

Genetic Analysis of Seed Cotton Yield and its Components in *Gossypium hirsutum* L.

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ABSTRACT

The present study was carried out in order to determine the type of gene action controlling plant height, number of bolls, boll weight, and seed cotton yield and lint percentage in *Gossypium hirsutum* L. Four varieties/lines were crossed in a complete diallel fashion, and F_1 population and their parents were grown in the field. The joint regression analysis of F_1 data revealed that the additive-dominance model was fully adequate for all the characters measured. The V_r/W_r graphs revealed that additive type of gene action with partial dominance was important for controlling these characters. The unit slope of regression lines for plant height ($b=0.99\pm0.23$), number of bolls ($b=1.14\pm0.10$), boll weight ($b=0.97\pm0.19$), seed cotton yield ($b=1.00\pm0.01$) and lint percentage ($b=1.10\pm0.05$) suggested the absence of epistatic component in the inheritance of the characters. It was revealed that GFS had maximum number of dominant genes for plant height, boll weight, seed cotton yield and lint percentage, and in contrast Tashkant-7 contained maximum number of recessive genes for plant height and boll weight, whilst for seed cotton yield and lint percentage S-12 carried the most recessive genes. The estimates of narrow-sense heritability ($h^2_{n.s.}$) for all the characters were high, and suggest that both pedigree and recurrent selection method may be useful to effect improvement in seed cotton yield and its components.

Key Words: Genetic analysis; Partial dominance; Additive gene action; Dominant genes; Heritability

INTRODUCTION

Amongst agricultural commodities of Pakistan, cotton is the main source of foreign exchange earnings. Although a great deal of research work had already been done in term of increasing total cotton production of the country, the average acre yield is still lower than that obtained in other cotton growing countries. This emphasizes the breeders to continue their efforts for exploiting the genetic resources available to them, through selection and breeding. The variation in exotic and local germplasm for the desirable characters may be used advantageously involving in plant improvement programme. To make such a programme a good success, the breeders are required to collect information about the genetic mechanisms governing various plant characters of economic importance in the parental plant material.

The previous work showed that inheritance of seed cotton yield and its components were controlled by the genes with additive and non additive loci. For example, the studies of Khan *et al.* (1999), Mukhtar *et al.* (2000), Iftikhar *et al.* (2001) and Subhan *et al.* (2002) revealed additive type of gene action with partial dominance, whilst Amin *et al.* (1997), Ajmal *et al.* (1998) and Shakeel *et al.* (2001) reported the presence of genes showing overdominance for these traits. Therefore, in order to obtain such information on seed cotton yield and its components in the plant material used here the F_1 data were analyzed following diallel technique of Hayman (1954a,b) and Jinks (1954). The Hayman-Jinks method provides useful information on the

genetic mechanism of plant traits in early generation like F_1 , and therefore was also used here.

MATERIALS AND METHODS

Four varieties/lines of *Gossypium hirsutum* L. namely GFS, Tashkant-7, S-12 and NIAB-999 having different origin and genetic makeup were grown in glasshouse with controlled temperature and light conditions during December, 2001, and were crossed in all possible combinations. The four parents were also selfed. The seeds of 12 F_1 crosses and the parents were planted in the field during June, 2002 in a randomized complete block design with three replications. In each replication, there were 10 plants spaced 75 cm between the rows and 30 cm within the rows. At maturity middle eight plants were measured for plant height, number of bolls, boll weight, seed cotton yield and lint percentage. Statistical analysis of 16 families was performed using simple analysis of variance technique (Steel & Torrie, 1980) in order to see whether the genotypic differences are significant. Only significant genotypic differences allow the use of Hayman-Jinks model of genetic analysis. Adequacy of the genetic model to the data set was determined using a scaling test, known as regression coefficient (b) analysis. According to Hayman (1954a) regression coefficient (b) must deviate significantly from zero, but not from unity if all the assumptions underlying the genetic model are fulfilled. For genetic analysis of F_1 data all the crosses were arranged into arrays. Variance (V_r) of the family means within an array and covariance (W_r) of

these means with non-recurrent parents were calculated from each diallel table. Other statistics necessary to estimate are variance of the parental means (V_oL_o), the means of array variance (V_1L_1), the variance of means of arrays (V_oL_1), and the means of array co-variances (W_oL_o). These statistics were used to estimate four genetic components of variation, D (additive effects of genes), H_1 and H_2 (dominance effects of genes), F, which provides an estimate of the relative frequency of dominant to recessive alleles in the parental lines, and the variation in the dominance over the loci. Heritability estimate of each character was calculated following Mather and Jinks (1982).

RESULTS AND DISCUSSION

Mean squares obtained from analysis of variance indicated significant differences among the parents and their F_1 progenies for all the five characters (Table I), and thus allowed the use of Hayman-Jinks model for genetic analysis of these characters. The array means of the characters, and variance (V_r) and covariance of the parents (W_r) are given in Table II. The regression coefficient for plant height ($b=0.99\pm0.23$), number of bolls ($b=1.14\pm0.10$), boll weight ($b=0.97\pm0.19$), seed cotton yield ($b=1.00\pm0.01$) and lint percentage ($b=1.10\pm0.05$) are given in Fig. 1, and these

deviated significantly from zero and were equal to unity, suggesting that the data were fit for genetic interpretation, and there was no evidence of the presence of epistatic interaction. A further verification of the fulfillment of the assumptions is suggested when the array points lie closer to the regression line, and this was found to be true in all the cases.

On the basis of simple Hayman-Jinks model, the V_r and W_r graphs (Fig. 1) revealed that the genes controlling the inheritance of plant height, number of bolls, boll weight, seed cotton yield and lint percentage appeared to interact cumulatively, because the regression lines (b) were all of unit slope, and intersection of the regression line of V_r/W_r graph above the origin signified the importance of partial dominance. The relative distribution of varieties along the regression line (Fig. 1) revealed that GFS having the lower values of V_r and W_r was present closer to the origin, and has carried the most dominant genes for all the characters except number of bolls where S-12 carried the maximum number of recessive genes. Tashkant-7 being located away contained the most recessive genes for plant height and boll weight, whilst for seed cotton yield and lint percentage S-12 carried the most recessive genes, and for number of bolls NIAB-999 had maximum number of recessive genes.

The significance of the components of variation i.e. D,

Table I. Mean squares obtained from analysis of variance of five characters of *Gossypium hirsutum* L.

Source of variation	Degree of freedom	Plant height	Number of bolls	Boll weight	Seed cotton yield	Lint percentage
Replications	2	43.711	55.332	0.024	39.382	0.079
Genotypes	15	320.367**	103.566*	0.068*	60.245*	1.204*
Error	30	112.041	46.667	0.030	28.600	0.526

Table II. Variance (V_r), Covariance (W_r) of the parents, and array means of five characters of *Gossypium hirsutum* L.

Varieties	Plant height	Number of bolls	Boll weight	Seed cotton yield	Lint percentage
GFS	161.92	32.15	2.93	78.79	34.29
Tashkant-7	148.82	26.59	3.15	74.18	34.56
S-12	150.20	24.69	2.90	70.55	34.80
NIAB-999	153.91	34.21	2.94	74.31	34.31
V_r	48.26	21.63	0.01	12.38	0.07
W_r	65.74	43.54	0.03	22.10	0.11

Table III. Estimates of components of variation in five characters of *Gossypium hirsutum* L.

Components of variation	Plant height	Number of bolls	Boll weight	Seed cotton yield	Lint percentage
V_oL_o	149.77	94.87	0.07	43.07	0.33
W_oL_o	65.74	43.54	0.03	22.10	0.14
V_oL_1	34.54	20.25	0.01	11.37	0.60
V_1L_1	48.26	21.63	0.01	12.38	0.07
E	44.21 ± 3.57	19.37 ± 0.52	0.012 ± 0.0002	12.01 ± 0.02	0.20 ± 0.001
D	$105.56^* \pm 7.98$	$75.50^* \pm 1.17$	$0.054^* \pm 0.005$	$31.06^* \pm 0.05$	$0.12^* \pm 0.003$
H_1	$79.79^* \pm 23.19$	$7.07^* \pm 3.42$	-208.07 ± 0.001	$3.97^* \pm 0.16$	-12.16 ± 0.01
H_2	-33.53 ± 21.41	-33.21 ± 3.15	-0.021 ± 0.001	-19.97 ± 0.14	-0.35 ± 0.01
F	-7.63 ± 20.49	-3.80 ± 3.02	$0.002^* \pm 0.001$	-14.28 ± 0.14	-0.10 ± 0.01
h	1.02	-0.14	0.03	1.72	-0.07
$(H_1/D)^{0.5}$	0.87	0.31		0.36	
$h^2_{(n.s.)}$	0.76	0.84	0.98	0.83	0.94

Note: If the value of a parameter divided by its S.E exceeds 1.96, then it is significant.

Fig. 1a. W_r/W_r graph for plant height (cm)

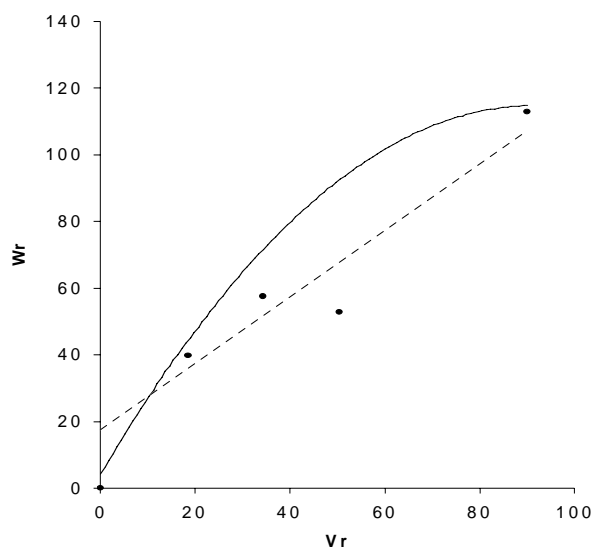


Fig.1b. W_r/W_r graph for number of bolls per plant

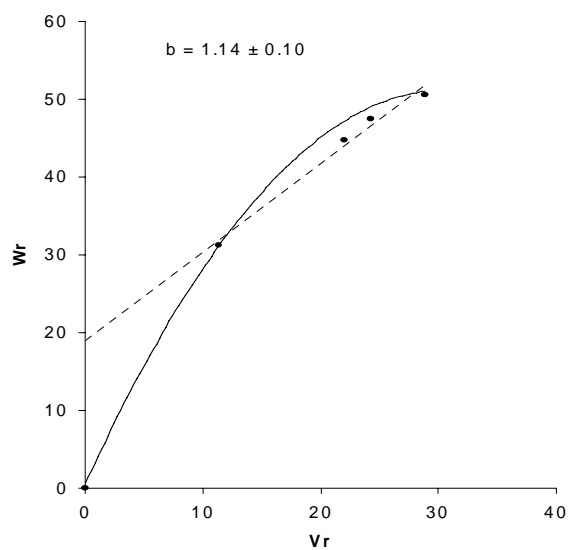


Fig.1c. W_r/W_r graph for boll weight (g)

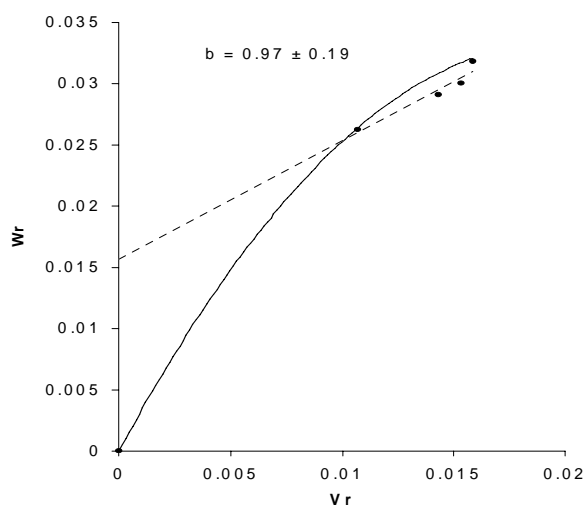


Fig.1d. W_r/W_r graph for seed cotton yield (g)

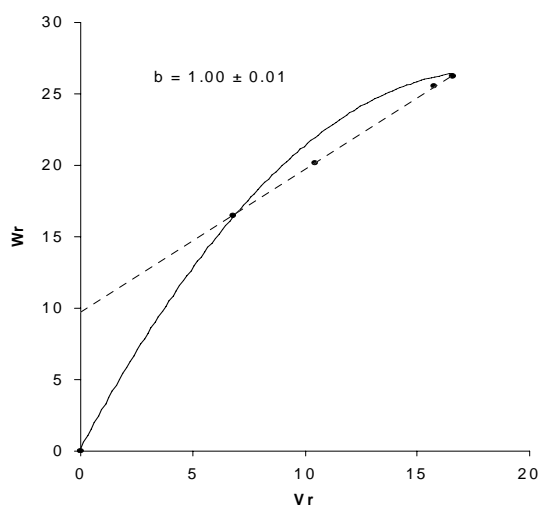
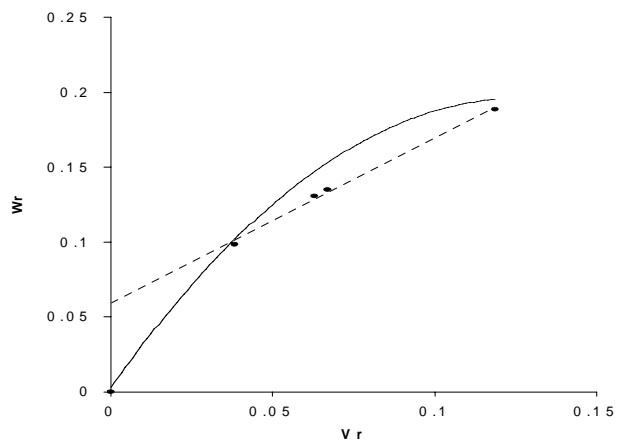


Fig.1e. W_r/W_r graph for lint percentage



H_1 , H_2 and F calculated in the five characters (Table III) is been discussed here. The additive component (D) for all the characters was significant, however dominant component (H_1) appeared to be significant for plant height, number of bolls and seed cotton yield. H_2 component was non-significant for all the characters, and similarly the values of F were non-significant except boll weight, and therefore not considered here. Although D and H_1 components were significant, the greater magnitude of D item for all the characters suggest that additive genetic effects were more pronounced than dominance effects in the genetic mechanism controlling all the characters, and the claim was strengthened by the position of regression lines in Fig. 1. These results agreed with those of Khan *et al.* (1995), Ahmad *et al.* (1997), Iftikhar *et al.* (2001) and Subhan *et al.* (2002).

The positive and significant value of F for boll weight revealed that there were more dominant genes than recessive alleles in the parents. Furthermore, the sign of h (mean F_1 - parental means), which measured the direction of dominance, were positive for plant height, boll weight and seed cotton yield (Table III), suggesting that dominance acted in the direction of the parents with higher expression of the characters, whilst for number of bolls and lint percentage, it was negative, indicating the lower expression of characters from parents to offspring. The degree of dominance, averaged over all loci, was indicated by the estimate of $(H_1/D)^{0.5}$. If there was complete dominance at every locus, the value of $(H_1/D)^{0.5}$ would have been 1, with partial, between 0 and 1 and with overdominance, greater than 1. Thus the estimates of $(H_1/D)^{0.5}$ for plant height (0.87), number of bolls (0.31) and seed cotton yield (0.36) indicated partial dominance, and agreed with the observations made in the Fig. 1.

The estimates of $h^2_{n.s}$ for all the characters, within the limits of present study were inflated. The high estimates might be expected since the genetic mechanism of all the characters appeared to be predominantly influenced by additive genetic effects. However, these estimates must be interpreted with caution, as the material has been tested under single environment, as suggested by Falconer and Mackey (1996). The presence of additive gene action and high heritabilities of seed cotton yield and its components

suggest that the F_2 populations may be amenable to selection, and both pedigree method and recurrent selection may be successful for improving the characters studied here. The extent to which the information derived here, applies to *Gossypium hirsutum* L. as a whole is uncertain, and thus may be substantiated by conducting another genetic study using a large number of parents / lines of the species.

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