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Genetic Analysis of Yield Components and Fiber Strength in Upland Cotton (*Gossypium hirsutum* L.)

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Abstract: In this study six different cotton genotypes, Nazilli-84, Acala SJ-5, Deltapine 5690, Carmen, Tamcot CAMD-E and PD 6186, were crossed in a half diallel mating scheme. The result of diallel analysis indicated that, the number of Bolls per Plant (B/P), Seed Cotton Weight per Plant (SCW/P), Lint Percentage (LP) and Earliness Ratio (ER) exhibited additive and dominance genetic effect but primarily dominance genetic effect, that fiber Strength (Str.) had about equal additive and dominance genetic effect and that seed cotton Weight per Boll (BW) exhibited primarily additive genetic effect. The highest heritability estimates were found in earliness ratio (0.53), fiber strength (0.50), seed cotton weight per boll (0.42) and lint percentage (0.40). The number of bolls per plant and seed cotton weight per plant showed moderate heritability estimates, 0.33 and 0.22, respectively. Results suggest some suitable parents which are; Nazilli 84 and Carmen for plant seed cotton yield and lint percentage; Acala SJ-5 for boll weight; DPL 5690 for number of bolls per plant; Tamcot CAMD-E for earliness ratio; PD 6168 for fiber strength. These varieties mentioned above could be suitable parents in cotton breeding program for further researches.

Key words: Cotton, yield components, inheritance, genetic analysis

INTRODUCTION

To improve yield capacity with high fiber properties, especially fiber strength due to the new spinning and weaving technology, has been a primary objective of cotton breeders. Therefore, along with the knowledge of heritability, magnitude and type of genetic variance has a great importance for cotton breeders dealing with simultaneous improvement of fiber quality and lint yield.

Most characteristics related to lint yield and fiber properties are quantitatively inherited in cotton. However, quantitative traits are difficult to study since: a) their expression is modified by environmental expression and management fluctuation; b) each trait is a composite of many other traits and influenced by many genes; c) the expression of an individual gene is often modified by the expression of other genes; d) linkage blocks are difficult to breakup; e) the optimum genotype for any environment-management system is likely to be different from that for another system^[1]. Thus, the purpose of all cotton breeders is to improve yield capacity with high fiber properties, especially fiber strength, in cotton by using simple genetic models and genetic parameters. The first step for successful breeding program is to select appropriate parents. Selection suitable parents is one of the most important criteria used to find the most

promising crosses and increase the efficiency of breeding program. The diallel analysis provides a systematic approach for the detection of appropriate parents, crosses superior for the investigated traits and understanding of genetic control of the trait. Also, it helps the plant breeders to choose the most efficient selection method by allowing estimate several genetic parameters^[2].

In the last 50 years, dramatic changes have been made in the speed of processing fibers in the textile industry. New spinning and weaving technology mandate plant breeders and geneticists to develop cultivars of upland cotton having improved fiber quality, especially fiber strength, without sacrificing yield potential. The negative association between lint yield and fiber strength, which has hampered the simultaneous improvement of these two important characters in cotton, was recognized in early cotton breeding studies^[3]. A number of breeding methods have been proposed to overcome the negative correlations between fiber quality parameters and lint yield components. Jensen^[4] proposed a diallel selective mating system and multiple parents to provide a large gene pool to break linkages and provide genetic advance at the same time. Culp and Harrell^[5] reported that to insure high yield, it was important to maintain high lint percent and number of bolls per unit land area. Scholl and Miller^[6] proposed that the genetic relationship between lint yield

and fiber strength probably resulted from pleiotropic effects. Meredith^[7] indicated that fiber strength was conditioned by relatively few major genes. Lint yield was not consistently correlated with fiber properties. Increased fiber strength was consistently associated with increased fiber length^[8,9]. This would indicate that it should be possible to simultaneously select for both fiber strength and length in conventional segregating populations.

The diallel analysis method has been widely used by plant breeders to estimate genetic parameters in the early generation. This method was applied to improve self and cross pollinated plants^[10-13]. In cotton, many researchers^[14-18] used diallel analysis method to show a considerable amount of useful genetic variability in cotton. To estimate genetic parameters, genetic variance and combining ability of parents and crosses, the diallel analysis method has been used in a broad (wide) plant species from hot pepper^[19] to mustard^[20].

Cotton breeders redirected their objectives toward producing stronger fibers to meet the continued demands of the textile industry. Information about the relationship between yield components and fiber quality parameters has a great importance for cotton breeders dealing with simultaneous improvement of fiber quality and lint yield per unit land area. This information, along with the knowledge of heritability and magnitude and type of genetic variance controlling fiber traits will allow breeders to develop more effective selection methods. The purposes of this research were to estimate genetic components for investigated characters and to determine appropriate parents for yield components and fiber strength among six different cotton genotypes.

MATERIALS AND METHODS

Genetic material

Nazilli 84: This variety constituted the check for this study due to the region standard variety. It is a moderately early cultivar with high yield and high ginning turnout.

Acala SJ-5: It displays vigorous growth habit, large boll and full season maturity.

Deltapine 5690: It is a compact and moderately early variety with having better fiber properties.

Carmen: It is very compact and moderate in growth habit and earliness.

Tamcot CAMD-E: It is a short season and moderately early cultivar and intermediate in height and growth habit.

PD 6186: It was released by the USDA-ARS in 1984 as a high fiber strength strain in South Carolina.

Six upland cotton genotypes, Nazilli-84, Acala SJ-5, Deltapine 5690, Carmen, Tamcot CAMD-E and PD 6186, representing a range of yield and fiber quality were (hand) crossed in a half diallel mating scheme. Parents and their 15 F_1 populations were grown at the Adnan Menderes University Agriculture Faculty Experiment Fields one row plots 6 m by 0.70 m apart in 2000. The experiment design was a randomized block design with four replications. Twenty well developed open bolls were hand harvested randomly from each row of parents and F_1 s. The bulked bolls from each genotype were ginned on laboratory roller gin. Seed cotton Weight per Boll (BW) and Lint Percentage (LP) were obtained from each boll samples. Seed Cotton Weight per Plant (SCW/P) was determined by dividing harvested total seed cotton to the number of plants in each plot. Earliness Ratio (ER) was found as the ratio of first hand harvest over total harvested seed cotton. The number of Bolls per Plant (B/P) was calculated by counting the open bolls from the randomly chosen 10 plants in each plot. High Volume Instrument (HVI) was used to measure fiber bundle Strength (Str.).

Data obtained from the 15 F_1 progenies and six parents were analyzed by the method proposed by Jinks-Hayman^[10-13]. Diallel analysis was applied to estimate genetic parameters for measured traits and to determine their inheritance. The diallel analysis was used to evaluate traits that significantly varied among the parents. The differences in phenotypes were assumed to be genetic differences. This biometrical genetic model is based on some assumption. The validity of assumptions for diallel analysis was tested by regression coefficient of W_r (Covariance) on V_r (Variance). The analysis of variance was performed by using SAS.

W_r+V_r : It estimates the order of dominance of parents. Low values of W_r+V_r indicate high levels of dominance while a high value indicates low dominance.

r (Y , W_r+V_r): The correlation of the mean parental phenotype values (y) and (W_r+V_r) values indicate the direction of dominance. A positive correlation indicates that recessive genes have positive effects while a negative correlation indicates that dominant genes have positive effects^[11].

D: It shows variation due to the additive gene effect.

F: It indicates the relative frequency of dominant and recessive alleles in the parent. While a negative F value indicates an excess of the recessive alleles in the parents, a positive value shows more dominant

alleles than recessive alleles in parents. A value of $F = 0$ indicates that either no genes exhibited dominance or that the dominant and recessive alleles of each gene are distributed equally among the parents^[21].

H₁ and H₂: They estimate components of variation due to the dominance effects of genes.

h²: It indicates the summation of dominance deviation over all loci. When the frequency of dominant and recessive alleles is equal, then $H_1=H_2=h^2$. Significant of h^2 confirms that dominance is unidirectional.

E: It is environmental component estimated by the error mean square from the analysis of variance.

(H₁/D)^{1/2}: It is a weighted measure of the average degree of dominance at each locus with a value of zero indicating no dominance, a value of 1 indicating complete dominance and a value greater than 1 indicating over dominance. Partial dominance results in a value between 0 and 1.

H₂/4H₁: It is an estimator of the average frequency of negative versus positive alleles at loci exhibiting dominance. It has maximum value of 0.25 when $p=q=0.5$.

KD/KR: It is a ratio of the total number of dominant to recessive genes in all parents.

Heritability: The formula of Crumpacker and Allard^[21] was used to estimate narrow sense heritability.

RESULTS AND DISCUSSION

Preliminary analysis of variance indicated that parents and their hybrids were significantly different from each other for all investigated traits in the study, which enable the diallel analysis to be run (Table 1).

Parental differences: The six parents used in this study varied significantly for each yield components and fiber strength (Table 2). Nazilli 84, Acala SJ-5, DPL 5690, Tamcot CAMD-E, PD 6168 and Carmen had the highest values in order of LP, BW, B/P, ER, Str. and SCW/P. These data indicated that the highest values of investigated characters did not follow the same pattern in every genotype.

F₁ Performance: Table 3 results showed that crosses of six cotton genotypes reflected variability as well as parents for studied characters. Among the crosses, 3x6 (DPL 5690 x Carmen) for boll number per plant (18.3) and

Table 1: Mean squares of yield components and fiber strength in half diallel cotton population

Source of variation	df	B/P No.	SCW/P (g)	BW (g)	LP (%)	ER (%)	Str. (g/tex)
Replication	3	21.9**	25.3	0.15	1.47	14.2	13.9
Genotypes (Parents and F ₁ s)	20	21.9**	848.1**	1.19**	8.06**	50.5**	14.6**
Error	60	5.9	132.7	0.18	1.99	8.5	2.3

** Significant at 0.01 level

Table 2: Means of yield components and fiber strength in half diallel cotton population for parents

Parents	B/P No.	SCW/P (g)	BW (g)	LP (%)	ER (%)	Str. (g/tex)
Nazilli 84	15.60bc*	71.00a	6.30b	44.80a	75.80a	23.30c
Acala SJ-5	14.00bc	61.60ab	7.30a	39.20d	70.40b	27.50b
DPL 5690	19.80a	68.80a	5.40c	42.70b	66.90bc	28.50ab
Tamcot CAMD-E	11.20c	42.80b	5.40c	41.30c	77.10a	24.10c
PD 6168	16.00a-c	63.30a	5.80c	42.60bc	72.20ab	30.10a
Carmen	14.90bc	74.10a	5.80bc	43.30ab	64.90c	28.10ab
LSD _{0.05}	3.94	20.01	0.62	1.69	5.28	2.39

* Means within columns followed by the same letter(s) are not different at 0.05 probability level

Table 3: Means of yield components and fiber strength in half diallel cotton population for hybrid combinations

Crosses	B/P No.	SCW/P (g)	BW (g)	LP (%)	ER (%)	Str. (g/tex)
1x2	14.40cd*	70.90ab	6.70a-c	43.90a-c	76.80ab	24.90de
1x3	16.40ab	77.50a	5.80f	44.40a	75.50a-c	23.60ef
1x4	12.40e	60.80ab	5.80f	43.20a-d	77.10ab	22.60f
1x5	15.90a-c	80.40a	5.90f	44.40a	77.30a	26.50a-d
1x6	14.80a-d	67.70ab	6.40b-e	43.90a-c	75.40a-c	25.10c-e
2x3	13.40c-e	80.30a	6.90ab	42.20cd	72.50d	27.80ab
2x4	10.30e	61.80ab	6.60a-d	41.70d	76.80ab	25.40c-e
2x5	13.20c-e	70.50ab	6.70a-c	42.80a-d	75.80a-c	26.20a-d
2x6	15.40a-d	84.30a	7.00a	43.70a-c	73.40cd	27.00a-c
3x4	12.70de	66.60ab	6.00ef	42.40b-d	78.50a	24.90de
3x5	16.50ab	73.10ab	6.40b-e	41.50d	75.80a-c	28.00a
3x6	18.30a	81.70a	5.80f	44.10ab	71.60d	27.70ab
4x5	12.30e	48.40b	5.50f	41.30d	77.70a	25.90b-d
4x6	13.10de	62.70ab	6.40b-e	42.60a-d	75.50a-c	25.90b-d
5x6	16.60ab	75.40a	6.30de	42.40b-d	75.30a-d	27.80ab
LSD _{0.05}	3.55	25.70	0.63	1.88	3.84	2.02

* Means within columns followed by the same letter(s) are not different at 0.05 probability level

2x6 (Acala SJ-5 x Carmen) for SCW/P (84.3 g) and BW (7.0 g) had the highest values. This result would be expected since DPL 5690, Carmen and Acala SJ-5 were the best in GCA for B/P, SCW/P and BW, respectively^[22]. Nazilli 84 x DPL 5690 and Nazilli 84 x PD 6168 for LP, DPL 5690 x Tamcot CAMD-E for ER and DPL 5690 x PD 6168 for fiber strength were in the first rank among 15 crosses.

Genetic analysis: The calculated W_r-V_r regression lines for studied characters differed from zero, but did not from one, which indicate that assumptions for diallel analysis were valid (Table 4). Dominance and phenotypic order of parents were similar for all measured characters, except for SCW/P and Str. The value of the correlation between (W_r+V_r) and Y_r was positive and significant for B/P, which indicates that dominant alleles have predominantly negative effects. Based on the phenotypic rank of

Table 4: Genetic parameters and ratios estimated from 6x6 diallel cross population in cotton

Crosses	B/P No.	SCW/P (g)	BW (g)	LP (%)	ER (%)	Str. (g/tex)
Test of assumptions						
Mean square of Wr-Vr	9.579	21741.000	0.042	1.038	15.418	0.962
Order of parents						
Dominance order (Wr+Vr)	421563.000	436215.000	215643.000	164352.000	415236.000	254163.000
Phenotypic order	351624.000	613524.000	214563.000	163542.000	415236.000	536241.000
Correlation of Yr and (Wr+Vr)	0.936**	0.415	-0.942**	-0.886*	-0.981**	0.347
Genetic components						
D	11.5±1.34**	226.1 ± 9.3**	0.445 ± 0.08**	4.45±0.77**	30.3 ± 2.29**	8.08±0.76**
F	4.6±3.386	-2.7 ± 23.4	-0.005 ± 0.19	1.75±1.94	21.5 ± 3.81**	2.88±1.91
H ₁	21.2±3.40**	744.2 ± 23.5**	0.425± 0.20	6.63±1.95*	39.4 ± 3.83**	8.10±1.92**
H ₂	17.5±3.05**	568.7 ± 21.1**	0.411 ± 0.18	5.01±1.75*	33.1 ± 3.43**	6.61±1.72*
h ²	1.99±2.09	170.9 ± 14.1**	0.232 ± 0.12	2.42±1.17	77.3 ± 2.31**	3.37±1.15*
E	1.66±0.51*	31.9 ± 3.5**	0.046 ± 0.03	0.49±0.29	2.2 ± 0.57**	0.70±0.28
Ratios of genetic components						
(H ₁ /D) ^{1/2}	1.355	1.814	0.977	1.221	1.139	1.001
H ₂ /4H ₁	0.206	0.191	0.241	0.189	0.209	0.204
KD/KR	1.343	0.993	0.988	1.409	1.902	1.434
Heritability (narrow sense)	0.33	0.21	0.42	0.40	0.53	0.50
** p < 0.01	t _{0.01} = 4.604	t _{0.01} = 4.604	t _{0.01} = 4.604	t _{0.01} = 4.604	t _{0.01} = 4.604	t _{0.01} = 4.604
* p < 0.05	t _{0.05} = 2.776	t _{0.05} = 2.776	t _{0.05} = 2.776	t _{0.05} = 2.776	t _{0.05} = 2.776	t _{0.05} = 2.776
	r _{0.01} = 0.917	r _{0.01} = 0.917	r _{0.01} = 0.917	r _{0.01} = 0.917	r _{0.01} = 0.917	r _{0.01} = 0.917
	r _{0.05} = 0.811	r _{0.05} = 0.811	r _{0.05} = 0.811	r _{0.05} = 0.811	r _{0.05} = 0.811	r _{0.05} = 0.811

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

parents, Tamcot CAMD-E carried the most dominant genes for B/P. Non significant values for correlation between (Wr+Vr) and Yr values for SCW/P and Str. indicate that some of the genes showed dominance and acted in the negative direction. On the other hand, negative and significant correlation between (Wr+Vr) and Yr indicates that the dominant alleles expressed increase in BW, LP and ER. Thus, Acala SJ-5, Nazilli 84 and Tamcot CAMD-E carry dominant alleles for BW, LP and ER, respectively.

The additive component (D) was significant for all measured properties (Table 4). As an indicator of the relative frequency of dominant and recessive alleles in the parents, F value was found to be positive and significant for ER which indicates an excess of the dominant alleles in the parents^[21]. Positive but non significant F values for B/P, LP and Str, shows asymmetry in frequency of dominant and recessive alleles in the parents, i. e. more dominant than recessive alleles. These results were supported by KD/KR, a ratio of the total number of dominant to recessive genes in all parents. The estimated KD/KR ratio for B/P, LP, ER and Str. was higher than 1, which indicates the presence of an excess of dominant genes, while KD/KR ratio for SCW/P and BW was lower than 1, which indicates the presence of an excess of recessive genes. Dominance components, (H₁ and H₂) were significant for all investigated characters, except for BW. The significant value of h² shows that dominance was unidirectional for SCW/P, ER and Str, but was not unidirectional for B/P, BW and LP due to the lack of significance for h². The significant environmental

component (E) indicated that environment factors had affect on the phenotypic expression of B/P, SCW/P and ER, which suggest that environmental effects also influence phenotypic difference in cotton cultivars. The ratio of (H₁/D)^{1/2}, measure of the average degree of dominance at each locus, was higher than 1 for all investigated characters, except for BW, which indicates over dominance for B/P, SCW/P, LP, ER and Str., but partial dominance for BW. H₂/4H₁ value, which estimates the average frequency of negative versus positive alleles at loci exhibiting dominance, was lower than 0.25 indicating the asymmetrical distribution of genes in the parents. Narrow sense heritability values for PL, BW, Str. and ER were in moderate range, 0.40, 0.42, 0.50 and 0.52, respectively, while it was very low for SCW/P, 0.21 and B/P, 0.33.

Genetic components in 6x6 half diallel cotton population were estimated by using the diallel analysis method proposed by Jinks^[12] and Hayman^[11]. Since additive genetic variance (D), dominance variance (H₁) and corrected dominance variance (H₂) were statistically significant from zero, it could be concluded that all investigated characters, except for BW, was under both the additive and dominance gene effect. However, dominant gene effects would be higher than additive gene effects for B/P, SCW/P, LP and ER since the estimated additive variance, D, was smaller than that of H₁ and H₂ and the overall degree of dominance ratio, (H₁/D)^{1/2}, was higher than 1. This result was in agreement with the results of previous studies^[16,23-25]. Boll weight and fiber strength were controlled by additive and additive-

dominant gene effects, respectively, which is consistent with previous results^[26]. Narrow sense heritability varied from 0.21 to 0.52 for investigated characters. For Boll Weight (BW) and fiber Strength (Str.), selection in early generation would be recommended due to the estimated heritability value and additive variance. However, B/P and SCW/P, having low heritability and LP and ER with moderate heritability level showed dominance variance. Thus, recurrent selection method would be appropriate for B/P, SCW/P, LP and ER.

It is concluded that, in order to improve investigated characters in cotton breeding program for further researches, some suitable parents were detected which were; Nazilli 84 and Carmen for plant seed cotton yield and lint percentage; Acala SJ-5 for boll weight; DPL 5690 for number of bolls per plant; Tamcot CAMD-E for earliness ratio; PD 6168 for fiber strength.

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