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ESTIMATION OF GENETIC PARAMETERS AND GENE ACTION FOR YIELD OF SEED COTTON AND LINT PERCENTAGE IN *GOSSYPIUM HIRSUTUM* L.

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Abstract: Gene action and genetic parameters for yield of seed cotton and lint percentage were studied in an eight parent diallel cross of upland cotton, which revealed that both additive and dominance components had prepondence in the inheritance of these characters. Asymmetrical distributions of dominant and recessive genes in the parents were observed. Low to moderate estimates of narrow sense heritability was obtained for both the characters.

Keywords: *Gossypium hirsutum* L., graphic analysis, lint percentage and gene action, yield of seed cotton.

INTRODUCTION

The breeding method to be adopted for improvement of a crop depends primarily on the nature of gene action involved in the expression of quantitative traits of economic importance. Diallel cross analysis leads to identification of parents with additive and non-additive effects. This in turn helps in choosing the parents to be included in a hybridization or population-breeding program.

The present investigation has been undertaken to know the type of gene action governing yield and lint percentage in upland cotton cultivars to identify the parents and crosses which could be exploited for the use in future breeding programme in cotton using diallel method [Sanyasi *et al*. 1982, Randhawa *et al.* 1986, Jugtap and Kolhe 1987, Tyagi 1988, Sing *et al.* 1990 and Murtaza *et al*. 1992] furnished information on additive and dominance gene effects. The importance of epistatic gene effect on yield and lint percentage was also reported by Khan and Khan [1993] and Murtaza *et al.* [1995].

MATERIALS AND METHODS

PLANT MATERIAL

From the elite working collection at Cotton Research Institute (CRI), Faisalabad, eight cultivars were chosen on the basis of their yield performance. These cultivars are denoted by their numbers and are followed throughout this research paper:

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

GLASSHOUSE CULTIVATION

Five seeds of all these cultivars were grown in 30 x 30 cm earthen pots (square) containing a mixture of equivalent volumes of sand, soil and farmyard manure from mid November 1993 to mid March 1994. Temperature within the glasshouse was maintained at 30ºC during day and 25ºC at night by using steam as well as electric heaters. The plants were exposed to natural sunlight and supplemented with artificial lighting, a photoperiod of 16 hours. Seedlings were thinned to one plant per pot 2 weeks after planting and after every 14 days 0.25 g of Urea (Nitrogen fertilizer) was added to each pot, plants were watered daily. The seed parents were emasculated manually and pollinated to produce enough hybrid seed. Extreme precautionary measures were taken to avoid pollen contamination from other varieties grown under the greenhouse.

FIELD EVALUATION

The seeds of 56F_1 hybrids and their parents were sown in the field (soil type was clay loam) on 1st June 1994 in a triplicate randomized complete block design. The growth protocol was identical for all the genotypes. The experimental plot was a 3.3-meter line single row with intra- and inter-row distance of 30 cm and 75 cm, respectively.

The F_1 hybrid and parents were self-pollinated to raise F_2 progeny. On 1st June 1995; F_2 progeny was sown in the same field also in a triplicated randomized complete block design (RCBD). The plot size for each cross in each replication was 3.3 x 6 meters. Ten plants in F_1 generation and sixty plants in F_2 generation in each replication were randomly chosen for all the data collection.

Yield of Seed Cotton (g)

The matured bolls were hand picked after every two weeks as soon as bolls started to open for both F_1 and F_2 generations; 150 days after planting (DAP) for three harvests and seed cotton was collected in Kraft paper bags. Picking was done when the dew had evaporated. The harvest was weighed on electronic balance (Mettler PE 360) and the average yield of seed cotton per plant for each genotype in each replication was then calculated and recorded.

Lint Percentage

Clean and dry samples of the seed cotton were weighed, then ginned separately with a single roller electric gin in the laboratory. The lint obtained from each sample was weighed and lint percentage was calculated by the following formula:

$$\text{Lint percentage} = \frac{\text{Weight of Lint in a Sample}}{\text{Weight of Seed Cotton in a Sample}} \times 100$$

STATISTICAL ANALYSIS

The data collected were subjected to the Fisher's analysis of variance as described by Steel and Torrie [1980]. While numerous methods of analyzing diallel data have been developed. Mather and Jinks [1971] concluded that Hayman [1954 a, b] analysis is the most useful for evaluating the mode of inheritance. So Hayman [1954 a, b] approach, as applied by Mather and Jinks [1977], 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 Senedcor and Cochron [1962].

The genetic parameters in F_1 population were computed as methodology given by Hayman [1954 a, b]. In F_2 generation the formulae for genetic parameters were modified as proposed by Verhalen and Murray [1969] and Verhalen *et al.* [1971].

RESULTS AND DISCUSSION

YIELD OF SEED COTTON PER PLANT

The results pertaining to analysis of variance [Steel and Torrie 1980] were presented in Table 1, which revealed that genotypic differences among cultivars were significant at 0.01 percent level of significance for both F_1 and F_2 generations; hence it permits to proceed for the analysis of the basic diallel data.

Table # 1. Estimates of mean square for Yield of Seed Cotton and Lint Percentage

Parameters		Mean Square Values	
		Genotypes	Error
Yield of Seed Cotton per plant	F_1	1660.1**	1011.66
	F_2	385.21**	32.9
Lint Percentage	F_1	26.69**	1.6
	F_2	15.27**	1.96

Table 2: Diallel analysis of variance for yield of Seed cotton and Lint percentage.

Parameters	Degree of Freedom	Yield of Seed Cotton Mean Squares			Degree of Freedom		Lint Percentage Mean Squares	
Item	F_1 and F_2	F_1	Retested	F_2	F_1	F_2	F_1	F_2
a	7	1589.00**	4669NS	3745.75**	6	7	202.46**	148.13**
b	28	3572.26**	1362NS	994.14**	21	28	70.35**	30.65**
b_1	1	10476.78*	3982NS	4601.48*	1	1	413.86**	9.80NS
b_2	7	3422.86*	1297 NS	956.79NS	6	7	29.18NS	27.66 NS
b_3	20	3279.32**	1245NS	826.85NS	14	20	63.45NS	32.74NS
c	7	4413.15**		517.79NS	6	7	95.87NS	40.68NS
d	21	3410.91**		720.21NS	15	21	38.39 NS	33.63NS
E	63	1296.89		704.62	48	63	50.17	26.62

** indicates significant differences at P< 0.01 probability level.
* indicates significant differences at P< 0.05 probability level.
NS = Non-significant, convention is followed throughout this research paper.

The diallel analysis of variance (Table 2) for yield of seed cotton in both the generations showed that (a) and (b) items were highly significant, which indicate the presence of additive and dominance effects. The significance of item (b_1) in both the generations showed the presence of directional dominance effects. The (b_2) was significant in F_1 generation indicating symmetrical distribution of genes, while it was non-significant in F_2 generation showing asymmetrical distribution of genes. The (b_3) item was also significant in F_1 generation showing presence of specific gene effects, while it was non-significant in F_2 generation, which indicated that specific gene effects were absent. The (c) and (d) items both were non-significant in F_2 generation showing the absence of maternal and reciprocal effects, while they were significant in F_1 generation so we retested (a) by (c) and b, b_1, b_2 and b_3 by (d). After retesting (a) became non-significant which means that additive effects were masked by the presence of maternal effects. Similarly after retesting b, b_1, b_2 and b_3 were also become non-significant, which indicated that dominance effects had been suppressed due to the reciprocal effects.

The analysis of V_r and W_r regression (Table 3) showed that regression coefficient depart significantly at 0.01 percent level of significance from unity but not from zero ($b=0.24\underline{+}0.18$) in F_1 generation, which indicated that non-additive variation including epitasis, multiple alleles and correlated genes distribution among the parents were present. Therefore, the data did not fulfill the diallel assumptions hence additive dominance model was partially inadequate.

Table 3: Test of Regression Coefficient of W_r on V_r for Yield and Lint Percentage.

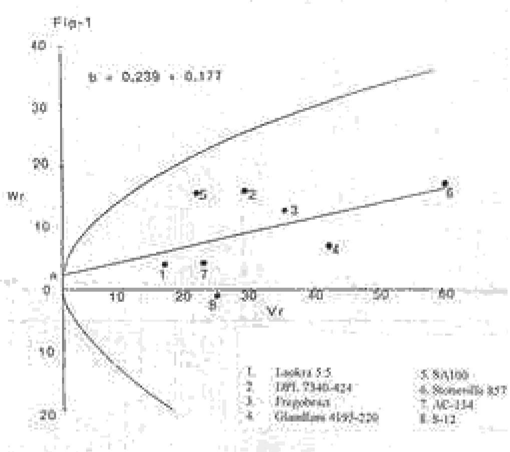
Parameters		Regression Coefficient (b)	Standard Error of Regression (SE (b))	t Value for b=0	t Value for b=1
Yield of Seed Cotton per plant	F_1	0.24	0.18	1.35 NS	4.29 *
	F_2	0.76	0.23	3.24*	1.05 NS
Lint Percentage	F_1	0.47	0.13	3.71*	4.18 **
	F_2	0.78	0.33	2.37 NS	0.68 NS

Table 4: Heterogeneity test for (Wr + Vr) and (Wr - Vr) estimates

Source	Yield of Seed Cotton Mean Square			Lint Percentage Mean Square			
	D. F.	F_1	F_2	D. F.	F_1	D. F.	F_2
Wr + Vr between array	7	308841.7 NS	27987.41*	6	42.57*	7	25.47 NS
Wr Vr within array	16	580204	6560.51	14	3.15	16	13.76
Wr – Vr between array	7	161272.8 NS	3398.32**	6	6.92 NS	7	8.22 NS
Wr-Vr within array	16	223119.9	825.94	14	3.1	16	7.54

The diallel data with variance and covariance for F_1 generation was presented in Table 4, which elaborated that there was no evidence of dominance effects as the mean square between arrays for W_r + V_r was non-significant, while the mean square between arrays for W_r - V_r was also non-significant, thus emphasizing partial adequacy of additive-dominance hypothesis [Mather and Jinks 1977].

W_r/ V_r graph for yield of seed cotton per plant in F_1 generation (Fig. 1) revealed that regression line intercepted the covariance axis on positive side (D > H_1) and signified the additive with partial dominance type of genetic mechanism for yield of seed cotton per plant. Fig.1 also showed that Laokra 5.5 possessed the maximum recessive alleles for this character. Wide scattering of array points on the regression line indicated much diversity for this character in the parents.
The W_r + V_r/P graph for yield of seed cotton per plant in F_1 generation (Fig. 2) showed negative correlation (r = -0.382), suggesting that genes for higher seed cotton yield tend to be dominant.



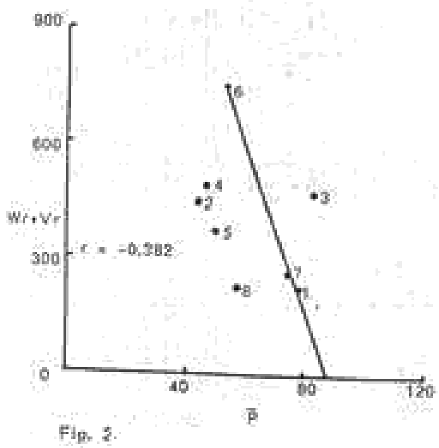


Fig. 1: W_r vs. V_r plot for yield of seed cotton per plant (F_1 generation).
Fig. 2: W_r+V_r vs.$\bar{P}$ plot for yield of seed cotton per plant (F_1 generation).

The results for regression analysis in F_2 generation of yield of seed cotton (Table 3) indicated that the regression coefficient (b = 0.76 $\pm$ 0.23) differ significantly at 0.05 percent level of significance from zero but not from unity, which indicated the adequacy of the additive-dominance model.
The analysis of variance of arrays Table 4 indicated that mean square between arrays of W_r + V_r at 0.05 and W_r - V_r were also significant at 0.01 percent level of significance. The significant W_r - V_r mean squares between arrays was due to the presence of non-allelic interaction, hence it invalidate the model and did not permit for further analysis [Mather and Jinks 1977].

LINT PERCENTAGE

In F_1 generation both test i.e. regression analysis and analysis of arrays invalidates the model, so rescaling was performed [Jinks 1954] and Laokra 5.5 was removed from the parental arrays and then the analysis proceeded as follows:

The variability among 56 genotypes, a pre-requisite for further analysis in F_1 population (Table 1) was confirmed from significant genotypic mean square at 0.01 probability level of significance of standard analysis of variance technique [Steel and Torrie 1980]. F_2 population also showed considerable variability at 0.01 percent probability level of significance. So further analysis of the data was preceded.

The items (a) and (b) both are highly significant in F_1 and F_2 generations (Table 2), thereby showing that additive and dominance effects are present. The (b_1) component was highly significant in F_1 generation only, so presence of directional dominance effects was confirmed, while they were absent in F_2 generation due to non-significance of b_1. The (b_2) and (b_3) both were non-significant which showed the asymmetrical distribution of genes with absence of specific gene effects. The items (c) and (d) were also non-significant which confirmed the absence of maternal and reciprocal effects.

The regression analysis (Table 3) showed that regression coefficient differs significantly from zero and unity in F_1 generation giving a clear evidence of the inadequacy of the additive dominance model.

Heterogeneity test for ($W_r + V_r$) and ($W_r - V_r$) presented in Table 4 showed that it was non-significant in F_2 generation, similarly ($W_r - V_r$) mean square for both the generation were also non-significant so its insignificance showed partial adequacy of additive-dominance model.

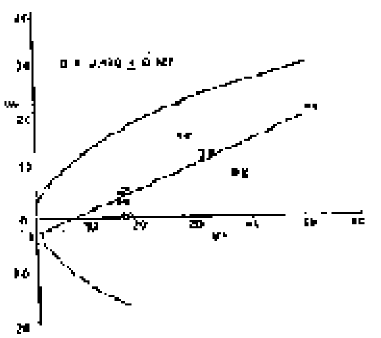


Fig. 3

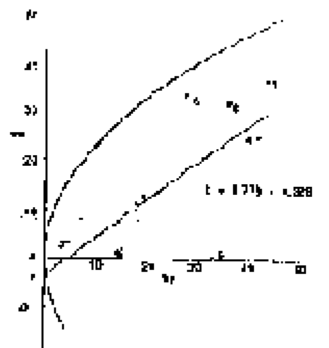
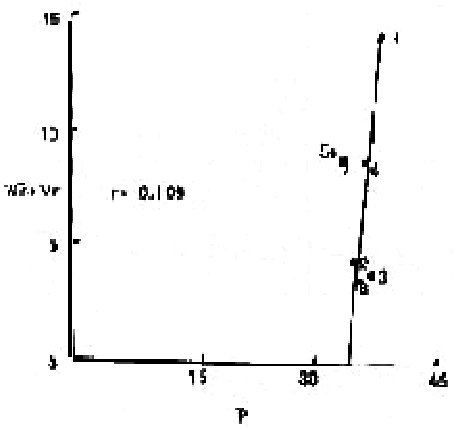


Fig. 4

Fig. 3: W_r vs. V_r plot for lint percentage (F_1 generation).
Fig. 4: W_r vs. V_r plot for lint percentage (F_2 generation).

The W_r vs. V_r plots for lint percentage (F_1 and F_2 generation) drawn in Figs. 3 and 4 indicated that regression line for both the generations touched W_r-axis below the origin ($D < H_1$), hence non-additive with over dominance type of gene action governed for the expression of lint percentage. The cultivar Fregobract possessed the most dominant genes being closest to the point of origin in both F_1 and F_2 generations. While Glandless 4195-220 in F_1 and Laokra 5.5 in F_2 generations had the maximum recessive genes for this character.

The W_r+V_r vs. $\overline{P}$ graphs given in Figs. 5 and 6 revealed that in general the plant with more lint percentage gave the larger values of $W_r + V_r$ and so must be carrying fewer dominant genes. The positive correlation in F_1 (r = 0.109) and F_2 (r = 0.048) indicated that genes, which lower the lint percentage, tend to be dominant.



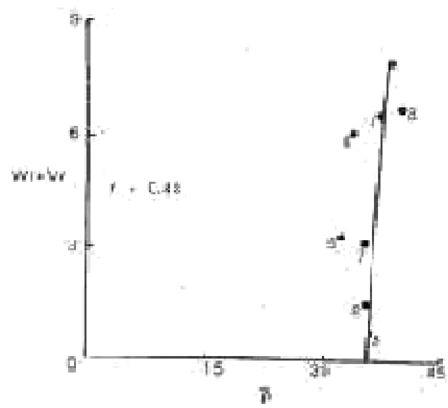


Fig. 5: W_r+V_r vs. $\overline{P}$ plot for lint percentage (F_1 generation).
Fig. 6: W_r+V_r vs. $\overline{P}$ plot for lint percentage (F_2 generation).

Table 5: Estimates of genetic parameters for yield of seed cotton and lint percentage.

Components of Variation	Yield of Seed Cotton		Lint Percentage	
	F_1	F_2	F_1	F_2
D	-125.6 NS ± 89.96	187.0* ± 23.91	2.89* ± 1.18	4.91* ± 0.90
H_1	105.75NS ± 206.8	1005.2* ±219.9	16.47* ± 2.85	24.70* ± 7.94
H_2	85.99NS ± 179.9	730.1* ± 191.3	14.54* ± 2.51	18.10* ± 6.91
h^2	354.43* ± 120.66	741.2* ± 628.3	22.28* ± 1.69	-7.25NS ± 4.63
F	-458.87* ± 212.56	314.9* ± 112.7	-1.45NS ± 2.84	5.14NS ± 4.07
E_2	358.87* ± 29.99	10.9 NS ± 7.9	0.54NS ± 0.42	0.65NS ± 0.29
$(H_1 / D)^{0.5}$	-0.420	1.16	2.39	1.15
$H_2 / 4H_1$	0.203	0.182	0.221	0.183
K_D / K_R	1.190	6.310	0.81	2.824
$K = h^2 / H_2$	4.120	1.020	1.532	-0.40
h^2 (ns)	0.500	0.574	0.43	0.43

GENETIC PARAMETERS

Estimates of the component of variation analysis given in Table 5 showed that dominance (H_1 and H_2) components of genetic variation exceed the additive component (D) supporting "over dominance" as confirmed from Figs. 3 and 4. While dominance components were non-significant for yield of seed cotton (in F_1) confirming the additive effects with partial dominance as clear from Fig. 1.

The existence of unequal gene frequencies in the parents was suggested by (H_1-H_2) as H_2 component was smaller than H_1. The asymmetrical distribution of genes in the parents was further evidenced by the value of proportion of genes with positive and negative effects ($H_2/4H_1$), from which it was found to be less than the maximum value of 0.25 for both characters in both generations.

The positive 'F' value for F_2 generation of both characters indicates gene asymmetry i.e. more dominant than recessive alleles. This was further confirmed by the proportion of dominant and recessive alleles, which were more than one, proving that dominant alleles were in excess. While it was found vice versa for F_1 generation.

The significant value of environmental component of variation (E_2) indicated that environment play an important role in the phenotypic expression of yield of seed cotton in F_1 generation.

The overall degree of dominance ratio $(H_1/D)^{0.5}$ was more than unity for both characters. This indicated the operation of over dominance. It also confirmed that quantitative traits are controlled by more than one group of genes.

Narrow sense heritability is a reflection of the amount of additive, fixable, heritable variation. Both characters showed h^2 (ns) in the moderate range. According to Hayman [1957] epistasis can decrease or increase degree of dominance, which also affect the heritability estimates.

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