الوراثية في منطقتي البحيرة ودمياط خلال موسمي ٢٠٠٢، ٢٠٠٣ م ويمكن تلخيص أهم النتائج فيما يلي:-

« أظهرت كلا من التراكيب الوراثية ومناطق الزراعة اختلافات عالية المعنوية لكل الصفات المدروسة وكان تأثير التفاعل بينها معنويًا لمعظم الصفات . كان تفاعل الدرجة الأولى بين المواد الوراثية والسنوات ، السنوات ومناطق الزراعة ، وتفاعل الدرجة الثانية بين المواد الوراثية والسنوات والمناطق تأثير غير معنوي لمعظم الصفات.

« سجل الهجين المبشر جيزة ٧٧ × بيما س ٦ أفضل القيم لصفات محصول القطن الزهر، معالم التكاثر، نسبة الإنبات، القدرة التخزينية، كثافة البذرة والتركيب الوراثي جيزة ٧٠ × بيما س ٦ أفضل القيم لصفات حجم البذرة ومعامل الزيت بالبذرة والتركيب الوراثي. جيزة ٨٧ × (جيزة ٧٧ × جيزة ٧٠) أفضل القيم لصفات النسبة المئوية للجنين ونسبة الزيت بالبذرة والجنين والتركيب الوراثي (جيزة ٧٧ × جيزة ٨٤) × (جيزة ٧٠ × جيزة ٥١) ب) أعلى القيم لصفات نسبة بروتين الجنين ونسبة الأحماض الدهنية الحرة للجنين والبذرة ورقم الحموضة للجنين.

« كان معامل الارتباط موجب وعالي المعنوية بين محصول القطن الزهر ومعامل الجنين ، معالم البذرة ، كثافة البذرة، بروتين البذرة، معامل بروتين البذرة، معامل الزيت للبذرة. كما وجد أيضا ارتباط موجب ومعنوي بين محصول القطن الزهر ونسبة الإنبات، النسبة المئوية للجنين، ونسبة الزيت للبذرة في حين وجد ارتباط معنوي سالب بين محصول القطن الزهر، التكاثر والنسبة المئوية للقصره

« كان معامل الارتباط معنويًا وموجبًا بين صفات البذرة الكيماوية (نسبة الزيت للبذرة، معامل زيت البذرة، نسبة البروتين للبذرة، النسبة المئوية لبروتين الجنين) مع صفات البذرة الفيزيائية (معامل الجنين، معالم البذرة، حجم البذرة ١٠٠) بذره والنسبة المئوية للجنين.

« سجلت قيم المكافئ الوراثي نسبة عالية لصفات بروتين القصره، الرطوبة % ، نسبة الزيت بالبذرة. كما سجلت نسبة متوسطة لصفات معالم البذرة، كثافة البذرة، معامل بروتين الزيت في حين سجلت نسبة منخفضة لصفات نسبة بروتين البذرة، نسبة بروتين الجنين، نسبة الزيت بالبذرة، النسبة المئوية للجنين، النسبة المئوية للقصره، و محصول القطن الزهر ونسبه التكاثر.

■ أظهرت النتائج ارتفاع قيم معامل الاختلاف الوراثي لصفات القدرة التخزينية، النسبة المئوية لبروتين القصره والنسبة المئوية لبروتين الجنين و تقارب قيم معامل الاختلاف الوراثي والمظهري لصفات وزن البذرة، نسبة الأحماض الدهنية الحرة بالجنين، رقم الحموضة للجنين، الكثافة النوعية للبذرة، النسبة المئوية للزيت مما يدل على أهمية الدور الذي يلعبه التباين الوراثي في وراثه هذه الصفات وإمكانية تحسينها.

■ انقسمت التراكيب الوراثية من حيث درجة التشابه إلى مجموعتين وراثيتين، ضمت المجموعة الأولى التركيب الوراثي (جيزة ٦٨ × جيزة ٤٥) × (جيزة ٨٤ × جيزة ٤٥) × جيزة ٤٥) في حين شملت المجموعة الثانية تحت مجموعتين، تكونت المجموعة الأولى من التركيب الوراثي (جيزة ٨٤ × ف ١٠٨ × (جيزة ٨٤ × جيزة ٤٥ × جيزة ٤٥) والتركيب الوراثي (جيزة ٧٧ × بيما ٦) × (جيزة ٨٧ × جيزة ٧٧ × جيزة ٧٠) في حين تكونت المجموعة الثانية من ٤ مجموعات فرعية شملت باقي المواد الوراثية