# ESTIMATION OF GENETIC COMPONENTS BY USING NORTH CAROLINA MATING DESIGN SYSTEM FOR DETECTION DESIRABLE GENE ACTION IN COTTON.

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## ABSTRACT

North Carolina design system is very effective in breaking undesirable linkage and lead to creating genetic variability in a population. One population was obtained by crossing two cultivars Giza 88 (G.88) and TNB1 followed by intermitting between each $F_2$ plants with original parents G.88 and TNB1. The results of the analysis of variance indicated that significant and highly significant mean squares for all the studied traits and these results indicating there were differences between them. The contribution of male or female parent was more pronounced in the genetic variation of the cross. The additive genetic variance was higher than dominance variance for most of the studied traits and potence ratio were less than one for these traits .On the other hand, the dominance portion of the genetic variation played the major role for inheritance of the other traits. Heritability in broad sense was larger than heritability in narrow sense for all the studied traits and the correlation coefficient was positive and significant between some of pair traits. These results recommended by recurrent selection for improvement of most the studied traits. While, many cycles of intermitting would dissipate the negative correlation.

## INTRODUCTION

The ultimate goal of cotton breeding program is to increase yielding capacity and improve fiber properties of stable commercial cotton varieties. Exploration of hybrid vigor and understanding of nature of gene action in cotton are considered the important application of the science of genetics in cotton breeding program.

Choice of the most efficient methodology mainly depends upon the type of gene action controlling the genetic variation. Therefore, unambiguous testes of the genetic components help the breeder to the rightful decision making about the most effective breeding method to be applied. In its respect, North Caroline design III ( Comstock and Robinson, 1948 and 1952) has been extensively applied to detect and estimate the components of the genetic variation, i.e. additive and dominance genetic variances, as well as, its very effective in breaking undesirable linkage and leading to cretin genetic variability in a population by creating heterozygosity. Assessment and quantifying the components of genetic variance controlling yield and its attributes as well as fiber properties in cotton have been studied by several researchers. Tyagi *et al.,* (1988) indicated that the biparental intermitted population was more amenable for improvement through selection than the selefed $F_3$. Abo-Arab (1999), Soliman (2003) and Abd El–Salam (2005) indicated that biparental system was more effective in breaking undesirable linkage.

In the light of the advantages N.C.D. III, the present investigation was target to estimate additive and dominance genetic variance, heritability in broad and narrow senses to help the breeder to chose the effective cotton breeding method and maximize breeding progress.

# MATERIALS AND METHODS

**Experimental material:-**

The materials were developed by crossing 32 $F_2$ plants of the cross G.88 x TNB1 used as a male with their original parents for the same cross which were G.88 and TNB1 varieties as females in 2008 growing season. Thus 32 hybrids were developed and sown by using single plant randomization in two replications in the eight sets, with row to row and plant to plant spacing of 70 cm. and 40 cm., respectively at Sakha Agricultural Research Station in 2009 growing season. Normal cultural practices were applied as recommended for ordinary cotton growing. Data were recorded on eight random plants for each replicate on the following traits:-

  1-Boll weight  in grams                 (B.W.)
  2-Seed cotton yield per plant in grams   (S.C.Y. /P.)
  3-Lint cotton yield per plant in grams    (L.C.Y. /P.)
  4- Lint percentage                   (L .P. %)
  5-Seed index in grams             (S.I.)
  6-Fiber fineness                   (F.F.)
  7- Fiber strength                 (F.S.)
  8- Fiber length at 2.5 %         (2.5 % S.L.)
  9-Uniformity ratio               (U.R. %)
  10- Yellowness degree         ( +b )

**Statistical analysis:**

North Carolina design III (N.C.D. III) as outlined by (Comstock and Robinson 1952) was performed to estimate different genetic components. The form of the analysis of variance is presented in Table 1.

**Table 1: Analysis of variance and expected mean squares in N.C.D. III.**

| S.O.V. | d.f. | M.S. | E.M.S. |
|---|---|---|---|
| Sets | S-1 | | |
| Reps/Sets | S(r-1) | | |
| Fem./Sets | S | | |
| Mal./sets | S(n-1) | M1 | $\sigma^2 e + 2r \sigma^2 m$ |
| Fem. x Mal./Sets | S(m-1) | M2 | $\sigma^2 e + r \sigma^2 ml$ |
| Error | S(2n-1)(r-1) | M3 | $\sigma^2 e$ |

**Where:**
**S    = Sets                r =Replications         m = Male in sets**
**$\sigma^2 e$ = M3 due to error/r and refer to environmental variance**
**$\sigma^2 ml$ = [M.S. due to interaction - M.S. due to error]/r**
**$\sigma^2 D = 2 \sigma^2 ml$.**
**Dominance variance, $\sigma^2 m$ [M.S. due to males./Sets - M.S. due to error]/2r**
**$\sigma^2 m = 1/4 \sigma^2 A$          $\sigma^2 A = 4 \sigma^2 m$,    Additive variance**

Proportional contribution of males, females and their interaction are presented by the magnitude of sum squares of these genotypes relative to the sum squares of crosses.

## RESULTS AND DISCUSSION

The analyses of variance and mean squares for ten studied traits in biparental crosses are shown in Table 2. The results cleared those significant or highly significant mean squares of sets for all the studied traits and these indicating found differences between them. Also, for females in sets the results illustrated those significant mean squares for all the studied traits with except seed index (S.I.) and yellowness degree (+b) traits. This result indicated that female parents differed markedly in their mean performance in the biparental cross. On the other hand, the results showed highly significant values of the mean squares due to males in sets for all the studied traits, with except boll weight (B.W.), lint percentage (L.P.%.) and seed index (S.I.). The results revealed overall differences between $F_2$ male plants in this cross, as well as, the results also cleared that the variance due to females was larger than the variance due to males for all the studied traits with a few exceptions i.e. fiber fineness (F.F.) and yellowness degree (+b). These results revealing that material effect play significant role in the inheritance of these traits. These results are agreement with many researchers i.e. Abo-Arab (1999), El-Harony (1999), Soliman *et al.,* (2007) and El-Mansy *et al.,* (2008).

In the same Table 2, the results cleared that the females x males interaction mean squares were significant and highly significant for lint cotton yield per plant ( L.C.Y./P.) , lint percentage (L.P.%.) , fiber fineness ( F.F.) , fiber strength ( F.S.) , span length at 2.5 % ( 2.5 % S.L.) and uniformity ratio (U.R.%) . These results indicated that females behaved some what differently from male to another and these males differed markedly in their genetic background. On the other hand, insignificant mean squares due to interaction reflect that the male or female changes nearly of similar magnitudes for these traits.

From the results in Table 3 cleared that the male or female parents appeared to contribute the maximum portion in the genetic variation for most of the studied traits. The contribution of male parents was more pronounced in all cases with except lint cotton yield per plant ( L.C.Y./P.) , span length at 2.5 % ( 2.5 % S.L.) and uniformity ratio (U.R.%) which had female contribution more than male contribution. On the other hand, the relatively high contributions of male x female interactions in most cases. This result convinced the focus to role of non- additive gene effects in addition to the additive effects in controlling these traits.

Assessment of the genetic variance components using N.C.D. III are summarized in Table 4. Regarding the relative magnitude of additive and dominance components variance were estimated. The values of additive variance were higher than those of dominance (non additive) variance for seed cotton yield per plant (S.C.Y. /P.), lint cotton yield per plant (L.C.Y./P.), seed index (S.I.), fiber fineness (F.F.) , span length at 2.5% ( 2.5 % S.L.) and yellowness degree (+b).

These results assuredly for potence ratio values which were less than one and explaining that additive variance of the above traits, these results agree with showed by Jagtap and Kolhe (1986), Soliman (2003), Abd El-Salam (2005) and El-Mansy *et al.,* (2008**)**. On the other hand, the magnitude of dominance components variance were larger than corresponding additive values for boll weight (B.W.), lint percentage (L.P %), fiber strength (F.S.) and uniformity ratio (U.R.%). These results confirmed and higher of heritability in broad sense ($h_{bs}$ %) and potence ratio values which were higher than unity. This finding showed the importance of over dominance gene effect which played the major role in the inheritance of the above traits. These results are agree with obtained by , Garg *et al.,* (1987), Abd EL-Bary (2003), Soliman (2003), Abd El-Salam (2005), El-Akheder and El-Mansy (2006), Soliman *et al.,* (2007) and El-Mansy *et al.,* (2008).

For heritability the results indicated that in broad sense ($h_{bs}$ %) the values ranged from 60.73 % for fiber strength (F.S.) to 94.82 % for uniformity ratio (U.R. %). On the other hand, the estimated values in narrow sense ($h_{ns}$ %) were less than in broad sense ($h_{bs}$ %) and ranged from 9.02 % for fiber strength (F.S.) to 67.80 % for seed cotton yield per plant (S.C.Y. /P.).

Estimation of correlation which occurs between each pair of traits in both biparental families is shown in Table 5. The results cleared that positive significant and highly significant correlations values between boll weight (B.W.) with seed cotton yield per plant (S.C.Y. /P.), also lint cotton yield per plant (L.C.Y. /P.) and span length at 2.5% (2.5% S.L.), same results between seed cotton yield per plant (S.C.Y. /P.) with lint cotton yield per plant (L.C.Y. /P.), span length at 2.5% (2.5% S.L.) and uniformity ratio (U.R. %), also the results indicated that significant and highly significant correlations values between lint cotton yield per plant (L.C.Y. /P.) with lint percentage (L.P.%), span length at 2.5% (2.5% S.L.) and uniformity ratio (U.R. %).

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# تقدير المكونات الوراثية باستخدام نظام تزاوج نورث كارولينا لاكتشاف الفعل الجينى المرغوب فى القطن

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أُجري هذا البحث بغرض تقدير مكونات التباين الوراثي وحساب معامل الارتباط وتقدير معامل التوريث في المدى الواسع والمدى الضيق باستخدام طريقة التهجين الرجعي لنباتات الجيل الثاني مع كلا الأبوين حيث تم الحصول علي 32 هجين للهجين ( جـ88  x  TNB1 ) وقد أجريت الدراسة فى محطة البحوث الزراعية بسخا – كفر الشيخ – مصر خلال الموسمين الزراعيين 2008 و2009.

أظهرت نتائج تحليل التباين لجميع الصفات وجود قدر كبير من الاختلافات مما يسمح بإجراء انتخاب كما أظهرت النتائج أن المساهمة النسبية لكل من الآباء والتفاعل في التباين كانت اكبر من المساهمة النسبية للأمهات لمعظم الصفات المدروسة.

كانت مساهمة الفعل الجيني المضيف اكبر من مساهمة الفعل الجيني غير المضيف لمعظم الصفات الموجودة تحت الدراسة مما انعكس ذلك علي درجة السيادة والتي كانت اقل من الواحد الصحيح وهذا يعني أن الفعل الإضافي هو المتحكم في وراثة هذه الصفات . بينما لعب الفعل الجيني السيادي( غير المضيف) دوراً اكبر في وراثة باقي الصفات وهذا يؤكده زيادة درجة السيادة عن الواحد الصحيح .

كما أظهرت النتائج أيضاً أن معامل الارتباط كان معنويا وموجبا لكثير من الصفات تحت الدراسة وأنه يُنصح بإستخدام طريقة الانتخاب المتكرر وهي الأفضل لتحسين هذه الصفات بينما يُنصح بإجراء عدد من دورات التزاوج داخل العشيرة للتغلب علي الارتباط السالب بين بعض أزواج الصفات محل الدراسة .

قام بتحكيم البحث

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|---|---|
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**Table 2:** **Analysis of variance and mean squares for yield and its components as well as fiber properties in the biparental crosses.**

| S.O.V. | d.f. | B.W. | S.C.Y./P. | L.C.Y./P. | L.P.% | S.I. | F.F. | F.S. | 2.5%S.L. | U.R.% | ( +b ) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Sets | 7 | 0.326** | 17991.7** | 2334.8** | 5.371* | 1.267* | 0.134** | 0.632* | 2.846** | 0.866** | 0.967** |
| Replications in sets | 8 | 0.055 | 1417.1 | 278.7 | 1.870 | 0.616 | 0.050 | 0.360 | 1.064** | 0.199 | 0.241 |
| Females in sets | 8 | 0.174* | 11924.9** | 1810.4** | 8.664** | 1.612 | 0.119** | 0.753** | 5.168** | 2.142** | 0.340 |
| Males in sets | 24 | 0.106 | 5943.8** | 560.9** | 3.545 | 1.229 | 0.132** | 0.721** | 1.092** | 0.614** | 1.193** |
| Interactions in sets | 24 | 0.109 | 2866.0 | 433.0* | 4.849* | 1.132 | 0.111** | 0.915** | 1.396** | 0.401** | 0.933 |
| Error | 56 | 0.065 | 1719.2 | 215.2 | 2.454 | 0.847 | 0.030 | 0.750 | 0.489 | 0.111 | 0.165 |

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

**Table 3: Proportion contribution as percent of males, females and their interactions for each trait.**

| Parameters | B.W. | S.C.Y./P. | L.C.Y./P. | L.P.% | S.I. | F.F. | F.S. | 2.5%S.L. | U.R.% | ( +b ) |
|---|---|---|---|---|---|---|---|---|---|---|
| Males | 38.87 | 46.49 | 35.12 | 31.47 | 42.39 | 46.69 | 38.17 | 25.94 | 35.62 | 53.24 |
| Females | 21.19 | 31.09 | 37.78 | 25.63 | 18.53 | 13.99 | 13.28 | 40.89 | 41.27 | 5.06 |
| Males x Females interaction | 39.94 | 22.42 | 27.10 | 42.90 | 39.08 | 39.32 | 48.54 | 33.17 | 23.24 | 41.70 |

**Table 4: The estimates of genetic parameters, additive, dominance, degree of dominance in the $F_2$ cotton crosses population.**

| Genetic parameters | B.W. | S.C.Y./P. | L.C.Y./P. | L.P.% | S.I. | F.F. | F.S. | 2.5%S.L. | U.R.% | (+b) |
|---|---|---|---|---|---|---|---|---|---|---|
| Additive | 0.0413 | 4224.500 | 345.7900 | 1.0910 | 0.3823 | 0.0627 | 0.0287 | 0.3975 | 0.3977 | 0.7282 |
| Dominance | 0.0442 | 1146.830 | 217.8038 | 2.3948 | 0.2855 | 0.0417 | 0.1646 | 0.0934 | 0.6099 | 0.4682 |
| $h_{bs}$% | 72.47 | 86.20 | 83.97 | 73.96 | 61.21 | 75.01 | 60.73 | 66.75 | 94.82 | 93.55 |
| $h_{ns}$% | 35.04 | 67.80 | 51.52 | 23.15 | 35.04 | 45.07 | 9.02 | 54.05 | 37.43 | 56.94 |
| D/A | 1.0300 | 0.521 | 0.794 | 1.482 | 0.864 | 0.816 | 2.395 | 1.533 | 1.238 | 0.802 |

**Table 5: Estimates of correlation coefficients among ten studied traits in the cross G.88 x TNB1.**

| Traits | S.C.Y./P. | L.C.Y./P. | L.P.% | S.I. | F.F. | F.S. | 2.5%S.L. | U.R.% | (+b) |
|---|---|---|---|---|---|---|---|---|---|
| B.W. | 0.325* | 0.348** | 0.174 | 0.290 | -0.138 | -0.143 | 0.461** | 0.257 | 0.052 |
| S.C.Y./P. | | 0.974** | 0.105 | 0.045 | 0.047 | 0.068 | 0.396** | 0.331** | -0.036 |
| L.C.Y./P. | | | 0.318* | 0.048 | 0.048 | 0.050 | 0.366** | 0.300* | -0.045 |
| L.P.% | | | | -0.018 | 0.068 | 0.011 | 0.044 | -0.013 | -0.033 |
| S.I. | | | | | -0.092 | 0.013 | 0.256 | 0.263 | 0.064 |
| F.F. | | | | | | 0.120 | 0.152 | 0.189 | 0.085 |
| F.S. | | | | | | | 0.026 | 0.115 | -0.143 |
| 2.5%S.L. | | | | | | | | 0.743 | 0.266 |
| U.R.% | | | | | | | | | 0.151 |
| ( +b ) | | | | | | | | | |

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