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Estimation of Genetic Effects in Upland Cotton for Fibre Strength and Staple Length

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ABSTRACT

Genetic effects were determined for fiber traits in upland cotton by 8 X 8 diallel cross experiment. Additive dominance effects were determined for fiber strength, while epistatic effects were present for staple length. Asymmetrical distribution of dominant and recessive genes in the parents was observed. Reciprocal effects were not present for both the characters.

Key Words: Genetic effects; Fiber strength; Staple length; Diallel analysis; Upland cotton

INTRODUCTION

Cotton is the raw material which is utilized by the spinners with the sole objective of producing better cotton products. Therefore, the most important and fundamental characteristics could be described as grade, staple length, fiber fineness and fiber strength suitable to produce a given product. Staple length and strength are ranked at the top in priority order for spinning. Stronger fibers are increasingly required by the modern rotor and friction spinning processes. Several natural and international cotton breeders have emphasized the use of diallel analysis for such studies (Verhalan & Murrey, 1967; Mirza & Khan, 1974; Innes *et al.*, 1975; Pathok, 1975; Singh *et al.*, 1987; Khan *et al.*, 1994; Khan *et al.*, 1990).

The purpose of our experiment was to obtain information on the genetic basis of variation and to investigate the nature of genetic systems controlling staple length and fibers strength in upland cotton.

MATERIALS AND METHODS

Plant material. Eight cultivars were selected for diallel crossing and are denoted by their numbers (Table I). Glass house cultivation and field evaluation have already been described (Murtaza *et al.*, 2002).

Table I. Particular attributes of cotton cultivars

Sr. No.	Cultivar name	Particular attribute
1	Laokra 5.5	Okra type leaf
2	DPL – 7340–424	Nectariless
3	Fregobract	Fregobracts
4	Glandless 4195–220	Glandless
5	SA100	Red leaves
6	Stoneville–857	Nectariless
7	S–12	High yielding Local Cultivar
8	AC–134	Local Cultivar

Staple length (mm). Staple length was measured from the representative samples by Digital Fiber graph model "530" at 2.5% span length and uniformity ratio at 50% divided by 2.5% were based on five specific readings.

Fiber strength (000 PPSI). The fiber strength tests were carried out on Presley flat bundle strength tester at zero gauge length. The Presley ratio (index) was computed by applying the formula:

Presley index = breaking load in pounds/bundle weight in mg

After calculating Presley index, the fiber strength was counted out by applying the following formula in 000PPSI Pounds/square inch.

Fiber strength = (Presley index x 10.8116) – 0.1200

Statistical analysis. The data collected were subjected to the Fisher's analysis of variance as described by Steel and Torrie (1980). Hayman (1954) approach, as used by Mather and Jinks (1982) was used in this study to analyze diallel data for the study of gene action. The standard error for the regression in slope was estimated according to Snedecor and Cochran (1962).

The genetic parameters in F_1 population were computed as described by Hayman (1954). In F_2 generation, the formula for genetic parameters was modified as proposed by Verhalen and Murray (1969) and Verhalen *et al.* (1971).

RESULTS AND DISCUSSION

Genotypic differences between parents and hybrids were established (Table II), and data were then subjected to Hayman (1954), and Mather and Jinks (1982) method of diallel analysis.

Staple length. The (a) and (b) items were significant (Table III) which showed presence of additive and dominance effects. The non significance of b_1 showed the absence of directional dominance effects. The b_2 item was significant in

Table II. Estimates of mean square (Genotype, Error) of staple length and fiber strength

Parameters	Mean Squares	
	Genotype	Error
Staple length		
F_1	4.86**	0.05
F_2	5.65**	0.31
Fiber strength		
F_1	25.19**	1.03
F_2	21.78**	0.70

** = Indicates significant differences at P <0.01 probability level

F_1 generation indicating symmetrical distribution of genes, while it was non significant in F_2 generation. The b_3 component was non significant in F_1 while it was significant in F_2 generation. The "c" item was non significant in F_1 generation, so there was absence of maternal effects. While vice versa in F_2 generation therefore, "a" item was retested for F_2 against "c" item and it became non–significant indicating that additive effects were marked by the presence of maternal effects. The "d" component was non significant in both the generations indicating absence of reciprocal effects for staple length.

The analysis of Vr and Wr regression shows that it was significantly differ from unity in F_1 and not for F_2 while, it was not differed from zero in both the generations (Table IV). The analysis of variance of arrays (Table V) elaborated that both Wr + Vr mean squares and Wr – Vr mean squares in both the generations varies from array to array at 0.01% level of significance. So, both the tests stave the validity of additive dominance model due to the presence of multiple allelism or correlated genes distribution. The highly significant Wr + Vr mean squares for both the generations indicated the presence of dominance for this character.

It was concluded that gene interaction and epistasis were involved in the inheritance of staple length. Involvement of gene interactions in staple length has already been reported by Verhalen and Murrey (1967), Mirza and Khan (1974), Khan *et al.* (1987) and Khan *et al.* (1990).

Fiber strength. The "a" item (Table III) was significant in both the generations suggesting the presence of additive gene effects controlling fiber strength. General dominance effects on "b" were also highly significant. The b_1 was non significant in both the generations which showed absence of directional dominance. The non–significant values of b_2 and b_3 showed that asymmetry of gene distribution, i.e. $H_1>H_2$, with absence of specific gene effects. The "c" and "d" items were also non significant in both the generations so absence of maternal and reciprocal effects were evident.

Table IV. Test of regression coefficient of W_r on V_r for staple length and fiber strength in *Gossypium hirsutum* L.

Parameter	Regression coefficient		Standard error of regression SE(b)	t–value for b–0	t–value for 1–b
Staple Length	F1	–0.04	0.137	–0.29ns	7.57*
	F2	0.452	0.256	1.77ns	2.14 ns
Fiber Strength	F1	0.700	0.232	3.02*	1.30 ns
	F2	1.093	0.286	3.83*	–0.325 ns

The regression coefficient for F_1 and F_2 generations (Table IV) departs significantly at 0.01% level of significance from zero but insignificantly differ at 0.05% level of significance from unity. So, the regression analysis qualified both the generations for diallel analysis. The second test i.e. analysis of variance of arrays (Table V) showed that mean squares for Wr + Vr was non significant for F_1 generation at 0.05% level, indicating the lack of dominance whereas in F_2 population it was significant at 0.01% level hence showed presence of dominance. While Wr – Vr for F_1 also non significant, while it was highly significant for F_2 population this significance indicates the presence of non allelic interactions, this invalidate the model and did not permit for further analysis. This being the case, it was not legitimate to produce graphs of Wr or Vr for F_2 population. This discrepancy may be due to different environmental conditions because the two populations were sown in two different years.

The graphic representation of F_1 population (Fig. 1) showed a straight regression line passing through ordinate point hence showed the absence of non–allelic interaction and independent distribution of genes array. The regression line cut the covariance axis above the origin ($D>H_1$), hence suggesting additive with partial dominance type of gene action. The cultivar SA–100 possessed the most dominant

Table III. Diallel analysis of variance table for staple length and fiber strength

Parameters / Item	Staple Length				Fiber Strength			
	D.F.		Mean squares		D.F.		Mean squares	
	F1	F2	F1	F2	F1	F2	F1	F2
a	7	7	30.60 **	31.54 **	6	7	251.67 **	177.0 **
b	28	28	17.41 **	19.88 **	21	28	46.93 NS	51.37 **
b1	1	1	6.56 NS	2.44 NS	1	1	15.21 NS	24.33 NS
b2	7	7	22.62 NS	8.41 NS	6	7	56.04 NS	76.55 NS
b3	20	20	16.12 NS	24.77 **	14	20	45.29 NS	43.91 NS
c	7	7	10.18 NS	26.48 **	6	7	39.01 NS	38.24 NS
d	21	21	6.88 NS	4.97 NS	15	21	60.01 NS	55.71 NS
e	63	63	9.61	10.67	63	63	48.37	42.12

Fig. 1. Wr/Vr graph for fibre strength (F1 generation)

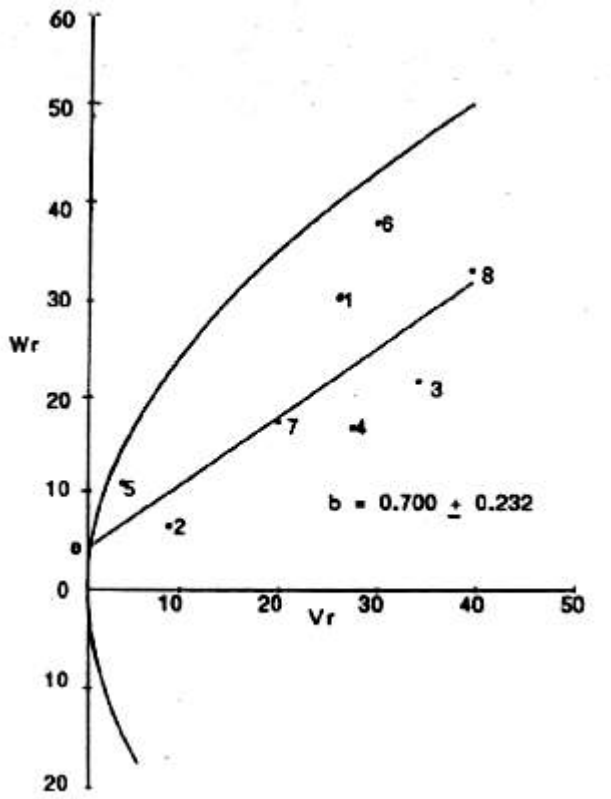
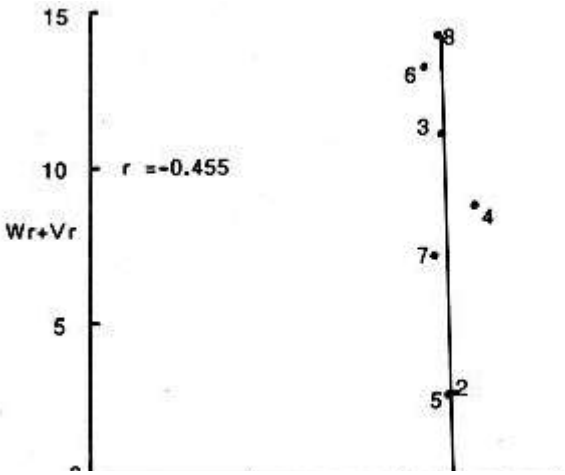


Fig. 2. $Wr + Vr\sqrt{P}$ **graph for fibre strength (F1 generation)**



Key to the parents

1 Laokra 5.5	5 SA 100
2 DPL 7340-424	6 Stoneville 857
3 Frego bract.	7 AC-134
4 Glandless 4195-220	8 S-12

Table V. Heterogeneity test for (W_r+V_r) and (W_r–V_r) estimates for staple length and fiber strength in *Gossypium hirsutum* L.

Source	Fiber strength				Staple length			
	F1		F2		F1		F2	
	d.f	M.S.	d.f	M.S.	d.f	M.S.	d.f	M.S.
$W_r + V_r$ between array	6	63.80ns	7	107.20**	7	1.03**	7	2.30**
$W_r + V_r$ within array	14	23.600	16	1.710	16	0.13	16	0.13
$W_r - V_r$ between array	6	8.002ns	7	11.25**	7	1.22**	7	0.65**
$W_r - V_r$ within array	14	2.982	16	0.738	16	0.03	16	0.15

genes being nearest to the origin, while S–12 had the maximum recessive genes being away from the origin. There was maximum diversity among the parents for this character as shown by wide scattered of array points on the regression line. The negative correlation (r = –0.46) (Fig. 2) between Wr + Vr and parental measurement suggesting that genes for fiber strength tend to be dominant. The additive with partial dominance type gene action have also been reported previously (Verhalen & Murrey, 1967; Innes *et al.*, 1975).

Genetic components of variation. Additive effects (D) were greater than (H_2) but less than (H_1) confirming the conclusion of additive with partial dominance in F_1 generation (Table VI).

The dominance (H_1 & H_2) effects were greater than additive (D) effects thus over–dominance in F_2 generation. The value of mean degree of dominance $(H_1/D)^{0.5}$ was found near to one in F_1 which showed partial dominance while it is greater than one for F_2 generation. It also indicates "over dominance type of gene action". The positive value of 'F' indicated that the number of dominant alleles were greater than the recessive alleles. The ratio of ¼ (H_2/H_1) was less than 0.25 indicating that positive and negative alleles frequencies overall loci were unequal. The different values of dominance (H_1 & H_2) effects i.e., 13.68 and 9.55 for F_1 and 66.99 and 42.45 for F_2 generation, also proved that the positive and negative alleles distribution was not equal. The value of the quantity $[(4KH_1)^{1/2} + F]/[(4KH_1)^{1/2} - F]$ was more than one, it also indicated that

Table VI. Estimates of components of variation for fiber strength

Components	F1	F2
D	12.14*±1.19	13.20* ± 1.42
H_1	13.68* ± 2.86	66.99* ± 13.09
H_2	9.55* ± 2.52	42.45* ± 11.40
H^2	0.62ns ± 1.69	1.46ns ± 7.64
F	8.42* ± 2.85	29.40* ± 6.71
E_2	0.44ns ± 0.42	0.234 ns ± 0.50
$(H1/D)^{0.5}$	1.06	1.128
$H_2/4H_1$	0.18	0.160
Kd/Kr	1.97	177.66
$K=h^2/H_2$	6.48	0.034
h^2 (ns)	0.56	0.781

dominant genes were greater than the recessive genes as proved by the positive value of F. The ratio h^2/H_2 indicated number of gene groups exhibiting dominance to some degree, and it was more than one. High estimates of h^2 (n.s) were obtained in both the generations. This offers a lot of scope for improvement of these characters through selection.

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