ESTIMATION OF GENE ACTION FOR FIBRE TRAITS IN UPLAND COTTON

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Abstract— The experiment was laidout in randomized complete block design with four replications in the experimental field of Botanical Garden, Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam for assessing the gene action for quality traits in a 5x5 complete diallel cross having five varieties of *Gossypium hirsutum* L.

The genetic components of variance revealed that dominance components (H1 and H2) and additive component (D) were highly significant for all the traits except staple length in dominance components. It was further observed that dominance components were greater in magnitude than additive components. The average degree of dominance for lint index, GOT%, staple length and fibre strength were more than a unity, displaying over dominance type of gene action, the positive non-significant F-value revealed that the dominant genes were less frequent than recessive genes in the parents and that they were in decreasing position as exhibited by h2 value. Estimated ratio of h2/H2 indicated that there were at least one group of genes controlling GOT%, two group of genes controlling lint index and fibre strength and three group of genes controlling staple length.

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1 Introduction

A systematic and successful hybridization programme for yield improvement in cotton (*Gossypium hirsutum* L) demands an understanding of the genetic architecture of quantitative and qualitative characters to be bred (Hayman, 1958) and requires information on (a) inheritance of yield and its morpho-physiological components, (b) the nature of relationship between yield and these components and (c) the efficacy of such genetic patterns in the selection process.

Estimating components of quantitative genetic variation may be justified at least for three reasons: Understanding fundamental genetic phenomena, predicting gain under selection in heterozygous population and identifying parents which might yield superior F1 hybrids (Chapman and McNeal, 1971). Sprauge (1966) listed three major factors that must be considered in the analysis of quantitative genetic variation i.e. the number of genes involved, type of gene action and genotype environment interaction. The diallel cross technique is one of the conventional approaches used in biometrical genetics to obtain adequate information regarding the inheritance of a quantitative and qualitative character. Diallel analysis as developed by Hayman (1958), Jinks (1954, 1956) and Jinks and Hayman (1958) provides a systematic approach for the depiction of parents and crosses superior for the traits under investigation and help plant breeder to choose the efficient method of selection for isolation of superior genotypes among

the offsprings of hybrid progenies under investigation. A diallel cross among selected parents can provide information on the genetic variances in a population derived by random mating of these parents. Since last decade, the analysis of diallel crosses received considerable emphasis in many plant breeding programmes, because it fulfils certain specific needs of plant breeders. The analysis provides a systematic approach for the detection of parents and crosses superior for the trait under investigation. Besides, it can help the plant breeder to choose most efficient method of selection as it provides estimates of various genetic parameters. Further breeding programme will have to rely more on such crosses which assemble genotype with high yield potential and a more stable performance after ascertaining the general and specific combining ability of our commercial cotton varieties.

Research work on the genetic improvement of cotton crop had been undertaken since independence and as a result, large numbers of varieties possessing harmonious combination of characteristics were evolved. In this context, present research programme was undertaken to study the nature of gene action in 5x5 parent dialle set of crosses of cotton in F2 generation.

2- MATERIAL AND METHODS

An experiment was conducted in the experimental area of Department of Plant Breeding and Genetics, Sindh Agriculture University Tandojam. Material consisted of five cultivars of upland cotton, *Gossypium hirsutum* L. viz. TH-3/83, NIAB-78, CIM-109, McNair-3150 and Reshmi sown in Randomized Complete Block Design with four replications. Before first irrigation, seedlings were thinned to maintain plant to plant distance of 30 cm, while row to row distance was kept 75 cm. All the required cultural and agronomical practices were adopted uniformly in all replications throughout the growing period. Data were collected for lint index, GOT%, staple length and fibre strength.

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The data were statistically analyzed after Steel and Torrie (1980). Graphical analysis was based on the variance and co-variance values (Vr/Wr graph) following the procedure developed by Jinks and Hayman (1958). The population parameters estimated were E, D, F, H1 and H2. E is the estimate of environmental variance, D is the additive genetic variance which may include a portion of the additive x additive epistatic variance as well as the additive genetic variance itself. H1 is the dominance genetic variance parameter, which may include the dominance genetic variance proper, dominance x dominance epiststic variance and additive x dominance as well as the portion of the additive x additive variance not included within D. H2 is the component of genetic variance due to non-additive (dominance) effects corrected for gene distribution. F is an indicator of the relative frequency of dominant and recessive alleles in the parents and may take a sign positive or negative.

The limiting parabola was constructed on the basis of formula $Wr2 = Vr \times Vp$ i.e, by ploting $Vr(Vr \times Vp)1/2$ points. The corresponding values for Wr for all observed Vr values were calculated as $(Vr \times Vp)1/2$, where Vp = variance of parents. The different arrays (varieties) were fitted within the limits of the parabola using the individual variance and covariance as their limiting points. Array nearest to the point of origin possessed most of the dominant genes, while the array that laid the farthest possessed most of the recessive genes, and the intermediate portion signified the presence of both dominant and recessive genes in the array.

2.1 Genetic Components of variation

The genetic components of variation were calculated using the modified formula of Hayman (1958) for genetic parameters as proposed by Verhalen and Murray (1969) and Verhalen *et al.* (1971).

Environmental Variation	$E = EMS / No.\ of\ reps.$
Additive variation	$D = Volo_2 - E$
Variation due to dominant effect of genes	$H_1 = 16\ V1L_2 - 16\ \underline{Wolo} + 4\ Volo_2 - \dfrac{4(5n-4)\ E_2}{n}$
Variation due to dominant efffect of genes correlated for gene distribution	$H_2 = 16V_1L_2 - 16\ Vo_2 - \dfrac{16(n-1)\ E}{n}$
Over all dominance effects of heterozygous loci	$h^2 = (4ML_1 - 4Mlo)^2 - \dfrac{16(n-1)\ E}{n}$
Covariance of additive and Non-additive effect in the rth array	$Fr = 4[Volo_2 - Wolo_2 + V_1L_2 - (\underline{Wri} + \underline{Vri})] - \dfrac{(n-2)E}{n}$
Relative frequency of dominant to recessive alleles	$F = 4\ Volo_2 - 8\ Wolo_2 - \dfrac{4(n-2)\ E}{n}$
A weighted measure of the average degree of dominance at each loci	$\frac{1}{4}[H_1/D]^{1/2}$
Proportion of dominant and recessive genes	$\dfrac{\frac{1}{4}(4DH1)1/2 + 1/2F}{\frac{1}{4}(4HD)1/2 - 1/2F}$
Heritability (n.s)	$h^2\ (n.s) = \dfrac{\frac{1}{4}\ D}{\frac{1}{4}\ D + 1/16H1 - 1/8F + E2}$
Heritability (b.s)	$h^2\ (b.s) = \dfrac{VF2\ VP1 \times VP2}{VF2}$
Genetic advance %	$\dfrac{GA}{\overline{X}} \times 100$
Genetic variance	$\dfrac{MSG - MSE}{r}$
Phenotypic variance	MSG/r

Where
M.S.E. = Error Mean Square; $Volo_2$ = Parental variance for F_2; V_1L_2 = Mean variance of arrays in F_2; $Wolo_1$ = Mean covariance between the parents and the arrays in F_1; $Volo_1$ = Variance of the mean of array in F_2; $(M1L1 - \underline{Mlo})^2 = 1/n(1/n\ grand\ total\ sum\ of\ diagonal\ values)^2$; $Wolo_2$ = Mean covariance between the parents and the arrays in F_2; M.S.G. = Mean squares of genotypes; M.S.E. = Mean squares of Error.

3- EXPERIMENTAL RESULTS

The present studies were carried out to assess the gene action and selection parameters for qualitative traits in 5x5 diallel cross of *Gossypium hirsutum* L. Five cultivars and their crosses were studied for assessing varietal performance

and graphical (Wr, Vr) approaches. The results of statistical analysis of the data through computer programme MSTAT-C and various genetic parameters for four traits are presented here in seriatim in following tables and paragraphs.

The analysis of variance (ANOVA) for parents and their F2 hybrids differed highly significantly (P>0.01) for lint index and differed significantly (P>0.05) for GOT% and staple length, indicating the presence of considerable genetic variability among the parents and their F2 hybrids for these traits.

The data presented in Table 1 revealed that Cross NIAB-78 x Reshmi exhibited highest lint index (4.537 gms) over all the entries, whereas hybrid Reshmi x Mc-Niar-3150 gave highest G.O.T.% (42.77%). Maximum staple length was obtained from cross of Reshmi x TH-3/83 (29.65 mm) and cross Reshmi x TH-3/83 had higher values (92.84) for fibre strength.

TABLE 1: MEAN PERFORMANCE OF PARENTS AND THEIR CROSSES FOR QUANTITATIVE AND QUALITATIVE TRAITS IN F2 GENERATION

S. No.	Parents and Crosses	Lint index (gms)	G.O.T. %	Staple length (mm)	Fibre strength (lbs/sq inch)
1	TH-3/83	3.374 h	35.11 j	29.35 abc	92.08
2	NIAB-78	4.049 c-f	40.45 bcd	28.32 c-h	91.76
3	CIM-109	3.778 fg	40.7 bc	28.49 b-h	92.27
4	Mc-Niar-3150	3.826 efg	40.16 bcd	27.73 ghi	92.16
5	Reshmi	4.349 ab	39.77 b-f	29.46 ab	92.22
6	TH-3/83 x NIAB-78	3.574 gh	38.14 f-I	28.84 a-f	92.23
7	TH-3/83 x CIM-109	3.79 fg	39.13 c-h	28.44 b-h	92.29
8	TH-3/83 x Mc-Niar-3150	3.863 efg	38.74 d-I	28.91 a-f	92.47
9	TH-3/83 x Reshmi	3.815 fg	38.15 f-I	28.81 a-f	91.84
10	NIAB-78 x CIM-109	3.623 gh	40.99 b	28.6 b-h	92.33
11	NIAB-78 x Mc-Niar-3150	3.946 def	41.05 b	29.18 a-e	91.97
12	NIAB-78 x Reshmi	4.537 a	40.53 bc	28.14 f-I	92.27
13	CIM-109 x Mc-Niar-3150	4.375 ab	40.22 bcd	28.74 a-g	92.46
14	CIM-109 x Reshmi	3.981 c-f	39.95 b-e	29.4 ab	92.33
15	Mc-Niar-3150 x Reshmi	4.24 bc	38.37 e-I	29.25 a-d	92.27
16	NIAB-78 x TH-3/83	3.4 h	37.13 I	27.68 hi	92.56
17	CIM-109 x TH-3/83	3.801 fg	37.51 hi	29.47 ab	92.48
18	Mc-Niar-3150 x TH-3/83	3.781 fg	37.43 I	28.5 b-h	92.35
19	Reshmi x TH-3/83	3.814 fg	37.87 ghi	29.65 a	92.84
20	CIM-109 x NIAB-78	3.617 gh	38.73 d-I	28.23 d-h	92.2
21	Mc-Niar-3150 x NIAB-78	3.65 gh	39.32 b-g	28.19 e-h	91.98
22	Reshmi x NIAB-78	4.102 b-e	40.1 bcd	28.59 b-h	92.22
23	Mc-Niar-3150 x CIM-109	3.62 gh	39.47 b-g	27.12 I	92.13
24	Reshmi x CIM-109	4.209 bcd	40.56 bc	28.79 a-f	92.26
25	Reshmi x Mc-Niar-3150	4.196 bcd	42.77 a	27.93 f-I	92.64
Source of variation	**DF**	**Mean Squares**			
Replication	3	0.487	8.548	0.643	0.101
Genotypes	24	0.368**	10.416**	1.689**	0.228
Error	72	0.078	2.629	0.542	0.205

Components of genetic variation and heritability

The means of genotypes arranged in diallel tables for each trait are presented in Table 2 to 4 and the Wr/Vr graphs plotted in figures 1 to 4 are discussed characterwise as under.

3.1 LINT INDEX

The array means presented in Table 2 showed that variety Reshmi had the highest array mean (4.1844 g) followed by variety Mc-Niar-3150 (4.0412 g). This shows that these varieties may prove better general combiners for higher lint index, while varieties TH-3/83, NIAB-78 and CIM-109 had the lowest array means (3.634, 3.7984 and 3.804 grams respectively) indicating poor general combiners for lower lint index. Among hybrids the cross NIAB-78 x Reshmi was best

combination showing highest value (4.537 g) for lint index whereas, cross NIAB-78 x TH-3/83 showed the lowest value (3.4 g) exhibiting SCA for lesser lint index.

TABLE 2 MEAN DIALLEL OF 5X5 PARENTAL CROSSES OF COTTON FOR LINT INDEX

	TH-3/83	NIAB-78	CIM-109	Mc-Niar-3150	Reshmi
TH-3/83	3.374	3.574	3.79	3.863	3.815
NIAB-78	3.4	4.049	3.623	3.946	4.537
CIM-109	3.801	3.617	3.778	4.375	3.981
Mc-Niar-3150	3.781	3.65	3.62	3.826	4.24
Reshmi	3.814	4.102	4.209	4.196	4.349

Figure 1 reveals that the regression line passed Wr axis below the origin, indicating over dominance type of gene action. From the position of array points on the regression line, it is observed that varieties Mc-Niar-3150, TH-3/83 and CIM-109 had maximum dominant genes as they were close to the origin. These results suggest that combinations of these varieties will produce lesser lint index. While varieties Reshmi and NIAB-78 had maximum recessive genes, as they were away from the origin, suggesting that combination of Reshmi and NIAB-78 will produce higher lint index. Positive value of correlation (Wr + Vr with parental values) indicated that recessive genes controlled the trait.
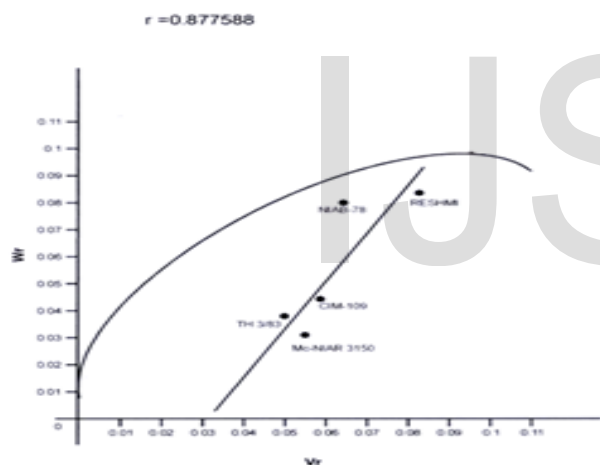

Figure 1. Wr/Vr graph for lint index

The genetic components of variance for lint index in F2 generation, (Table 6) revealed that the dominance components (H1=0.689 and H2=0.761) were highly significant and greater than additive components (D=0.0514) and the average degree of dominance ($\sqrt{1/4(H1/D)}$= 1.83) was more than one, displaying over dominance type of gene action, which was also confirmed in Wr/Vr graph. The positive and non-significant value of F and the value of ($\sqrt{1/4(4DH1)}$ + F/$\sqrt{1/4(4DH1)}$ - F (2.0042) revealed that the dominant genes were more frequent than recessive genes in the parents and that they were in decreasing position as exhibited by h2 (0.997**). The value of H1 was lesser than H2 indicating that positive and negative genes were symmetrical in the parents as confirmed by the value H2/4H1 (0.276) which is nearer to 0.25, whereas the estimated ratio h2/H2 (1.3104) indicated that there were at least two group of genes controlling lint index and that genes exhibited some degree of dominance. Further,

the value of r2 (0.770) showed the complete dominance of parents. Heritability in narrow sense (h2 n.s), is the ratio of additive or additive x additive variance to the total phenotypic variance, showed low heritability (0.191) with additive genes (Table 6).

As far as the character lint index was concerned, TH-3/83 and Reshmi proved to be the best general combiners, which could be utilized in the production of pure line varieties. The crosses of Reshmi with NIAB-78 and Mc-Niar-3150 were the best specific combiners for this trait and form the potential material for the development of hybrid cottons. EL-Adl et al. (2001), Meena et al. (2001), Zia et al. (2001), Laxman and Ganesh (2003), Mehetre et al. (2003) and Odhano (2003) have also obtained significant general and specific combining ability variances for this trait. The Wr/Vr graph proved the partial and over dominance type of gene action underlying these trait respectively. The negative value of "r" have indicated that the lint index is controlled by recessive genes. These results are in agreement with the results of Subhan et al. (2001) who also reported over dominance type of gene action for these traits.

Ginning Outturn Percentage

The array means presented in Table 3 showed that variety Mc-Niar-3150 had the highest array mean (40.5872%) followed by variety CIM-109 (40.171%) indicating that these varieties may prove better general combiners for higher GOT%, while variety TH-3/83 had the lowest array mean (37.0092%) indicating poor general combiner for GOT%. Among hybrids the progeny of cross Reshmi x Mc-Niar-3150 was the best combination showing highest value (42.768 %) for GOT% whereas, cross NIAB-78 x TH-3/83 showed the lowest value (37.126%) exhibiting SCA for lesser GOT%.

TABLE 3 MEAN DIALLEL OF 5X5 PARENTAL CROSSES OF COTTON FOR G.O.T. %

	TH-3/83	NIAB-78	CIM-109	Mc-Niar-3150	Reshmi
TH-3/83	35.11	38.139	39.131	38.738	38.145
NIAB-78	37.126	40.446	40.995	41.054	40.531
CIM-109	37.506	38.732	40.704	40.22	39.947
Mc-Niar-3150	37.432	39.318	39.469	40.156	38.365
Reshmi	37.872	40.104	40.556	42.768	39.768

Figure 2 reveals that the regression line passed Wr axis above the origin, indicating partial dominance type of gene action. From the position of array points on the regression line, it is observed that varieties CIM-109, NIAB-78 and Reshmi had maximum dominant genes as they were close to the origin, suggesting that combinations of these varieties will produce higher GOT%. While variety Mc-Niar-3150 had maximum recessive genes, as it was away from the origin, suggesting that combination of TH-3/83 and Mc-Niar-3150 will produce lesser GOT%. Negative values of correlation (Wr + Vr with parental values) indicated that dominant genes controlled the trait.
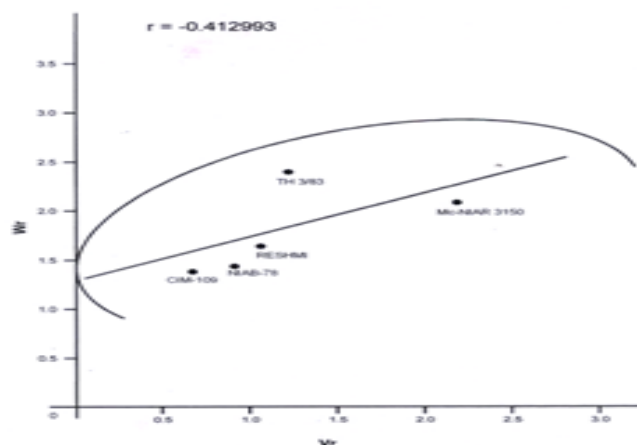
Figure 2. Wr/Vr graph for GOT%

The genetic components of variance for GOT% in F2 generation (Table 6) revealed that the dominance components (H1=31.856** and H2=44.997**) were highly significant and greater than additive component (D=2.8141) and the average degree of dominance ($\sqrt{1/4(H1/D)}$= -1.6823) was less than one, displaying partial dominance type of gene action, which was also confirmed in Wr/Vr graph. The positive and non-significant value of F (1.07) and the value of ($\sqrt{1/4(4DH1)}$ + F/$\sqrt{1/4(4DH1)}$ - F (0.9941) revealed that the dominant genes were more frequent than recessive genes in the parents and that they were in decreasing position as exhibited by h2 (0.748). The value of H1 was greater than H2 indicating that positive and negative genes were asymmetrical in the parents as confirmed by the value H2/4H1 (0.353) which is greater than 0.25, whereas the estimated ratio h2 /H2 (0.748) indicated that there was only one group of gene controlling GOT% and that genes exhibited some degree of partial dominance. The r2 value (0.171) also showed the partial dominance of parents. Heritability in narrow sense (h2 n.s) showed moderate to high heritability (0.605) with additive genes (Table 6).

As regards the character GOT%, Mc-Niar-3150 and CIM-109 proved to be the best general combiners followed by Reshmi and NIAB-78 showing the highest array means for this trait. Therefore, it is most probable that these varieties when used in the breeding programmes aimed at the improvement of GOT% would give transgressive segregates, which in turn could lead to the development of varieties with higher GOT%. The crosses Reshmi x Mc-Niar-3150 and NIAB-78 x Mc-Niar-3150 were the best specific combiners for this trait and would prove to be the best potential material to be exploited in the development of hybrid cottons. Baloch *et al*. (2003), Meheter *et al*. (2003), Odhano (2003) and Anisa *et al*. (2004) have also obtained significant GCA and SCA in their material for this trait. The perusal of Wr/Vr graph indicates that this character is controlled by partial dominance type of gene action, supported by negative "r" value which indicated that this character was controlled by dominant genes. The Wr/Vr graph indicated that varieties TH-3/83 and Mc-Niar-3150 had most of the dominant genes. These results are in partial agreement to Ahmed *et al*. (1997) and Khan *et al*. (2002) who reported over dominance type of gene action for this

character. Abro (2003) has also reported complete dominance for the control of this character. These results proved Mc-Nair-3150 and CIM-109 as the useful potential material to be exploited in the development of hybrid cottons.

3.2 STAPLE LENGTH

The array means presented in Table 4 showed that variety Reshmi had the highest array mean (29.0602 mm) followed by variety TH-3/83 (28.9318 mm) and that these varieties may prove better general combiners for longer staple length, while varieties CIM-109 and NIAB-78 had the lowest array means (28.2886 and 28.4344 mm respectively) indicating poor general combiners for shorter staple length. Among hybrids, the cross of Reshmi x TH-3/83 produced best progeny showing highest value (29.651 mm) for longer staple length whereas, cross Mc-Niar-3150 x CIM-109 showed the lowest value (27.124 mm) exhibiting SCA for shorter staple length.

TABLE 4 MEAN DIALLEL OF 5X5 PARENTAL CROSSES OF COTTON FOR STAPLE LENGTH

	TH-3/83	NIAB-78	CIM-109	Mc-Niar-3150	Reshmi
TH-3/83	29.352	28.841	28.437	28.908	28.809
NIAB-78	27.681	28.322	28.603	29.182	28.139
CIM-109	29.471	28.234	28.488	28.74	29.395
Mc-Niar-3150	28.504	28.186	27.124	27.729	29.247
Reshmi	29.651	28.589	28.791	27.93	29.711

Figure 3 reveals that the regression line passed through Wr axis above the origin, indicating partial dominance type of gene action. From the position of array points on the regression line indicated that varieties NIAB-78, Mc-Niar-3150 and Reshmi had maximum dominant genes as they were close to the origin, suggesting that combinations of these varieties will produce shorter staple length. While varieties CIM-109 and TH-3/83 had maximum recessive genes, being away from the origin, suggesting that combination of CIM-109 and TH-3/83 will produce longer staple length. Positive value of correlation (Wr + Vr with parental values) indicated that recessive genes controlled the trait.
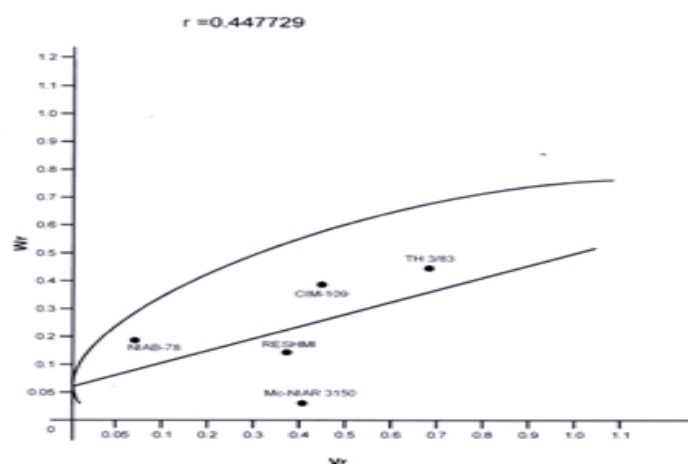

Figure 3. Wr/Vr graph for staple length

The genetic components of variance for staple length in F2 generation (Table 6) revealed that the dominance components (H1=4.065** and H2=2.412*) were significant and greater than additive component (D=0.102) and the average degree of dominance ($\sqrt{1/4(H1/D)}$= -3.158) was less than one, displaying partial dominance type of gene action, which was also confirmed in Wr/Vr graph. The positive and non-significant value of F (0.652) and the value of ($\sqrt{1/4(4DH1)}$ + F/$\sqrt{1/4(4DH1)}$ - F (2.889) revealed that the dominant genes were less frequent than recessive genes in the parents and that they were in increasing position as exhibited by h2 (6.9135**). The value of H1 was greater than H2 indicating that positive and negative genes were symmetrical in the parents as confirmed by the value H2/4H1 (0.1483) which is lesser than 0.25, whereas the estimated ratio h2 /H2 (2.867) indicated that there were at least three group of genes controlling staple length and that genes exhibited some degree of dominance. Further more the value of r2 (0.2005) also showed the partial dominance of parents. Heritability in narrow sense (h2 n.s), which is the ratio of additive or additive x additive variance to the total phenotypic variance, showed low heritability (0.061) with additive genes.

With respect to the character staple length, the results depicted variety Reshmi, as the best general combiner for this trait, whereas the crosses of Reshmi with TH-3/83 and Mc-Niar-3150 made the best specific combinations. Therefore, the variety Reshmi, TH-3/83 and Mc-Niar-3150 could be successfully exploited for the production of pure lines and hybrid cotton with respect to increased staple length. Iqbal (2002), Odhano (2003) and Anisa *et al.* (2004) have also reported significant GCA and SCA values for this trait. It is evident from Wr/Vr graph that the character staple length was controlled by partial dominance type of gene action. These results are in contradiction with the findings of Ahmed *et al.* (1997) who reported that this character was controlled by over dominance type of gene action. The results may be due to the different genetic background of the material used their experiments. The correlation coefficient between Wr+Vr and parental means revealed that increased staple length was the function of recessive genes.

3.3 FIBRE STRENGTH

The array means presented in Table 5 show that variety TH-3/83 had the highest array mean (92.462 lbs/sq inch) followed by variety Mc-Niar-3150 (92.3392 lbs/sq inch). It means that these varieties may prove better general combiners for stronger fibre, while varieties NIAB-78 and Reshmi had the lowest array means (92.078 and 92.1864 lbs/sq inch respectively) indicating general combining ability for weaker fibre. Among hybrids the cross Reshmi x TH-3/83 was best combination showing highest value (92.837 lbs/sq inch) for stronger fibre whereas, cross TH-3/83 x Reshmi showed the lowest value (91.843 lbs/sq inch) exhibiting SCA for weaker fibre.

TABLE 5 MEAN DIALLEL OF 5X5 PARENTAL CROSSES OF COTTON FOR FIBRE STRENGTH

	TH-3/83	NIAB-78	CIM-109	Mc-Niar-3150	Reshmi
TH-3/83	92.08	92.233	92.288	92.467	91.843
NIAB-78	92.556	91.762	92.332	91.967	92.268
CIM-109	92.484	92.197	92.271	92.456	92.331
Mc-Niar-3150	92.353	91.982	92.128	92.162	92.268
Reshmi	92.837	92.216	92.26	92.644	92.222

Figure 4 reveals that the regression line passed Wr axis below the origin, indicating over dominance type of gene action. From the position of array points on the regression line, it is observed that varieties CIM-109, Reshmi and TH-3/83 had maximum dominant genes as they were close to the origin, suggesting that combinations of these varieties will produce stronger fibre. While Mc-Niar-3150 and NIAB-78 had maximum recessive genes, as it was away from the origin, suggesting that combination of these varieties (Mc-Niar-3150 and NIAB-78) will produce weaker fibre. Negative values of correlation (Wr + Vr with parental values) indicated that dominant genes controlled the trait.
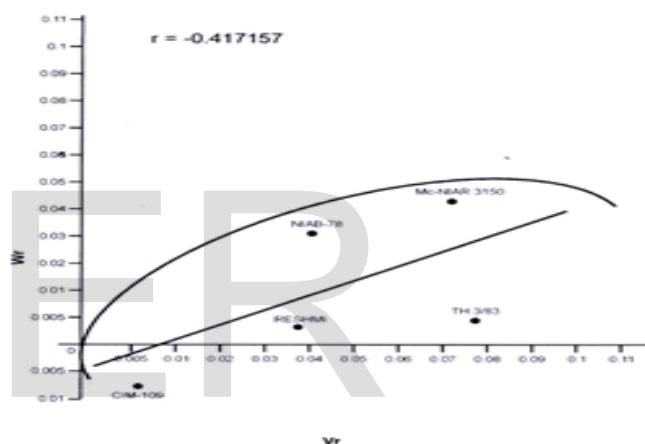

Figure 4. Wr/Vr graph for fibre strength

The genetic components of variance for fibre strength in F2 generation revealed that the dominance components (H1, H2 and D) were highly significant and the dominance components were greater than additive components and the average degree of dominance ($\sqrt{1/4(H1/D)}$= 1.74822) was more than one, displaying over dominance type of gene action, which was also confirmed in Wr/Vr graph. The positive and highly significant value of F (0.008945) and the value of ($\sqrt{1/4(4DH1)}$ + F/$\sqrt{1/4(4DH1)}$ - F (0.942526) revealed that the dominant genes were more frequent than recessive genes in the parents and that they were in increasing position as exhibited by h2 (0.063925**). The value of H1 was greater than H2 indicating that positive and negative genes were asymmetrical in the parents as confirmed by the value H2/4H1 (0.2109) which is lesser to 0.25, whereas the estimated ratio h2 /H2 (1.3323) indicated that there were at least two group of genes controlling fibre strength. Furthermore the value of r2 (0.3723) showed the over dominance of parents. Heritability in narrow sense (h2 n.s) showed moderate heritability (0.6552) with additive genes (Table 6).

TABLE 6 ESTIMATES OF GENETIC COMPONENTS OF VARIATION IN 5X5 PARENTAL DIALLEL OF COTTON FOR LINT INDEX, GOT%, STAPLE LENGTH AND FIBRE STRENGTH

	Lint index	GOT	Staple length	Fibre strength
D	0.051441**	2.814105**	0.101953n.s	0.004651**
H_1	0.68873**	31.85574**	4.066618**	0.056856**
H_2	0.761003**	44.99692**	2.41154*	0.047981**
F	0.117835n.s	1.069259n.s	0.651746n.s	0.008945*
h^2	0.997217**	33.63844**	6.913364**	0.063925**
E	0.078**	2.629**	0.542**	0.005**
$[1/4(H_1/D)]1/2$	1.829535	1.682263	3.157811	1.74822
$H_2/4H_1$	0.276234	0.35313	0.148252	0.210976
$\frac{1}{4}(4DH_1)1/2+1/2F/1/4(4DH_1)1/2-1/2 F$	2.004156	0.994054	2.888789	0.942526
h^2/H_2	1.310398	0.747572	2.866784	1.332297
R	0.877588	-0.412993	0.447729	-0.610166
r^2	0.77016	0.17056	0.200461	0.372302
Heritability (n.s)	0.190652	0.604751	0.060406	0.655186

With respect to the character fibre strength, the results revealed that varieties Reshmi and NIAB-78, were the best general combiners for these traits, whereas the crosses of Reshmi with TH-3/83 and Mc-Niar-3150 made the best specific combinations. Therefore, the variety Reshmi, TH-3/83 and Mc-Niar-3150 could be successfully exploited for the production of pure lines and hybrid cotton with respect to increased fibre strength. Iqbal (2002), Odhano (2003) and Anisa *et al.* (2004) have also reported significant GCA and SCA values for this trait. It is evident from Wr/Vr graph that the character fibre strength was controlled by over dominance type of gene action. These results are in accordance with the findings of Ahmed *et al.* (1997) who also reported that this character was controlled by over dominance type of gene action. The correlation coefficient between Wr+Vr and parental means revealed that increasing magnitude of these traits was the function of dominant genes.

4- CONCLUSION

The genetic components of variance revealed that dominace (H1 and H2) and additive component (D) were highly significant. The regression line exhibited that characters are controlled by dominance and over dominance type of gene action.

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