

DIALLEL ANALYSIS OF COTTON HYBRIDS
(*G. barbadense* L.)
1. EARLINESS CHARACTERS OF F₁s AND F₂s

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(Manuscript received 18 February, 1997)

Abstract

Hayman's diallel cross analysis was employed to investigate the nature of genetic system controlling some earliness characters in nine Egyptian cotton varieties and their half diallel crosses. The information obtained with regard to D and H₁ suggested that in all traits, additive part of the genetic variance was more important than dominance concerning gene distribution, and all traits expressed unequal gene distribution. Most of dominant genes had negative effects in all characters except days to first flower in F₂ generation. Dominance degree was over dominance for all traits except days to first flower in F₁, which exhibited complete dominance and position of first fruiting node in F₁.

The narrow sense heritability values of more than 0.50 were determined for all traits in F₁ generation. However, in F₂, generation, it was 0.12, 0.38 and 0.33 for days to first flower, position of first fruiting node and days to boll opening, respectively.

For all traits in F₁, the W_r/V_r regression coefficients were not significantly different from unit slope, indicating additive gene action with partial dominance. In F₂, the W_r/V_r regression coefficients were not significantly different from unit. The results reached from the distribution of parents along and/or around the regression line suggested that Giza 83 was best parent for breeding program for earliness trait.

INTRODUCTION

The choice of selection and breeding procedures for genetic improvement of cotton or any crop, is largely conditioned by the type and relative amounts of genetic variance components in the population. The exploitation of genetically diverse stock in cross combinations helps to identify promising hybrid and/or to develop superior inbred lines. The diallel cross analysis has been used by many investigators to assist in the investigation of nature of heterosis and partition the genetic variance into its

components by using Hayman's method to obtain and test various genetic estimates (Al Rawi and Kohel 1969, Silva and Alves 1983, Wariboko 1983 Khajidoni *et al.* 1984, El-Feki 1986, Udayakumar *et al.*, 1984 and El-Feki *et al.* 1995).

The present study was designed to estimate some types of gene action controlling the inheritance of some earliness characters of cotton raised after crossing nine parents in half diallel. The heritability estimates for these characters were also calculated. Also, to identify those parents which carry the dominant alleles.

MATERIALS AND METHODS

The field work of this study was carried out at Sakha Research Station, Agricultural Research Center, Egypt. Nine cotton cultivars (*G.barbadense* L.) namely; Giza 83 (1), Giza 81 (2), Giza 80 (3), Giza 45 (4), Giza 85 (5), Giza 70 (6), Giza 84 (7), Giza 77 (8) and Giza 45 (9), were used as experimental materials. The entries will be identified by numbers 1 through 9 respectively. All possible crosses without reciprocals were made among these nine lines in 1993 to obtain F₁'s hybrid seeds enough for common agronomic practices followed in farmer fields. The parental varieties and F₁ hybrids (45 entries) were grown in 1994 and F₂ and parental varieties were grown in 1995 in a randomized complete block design experiments with two replicates and three-row plot. The rows were 4 meter long and 65 cm. apart. Hills were spaced at 20 cm. within row and seedlings were thinned to two plants/hill.

The following observations and measurements were recorded on 10 individual guarded plants from middle row in each plot: (1) Days to first flower, (2) position of first fruiting node and (3) days to first boll opening.

Partitioning the genetic variance to its components, as recommended by Hayman (1954), Jinks (1954) and Mather and Jinks (1971) for diallel crosses, was used to estimate the relative magnitude of the genetic components of the quantitative variability, and to provide information on the genetic mechanisms by which traits are inherited. To interpret the genetic control of each character, the (V_r , W_r) graphs for each trait in the F₁ and F₂ diallel crosses were developed according to Jinks (1954) and Hayman (1954) after computation of covariance-variance regression.

RESULTS AND DISCUSSION

The mean squares values were obtained from ordinary variance analysis for earliness characters, it is clear that all genotypes differed significantly (Table 1). This result ascertains the fact of previous assumption for distinct genotypic background of the parents involved. Consequently, various comparisons suggested to be done are valid and should be conducted to fulfill the objectives of the present study.

The validity to Hayman assumption :

Assumption and tests for their validity are as follows:

1. Diploid segregation: *Gossypium barbadense* L. is tetraploid ($4n = 52$) and segregates in diploid manner,
2. Homozygous parents: The parental lines were maintained by self fertilization for three cycles and were assumed to be homozygous,
3. No reciprocal difference: The entries in the diallel table were replaced by their mean reciprocal for all characters prior to analysis,
4. No genotype-environmental interaction: Insignificant variance for replicates showed insignificant genotype-environmental interaction,
5. No epistasis.
6. No multiple alleles and,
7. Uncorrelated gene distribution may be fulfilled through inspection,

Variance and covariance (V_r and W_r) interrelationships, are shown in Table (1). Data indicate that t^2 which represents uniformity was insignificant for days to first flower, position of first fruiting node and days to first bolls for F_1 and F_2 . This result reveals that there is no evidence of non-allelic interactions variance components and the existence of allelic interaction i.e., the validity of additive-dominance model.

Table 1. Mean square variance and uniformity of W_r , V_r for validity assumption made by Hayman.

Source of variance	Days to first flower		Position of first fruiting node		Days to first boll opening	
	F_1	F_2	F_1	F_2	F_1	F_2
Replication	0.6548	6.7788	0.4150	0.0640	1.7361	14.8028*
Genotypes	7.8146	1.6517*	1.5530*	0.4890*	2.6755*	6.7180*
Error	1.2207	0.6647	0.2790	0.2126	1.2184	2.9012
t^2	0.3877	4.6600	0.5606	0.0950	0.9021	1.0912
b	0.8048*	0.2781*	1.1034*	0.4800*	0.9391*	0.1634
S.E.	0.1174	0.0819	0.0625	0.2400	0.5081	0.1550

* ($P < 0.05$)

A further approach to test adequacy of additive-dominance model is the joint regression coefficient of W_r on V_r (Table, 1). Data in Table (1) indicates that the regression of W_r/V_r obtained in F_1 were not significantly different from unit slope and in the same time significantly different from slope zero indicating additive gene action with partial dominance. While in F_2 , the regression of W_r/V_r gave values which were significantly different from unit and zero slope in the same time indicating the presence of dominance as well as non-additive effects.

Genetic parameters :

Table (2) summarizes the estimates of genetic variance component in addition to Hayman's genetic parameters from F_1 and F_2 diallel analysis for the studied traits. The data showed the significance of additive "D" and dominance effects (H_1 and (H_1 and/or H_2) with exception of component D on H_2 for days to first flower in F_2 which are shown in Table (2). Regarding the number of standard units for D and (H_1 and / or H_2) indicated that these additive effects were more important portion in the genetic variance. These results are generally in agreement with those obtained by El-Feki (1986) and El-Feki *et al.* (1995).

H_1 greater than H_2 indicates that positive and negative alleles at the loci for these traits are not equal proportion in the parents for F_1 and F_2 . The h_2 values of F_1 and F_2 , over all dominance effects of heterozygous loci was significant for all traits, these results indicated that dominant genes had negative effect except the days to first flower in F_1 . Covariance of additive and non-additive effects (F) were significant in F_1 generation. These results suggesting greater frequency of dominate genes were positive for position of first fruiting node and days to boll opening, while it was negative for day to first flower, however, in F_2 it was not significant (Table 2), this estimator was not enough to determine of dominant allele in F_2 .

Genetic ratio and estimator were computed using genetic parameters obtained in Table (2) to provide further information about the genetic system operating for each trait. The mean values of these estimates are presented in Table (2). Dominance degree indicated complete dominance for days to first flower in F_1 generation. El-Feki (1986) obtained over-dominance for this trait, however, in F_2 it was over-dominance. Position of first fruiting node exhibited partial dominance in F_1 generation and over-dominance in F_2 El-Feki (1986) indicated over-dominance for this trait. While days to first boll opening exhibited over-dominance in the two generations. The results obtained by El-Feki (1986) indicated over dominance for first boll opening.

Table 2. Mean estimates of genetic and environmental variance components for F₁ and F₂ diallel crosses.

Source of variance	Days to first flower		Position of first fruiting node		Days to first boll opening	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
D	5.07* ± 0.44	0.41 ± 0.37	0.53* ± 0.02	0.35* ± 0.09	3.03* ± 0.59	4.36* ± 1.25
F	3.99* ± 1.03	-0.13 ± 1.74	-0.17* ± 0.04	0.64 ± 0.44	5.01* ± 1.37	8.32 ± 5.82
H ₁	5.15* ± 0.98	6.52* ± 3.29	0.19* ± 0.03	1.84* ± 0.82	5.03* ± 1.30	27.39* ± 11.03
H ₂	3.72* ± 0.84	-1.08 ± 2.83	0.12* ± 0.03	1.73* ± 0.71	2.90* ± 1.21	28.16* ± 9.48
h ₂	3.72* ± 0.84	-4.43* ± 1.89	-0.27* ± 0.02	-1.48* ± 0.47	-0.08* ± 0.75	-19.49* ± 6.35
E	9.02* ± 0.14	0.33* ± 0.12	0.14* ± 0.01	0.11* ± 0.03	0.61* ± 0.19	1.45* ± 0.39
Degree of dominance	1.00	1.99	0.60	1.14	1.29	1.25
Pq	0.18	0.04	0.16	0.23	0.14	0.25
K _D /K _R	2.28	0.85	0.57	2.98	4.59	7.39
K	2.42	4.09	2.18	0.85	0.03	0.69
Correlation parental	0.94*	-0.03	0.44	0.45	0.52	0.43
	50.1	12.0	78.1	38.1	53.0	33.9

* (P<0.05)

Estimates of the average frequency of negative vs positive alleles at all loci exhibiting dominance (pq) showed that the positive and negative alleles were not equally distributed among the parents in all traits of F_1 and F_2 generations.

Estimates of the ratio of dominant to recessive alleles in the parents (K_D/K_R) were greater than unity for all traits in the two generations, except days to first flower in F_2 and position of first fruiting node in F_1 . This implies an excess of dominant genes in the parents for each trait; as previously discussed concerning the positive values F component except for the two traits.

The number of effective factors (K) has been described by Mather and Jinks (1971) as the smallest unit of heritability material that is capable of being recognized by methods of biometrical genetics. Estimates of number of effective factor (K) ranged from 2 in F_1 generation to 5 in F_2 generation for days to first flower. However, it ranged from 3 in F_1 to 1 in F_2 for position of first fruiting node. One effective factor controls parental difference regarding days to first boll opening in two generations. A high correlation indicates that the most dominant alleles act in one direction and most recessive alleles act in the opposite direction (Hayman, 1954). Positive and significant (r) values were noticed for days to first flower in F_1 generation indicating that most of dominant genes had negative effects. The data in Table (2) showed that the (r) values were enough to determine the direction of dominance in F_1 and F_2 for all traits with exception of days to first flower in F_2 , because it has a low correlation which could not be useful to formulate an idea about the direction for this trait.

Table (2) showed the values of narrow sense heritability were more than 50% in F_1 of all traits, while in F_2 the values were 38.1 and 33.9% for position of first fruiting node and days to first boll opening respectively. This assured by previously mentioned concerning that dominance and additive genetic variance were found with exception position of first node fruiting node in F_1 . The low value of narrow sense heritability of days to first flower in F_2 was due to insignificant additive genetic variance. El-Feki (1986) revealed low narrow sense heritability (below 30%) for position of first fruiting node, medium narrow sense heritability (30%-40%) for first flower and high narrow sense heritability for days to first boll opening.

Wr/Vr Graphic analysis :

Figures (1 to 6) represent the graphical analysis of the regression of W_r (parent-off spring covariance) on V_r (parental array variance) and their limiting

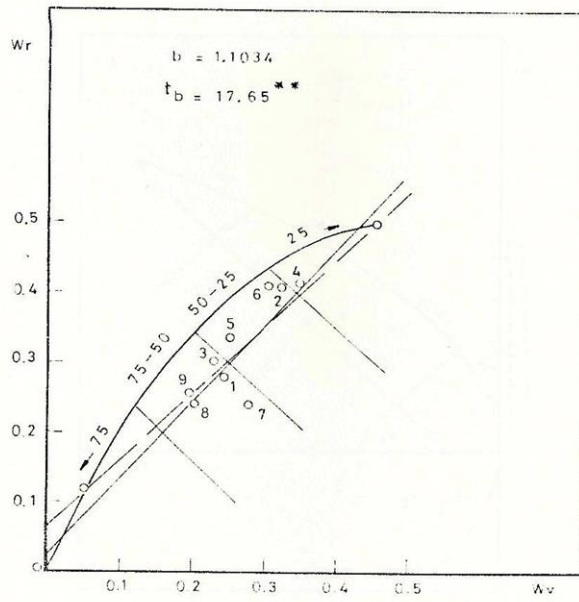


Fig. 1. Days to first flower (F_1).

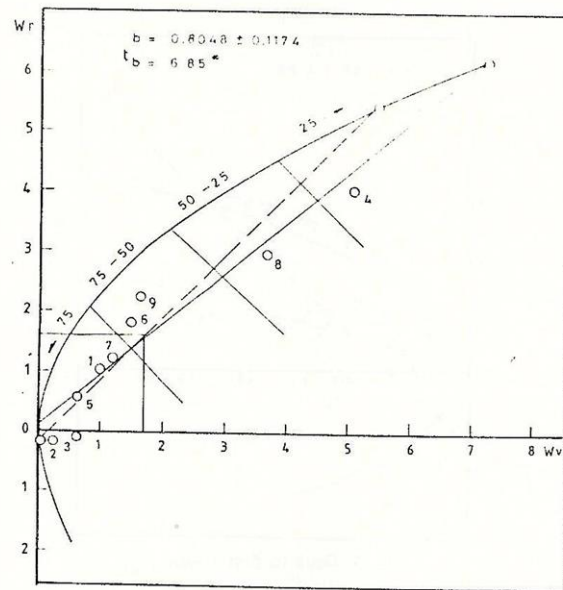


Fig. 2. Position of first fruiting node (F_1).

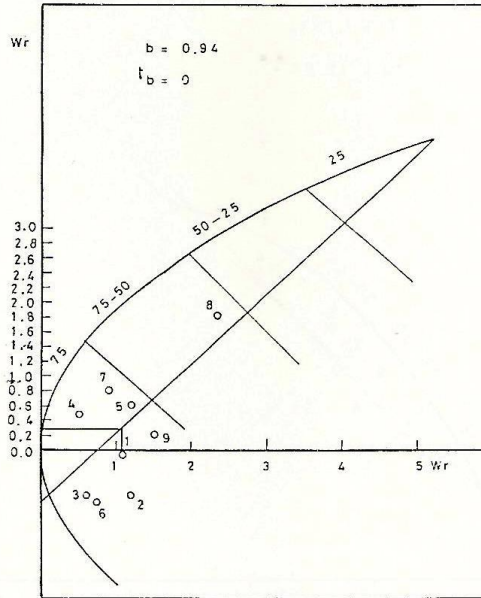


Fig. 3. Days first boll opening (F_1).

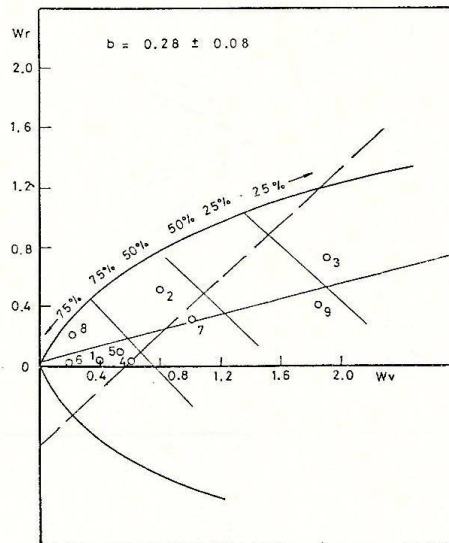


Fig. 4. Days to first flower (F_2).

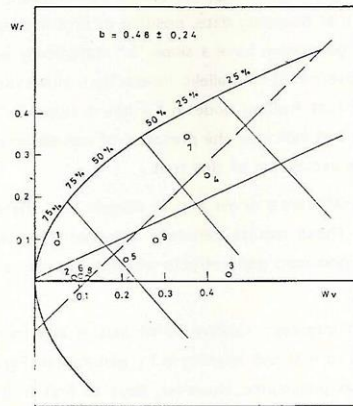


Fig. 5. Position of first fruiting node (F_2).

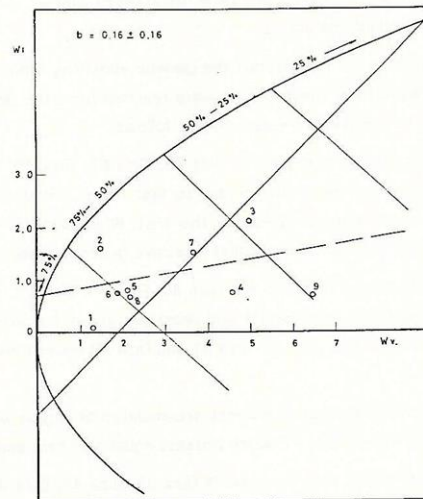


Fig. 6. Opening of the first boll (F_2).

parabola from F_1 and F_2 diallel analysis for all the investigated characters. Figures (1, 2 and 3) illustrate that flowering date, position of first fruiting node and days to first boll opening in F_1 generation have a slope "b" statistically equal to unity ($b=1$) which indicates the absence of non-allelic interaction. However, for days to first flower and position of first fruiting node in F_2 has a slope "b" statistically differ significantly from unity and indicates the presence of non-allelic interaction between factors determining the expression of this trait .

The insignificant difference of W_r and V_r reveals that there is no evidence of non-allelic interaction. These results generally demonstrate non-allelic interaction as well as additive and dominant gene effects which might play a role in the expression of these traits.

With respect to Y intercept, relative to W_r axis, it was found that all traits in F_2 generation and days to first boll opening in F_1 generation (Figures 3, 4, 5 and 6) were controlled by over-dominance. However, days to first fruiting node was controlled by partial dominance (Figure 2) in F_1 . The results obtained from the intercept with ordinate showed that the degree of dominance was consistent with the results obtained previously from the value of $\checkmark H_1/D$ in F_1 and $\checkmark 1/4 H_1/D$ in F_2 (Table 2) for all the studied characters.

Figures (1 to 6), also explain the genetic variability among the parents for all the studied characters. These results were reached from the distribution of parents along and/or around the regression line as follows:

Figure (1) shows that parents Giza 83, Giza 81, Giza 80, Giza 85 and Giza 84 appeared most dominant genes for day to first flower, on the other hand, Giza 45 contains excess of recessive genes for this trait. While Giza 70, Giza 75 and Giza 77 contain equal position of dominant and recessive genes for this trait.

Figure (2) shows that Giza 83, Giza 80, Giza 84, Giza 77, Giza 75 and Giza 85 contain equal position of dominant and recessive genes for position of first fruiting node. On the other hand, Giza 45, Giza 81 and Giza 70 poses most of recessive genes for this trait.

Figure (3) shows that all parents accumulated at region which contain $P > 75\%$ dominant genes except Giza 77 which possess equal dominant and recessive genes.

Figure (4) shows that the parents Giza 83, Giza 45, Giza 85, Giza 70 and Giza 77 contain most dominant genes for the first flower in F_2 , while Giza 80 and 75 appeared to poses most recessive genes for this trait. The varieties Giza 81 and Giza 84 have equal portion of dominant and recessive genes for this trait.

Figure (5) illustrated that Giza 83, Giza 81, Giza 70 and Giza 77 contain 75% dominant genes, while Giza 85, Giza 80 and Giza 45 contain equal dominant and recessive genes and Giza 84 and Giza 85 appeared to possess most of recessive genes for position of first fruiting node.

Figure (6) shows that varieties Giza 83, Giza 81, Giza 85, Giza 70 and Giza 77 contain most dominant genes, while Giza 80, Giza 45, Giza 84 and Giza 75 contain equal portion of dominant and recessive genes.

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التحليل لهجن القطن بطريقة كل الهجن الممكنة (*G.barbadense*) ١ . صفات التبيكير للجيلين الأول والثانى

طلعت أحمد الفقى ، محمد عبد الباقي على الجليل ، عبد المعطى محمد زينة

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يهدف هذا البحث إلى دراسة الفعل الجينى فى بعض الصفات الهامة المرتبطة بالتبيكير. استخدم فى هذا البحث تسعة أصناف هى جيزة ٨٢ ، جيزة ٨١ ، جيزة ٨٠ ، جيزة ٤٥ ، جيزة ٧٠ ، جيزة ٨٤ ، جيزة ٧٧ و جيزة ٧٥ . وأجريت الدراسة بمحطة البحوث الزراعية فى موسمى ١٩٩٤ ، ١٩٩٥ لهجن فى نصف دائرة كاملة بين الأصناف السابقة وتم التهجين بمحطة زراعة كلية الزراعة بالأسكندرية سنة ١٩٩٣ .

فى موسم ١٩٩٤ تم زراعة الآباء والهجن الناتجة فى تجربة تصميم قطاعات كاملة العشوائية فى مكررين، فى نهاية الموسم تم جنى كل تركيب وراثى فى كل مكرر على حدة وتم دراسة البذرة الناتجة فى موسم ١٩٩٥ للحصول على الجيل الثانى وأخذت بيانات التبيكير على ١٠ نباتات فى كل مكرر.

وكانت النتائج كما يلى :

- ١ . كان للتأثير المضيف الدور الرئيسى فى وراثة هذه الصفات.
- ٢ . درجة السيادة سيادة تفوقية لكل الصفات عدا عدد الأيام لظهور أول زهرة فى الجيل الأول كانت سيادة تامة وكذلك مع أول عقدة ثمرية بالجيل الأول.
- ٣ . معظم الجينات السائدة تعمل فى الاتجاه السالب عدا عدد الأيام لظهور أول زهرة فى الجيل الثانى.
- ٤ . فى الجيل الأول كانت الكفاءة الوراثية للصفات أكثر من ٥٠٪ بينما كنت فى الجيل الثانى ١٢٪ ، ٢٨٪ ، ٩٠٪ ، ٣٣٪ لصفات عدد الأيام اللازمة لظهور أول زهرة وموقع العقدة الثمرية الأولى وعدد الأيام اللازمة لتفتح أول لوزة على التوالي.
- ٥ . كان معامل إنحدار Wt/Vt فى الجيل الأول لا يختلف عن الوحدة معنوياً مما يدل على وجود الأثر المضيف مع جزء من السيادة نجد المعامل يختلف فى الجيل الثانى عن الوحدة.
- ٦ . من توزيع الأصناف على خط الانحدار يتضح أن الصنف جيزة ٨٢ هو أفضل الأصناف من ناحية التبيكير.