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Nature of Gene Action for Certain Agronomic Characters in *Gossypium hirsutum* L.

[1]*Farah Naz Kaleri,* [2]*Muhammad Abdul Rehman Rashid,*
[1]*Shahnawaz Mari,* [1]*Zahoor Ahmed Soomro and* [1]*Siraj Ahmed Channa*

[1]Department of Plant Breeding and Genetics, Sindh Agriculture University Tandojam-70060, Pakistan
[2]Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan

Abstract: An experiment was conducted to investigate the gene action for plant height, GOT% and seed index of five commercial varieties and ten direct crosses in Randomized Complete Block Design with four replications during kharif 2004. Results revealed that parent Acala-P_3 was good general combiner for plant height and GOT% whereas DPL-25 and DPL-7340-424 were good general combiner for seed index. Cross Qalandri×Sarmast and Qalandri×Acala-P_3 was the best combiner for plant height and seed index respectively while Acala-P_3×DPL-7340-424 was best specific combiner for GOT%. Further results revealed that plant height, seed index and GOT% were controlled by over dominance type of gene action. Regression line and Fr values confirm the gene action for the studied traits. Seed index and GOT% were controlled by one group of genes whereas plant height was controlled by three groups of genes.

Key words: *Gossypium hirsutum* L. · Gene action · Diallel mating · Agronomic traits

INTRODUCTION

Crop improvement is a one of the goals accomplished by higher degree selection of genotypes with extra ordinary performance. A significant variation in population is the main requirement for selection of superior plants which can attain by intercrossing of unrelated genotypes followed by phenotypic selection. The selection of parental lines for breeding of a specific trait always based on the type and extent of genetic control for that specific trait which can directly influenced by different environmental factors.

There are several mating systems have been designed to dissect the genetic and environmental control of complex quantitative traits. Diallel crossing is one of the most common adapted mating systems for crop improvement. The diallel analysis proposed by Jinks [1] and Hayman [2, 3, 4, 5] endeavors to dissect the total variation, in genotypic and environmental components and it further sub-divides genotypic variation, into additive and dominance components. These values can be used to draw inference about the genetic system. This method provides unique information about the nature of genetic system and together it clearly resolves the mechanism of inheritance.

The present study was designed to evaluate the inheritance pattern of plant height, GOT% and seed index from commercially cultivated cotton varieties. The half diallel crossing pattern was applied to achieve required results.

MATERIALS AND METHODS

The experiment was conducted during the kharif season of 2004 at the experimental field of Botanical Garden of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam. Five parental varieties of *Gossypium hirsutum* L. (Qalandri, Acala-P_3, DPL-25, Sarmast, DPL-7340-424) were grown and crossed inter specifically in half diallel mating system. Three seeds per hill for parental lines and ten F_1genotypes were sown by dibbling method in Randomized Complete Block Design (RCBD) with four replications and thinned to one seedling per hill to ensure uniform stand of only one plant per hill. The 30 cm plant×plant and 75 cm row×row distance was maintained. All the standard cultural practices were applied.

Ten guarded plants per genotype were randomly selected and tagged from each replication. At maturity data was collected for plant height (cm), seed index and

Corresponding Author: Muhammad Abdul Rehman Rashid, Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. Pakistan. E-mail: rashidpbg@hotmail.com.

ginning outturn percentage (GOT%). Plant height of selected plants was measured in centimeters (cm) from the soil surface to the tip of the main stem of the plant. A sample of hundred (delinted) cotton seeds were taken at random from each selected plants and their weight was recorded by electric balance in grams as seed index per plant. The samples from each plant were ginned separately with electric saw gin machine, after drying and cleaning them from dust and other foreign matter and were weighed. The ginning outturn percentage was calculated by using following formula.

$$\text{GOT \%} = \frac{\text{Weight of lint}}{\text{Weight of seed cotton yield}} \text{X } 100$$

To evaluate the variation among genotypes, data was analyzed by analysis of variance described by Steel *et al.* [6]. Genetic differences, the nature of gene action and other genetic components for selectedagronomic traits were studied through diallel analysis proposed by Hayman [2, 3] and Jinks [1].

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) of means showed the highly significant variation (P>0.01) among genotypes while the variation among replications was non-significant Table 1. The data about average performance revealed the Qalandri and DPL-7340-424 as tallest (106.35cm) and shortest statured parent (88.27cm). Among the F_1 hybrids Qalandri × Sarmast proved as tallest plants (116.50cm), whereas Sarmast×DPL-7340-424 had the short stature plants with a height of 106.15cm.DPL-25 was ranked first for seed index (8.83g) and Acala-$P_3$was lowest (7.225g). In hybrids, Qalandri×Acala-P_3 attained (9.142g) seed index, while Sarmast×DPL-7340-424 attained minimum as (7.92g). Maximum G.O.T% was obtained from Sarmast (33.6%) and Acala-P_3 x DPL-7340-424(35.63%), while DPL-7340-424 and Sarmast×Acala-P_3 gave the lowest (33.25% and 33.53%) ginning outturn percentage.

Combining Ability: The higher array means of Acala-P_3indicated as a best general combiner for plant height and GOT%, while DPL-25 found as a best general combiner for seed index. On the other hand, with lowest array mean for plant height, DPL-7340-424 was found as a good general combiner to induce dwarfness and simultaneously to improve seed index. Among hybrids the cross Qalandri×Sarmast showed highest value of array means for plant height whereas, the cross Sarmast×DPL-7340-424 was best specific combination for dwarfness but gave the lowest seed index. The cross Qalandri×Acala-P_3 proved better specific combiner for the seed index followed by Acala-P_3×DPL-7340-424 which was a best combination for GOT%. For GOT%, the hybrid Sarmast×DPL-25 also had an attractive combining ability.

Gene Action: The inheritance pattern of the subjected traits was found to be governed by over dominance type of gene action (Fig. 1a, 2a, 3a) as in Wr/Vr graphs the regression line intersected the Wr axis below origin. From the position of array points on the regression line, it was observed that varieties Qalandri, Sarmast and Acala-P_3 had maximum dominant genes for plant height as they were close to the origin, while DPL-7340-424 and DPL-25 had maximum recessive genes (Fig. 1a). It can predict that the combination of DPL-7340-424×DPL-25 will produce dwarf plants. For seed index, DPL-25 had maximum dominant, while variety Acala-P_3 possessed most recessive genes (Fig. 2a). Similarly, Sarmast and DPL-7340-424 showed the availability of maximum dominant and recessive genes for GOT% (Fig. 3a). Negative values of correlation (Wr + Vr with parental values) indicated that all three traits governed by dominant genes (Fig. 1b, 2b, 3b).

The non-significant value of "t" test for subjected traits confirmed the adequacy of the additive dominance model with no non-allelic interaction (epistatic) and indicates that genes were independent in their action for their random combinations. The regression analysis further manifested that regression coefficient (b) differed non-significantly from zero but significantly from unity which do not fulfill the assumptions of Hayman and Jinks model and make the model partially adequate (Table 6).

Plant Height: The genetic components of variance for plant height in F1 generation revealed that additive (D), dominance (H_1, H_2) and heritability (h^2) components were significant while environmental variation (E) and F value were non-significant (Table 7). The dominance components (H_1, H_2) were greater than additive components and the average degree of dominance (vH_1/D=1.7843) 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 $v4DH_1$+ F/$v4DH_1$-F (1.7824) revealed that the dominant genes were more frequent than recessive genes in the parents and that they were in increasing position as exhibited by h^2. The value of H_1 was greater than H_2 indicating that positive and negative genes were symmetrical in the parents as also confirmed

Table 1: ANOVA (mean squares) for various quantitative characters

Source of variation	D.F	Plant height (cm)	Seed index (g)	G.O.T %
Replications	3	15.80	0.021	0.303
Genotypes	14	271.89**	1.008**	2.279**
Error	42	18.80	0.069	0.203

** = Significant at P>0.01.

Table 2: Average performance of 10 F1 hybrids and their five parents for various characters in cotton (*Gossypium hirsutum* L.).

Genotypes	Plant height (cm)	G.O.T %	Seed index (g)
Qalandri X Sarmast	116.50	33.96	8.367
Qalandri X Acala-P_3	113.95	33.90	9.142
Qalandri X DPL-25	106.47	35.07	7.972
Qalandri X DPL-7340 –424	109.47	34.39	8.640
Sarmast X Acala-P_3	111.77	33.53	8.157
Sarmast X DPL-25	111.15	35.28	8.872
Sarmast X DPL-7340-424	106.15	34.18	7.920
Acala-P_3 X DPL-25	115.50	34.55	8.652
Acala-P_3 X DPL-7340 –424	111.92	35.63	9.115
DPL-25 X DPL-7340-424	114.12	33.58	8.585
Qalandri	106.35	33.37	8.287
Sarmast	105.07	33.68	8.577
Acala-P_3	102.50	33.50	7.225
DPL-25	91.32	33.36	8.830
DPL-7340-424	88.27	33.25	8.230
LSD (5 %)	5.154	0.536	0.312

Table 3: 5 x 5 diallel average plant height, variance (Vr) and covariance (Wr) for F1 generation of *Gossypium hirsutum* L.

Varieties	Qalandri	Sarmast	Acala-P_3	DPL-25	DPL-7340-424	Wr+Vr	Vr	Wr
Qalandri	106.35	116.50	113.95	106.475	109.475	35.586	20.591	14.995
Sarmast	116.50	105.075	117.75	111.15	106.15	35.610	21.429	14.181
Acala-P_3	113.95	111.775	102.50	115.50	111.925	13.737	25.644	-11.926
DPL-25	106.475	111.15	115.15	91.325	114.125	119.928	95.916	24.012
DPL-7340-424	109.475	106.15	111.925	114.125	88.275	150.578	106.849	43.729
Total	552.75	550.65	555.65	538.575	529.95	355.439	270.428	85.011
Mean	110.55	110.13	111.13	107.715	105.99	71.088	54.086	17.002

- Bold diagonal values represent parental values.
- Upper diagonal values represent direct cross values.
- Lower values represent alternate reciprocal cross values.
- Vr represent variance values.
- Wr represent covariance values.

Table 4: 5 x 5 diallel average seed index (g) variance (Vr) and covariance (Wr) for F1 generation of *Gossypium hirsutum* L.

Varieties	Qalandri	Sarmast	Acala-P_3	DPL-25	DPL-7340-424	Wr+ Vr	Vr	Wr
Qalandri	8.2875	8.3675	9.1425	7.9725	8.640	-0.0622	0.1929	-0.2551
Sarmast	8.3675	8.5775	8.1575	8.8725	7.920	0.2825	0.1357	0.1468
Acala-P_3	9.1425	8.1575	7.225	8.6525	9.115	0.9599	0.6372	0.3227
DPL-25	7.9725	8.8725	8.6525	8.830	8.585	0.1666	0.1306	0.036
DPL-7340-424	8.640	7.920	9.115	8.585	8.230	0.0134	0.2036	-0.1901
Total	42.41	41.895	42.2925	42.9125	42.49	1.3602	1.300	0.0603
Mean	8.482	8.379	8.4585	8.5825	8.498	0.2720	0.260	0.0121

- Bold diagonal values represent parental values.
- Upper diagonal values represent direct cross values.
- Lower values represent alternate reciprocal cross values.
- Vr represent variance values.
- Wr represent covariance values.

Table 5: 5 x 5 diallel average GOT% variance (Vr) and covariance (Wr) for F1 generation of *Gossypium hirsutum* L.

Varieties	Qalandri	Sarmast	Acala-P_3	DPL-25	DPL-7340-424	Wr+Vr	Vr	Wr
Qalandri	33.373	33.960	33.90	35.075	34.393	0.3713	0.4041	-0.0328
Sarmast	33.960	33.685	33.533	35.285	34.178	0.4204	0.4799	-0.06
Acala-P_3	33.90	33.533	33.505	34.555	35.635	0.6778	0.800	-0.1222
DPL-25	35.075	35.285	34.555	33.360	33.585	0.8559	0.7512	0.1047
DPL-7340-424	34.393	34.178	35.635	33.585	33.250	0.9206	0.8443	0.0762
Total	170.701	170.641	171.128	171.86	171.041	3.246	3.2795	-0.0341
Mean	34.1402	34.1282	34.2256	34.372	34.2082	0.6492	0.6559	-0.0068

- Bold diagonal values represent parental values.
- Upper diagonal values represent direct cross values.
- Lower values represent alternate reciprocal cross values.
- Vr represent variance values.
- Wr represent covariance values.

Table 6: Regression Analysis

Parameters	t^2-Test	b/SE	bo	b1
Plant height	5.3371^{NS}	0.3565 ± 0.1701	2.0956 ^{NS}	3.7823*
Seed index	0.0607^{NS}	0.6954 ± 0.5051	1.3766^{NS}	0.6029 ^{NS}
GOT%	2.2386^{NS}	0.1594 ± 0.2586	0.6165^{NS}	3.2500*

Table 7: Genetic components of variance for F1

Components	Plant Height	Seed index	GOT%
D	64.5177 ± 23.7871*	0.3568 ± 0.1531*	-0.0247± 0.1474 ^{NS}
H_1	205.4102 ± 64.2401*	1.3220 ± 0.4135*	2.5418± 0.3981**
H2	188.16636 ± 58.2665*	0.9851 ± 0.375*	2.4807± 0.3611**
F	64.7473 ± 63.2638 ^{NS}	0.6789 ± 04072 ^{NS}	0.9811± 0.3920 ^{NS}
h2	429.4971 ± 39.3388**	0.2393 ± 0.2532 ^{NS}	2.4015± 0.2437**
E	4.6507 ± 9.7110 ^{NS}	0.0166 ± 0.0625 ^{NS}	0.0524± 0.0601 ^{NS}
vH1/D	1.7843	1.9247	v-102.8884
H2/4H1	0.2290	0.1862	0.2439
v4DH1+F /v4DH1-F	1.7824	2.9542	v-102.89+0.019/
v-102.89-0.019 h^2 /H2	2.2825	0.2429	0.9680
R	-0.9504	-0.7739	-0.6262
r^2	0.9034	0.5988	0.3921
Heritability (h^2) (n.s)	0.1413	0.0274	0.0124
S^2	471.5256	0.0195	0.0181

Table 8: F_1, Fr-values

Cultivars	Plant height	Seed index	GOT%
Qalandri	135.7505	1.3473	0.5751
Sarmast	135.7022	0.6580	0.4769
Acala-P_3	179.4487	-0.6967	-0.0377
DPL-25	-32.9321	0.8898	-0.3940
DPL-7340-424	-94.2324	1.1960	-0.5233
Fri	64.7473	0.6789	0.0194

by the value $H_2/4H_1$ (0.229) which is nearer to 0.25, whereas the estimated ratio h^2/H_2 (2.2825) indicated that there were at least three groups of genes controlling plant height and that genes exhibited some degree of dominance. Further, the value of r^2 (0.9034) showed the complete dominance of parents. Heritability in narrow sense (h^2n.s), which is the ratio of additive or additive×additive variance to the total phenotypic variance, showed low heritability of additive genes.

Table 8 depicted maximum and minimum Fr values with positive and negative sign. It revealed the dominant and recessive gene frequencies respectively while Fig. 1b indicated that the dwarf varieties, in general the shorter varieties gave larger values of Wr+Vr than the taller varieties and were far away from the origin.

Seed Index (g): For components of variation, it was observed that only additive (D) and dominance components were significant, while F, h^2 and E were non-significant. Both H_1 and H_2 components were greater than that of additive and mean degree of dominance (vH_1/D=1.9247) was more than 1, predicting over dominance type of gene action. The unequal value of dominance components (H_1, H_2) indicated asymmetric distribution of positive and negative genes as confirmed by the H_2/4H1 (0.1862). Both the positive and

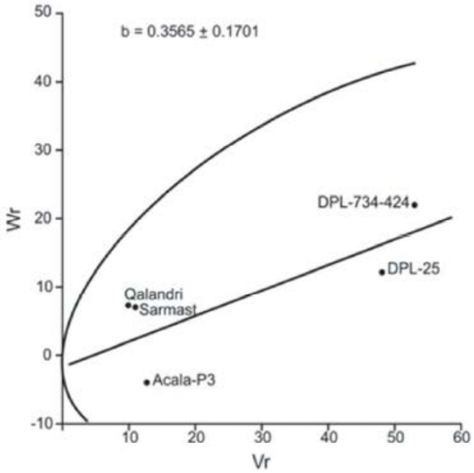

Fig. 1a: Wr/Vr Graph of Plant Height

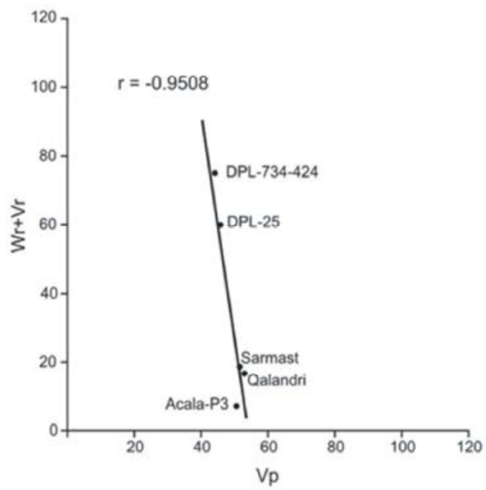

Fig. 1b: Wr+Vr/Vp Graph of Plant Height

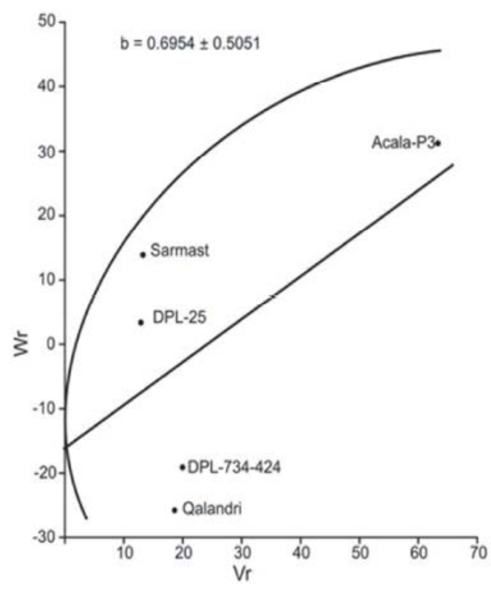

Fig. 2a: Wr/Vr Graph of Seed Index

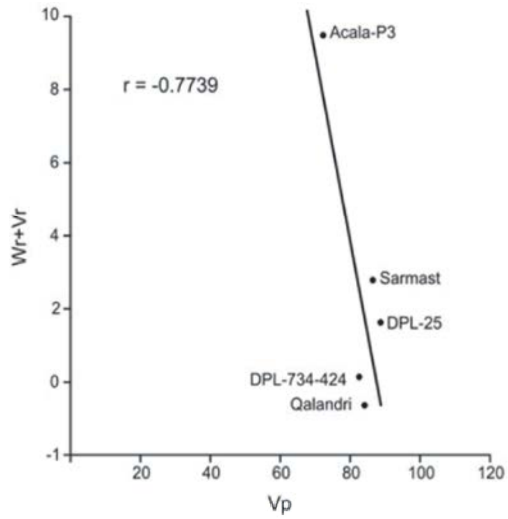

Fig. 2b: Wr+Vr/Vp Graph of Seed Index

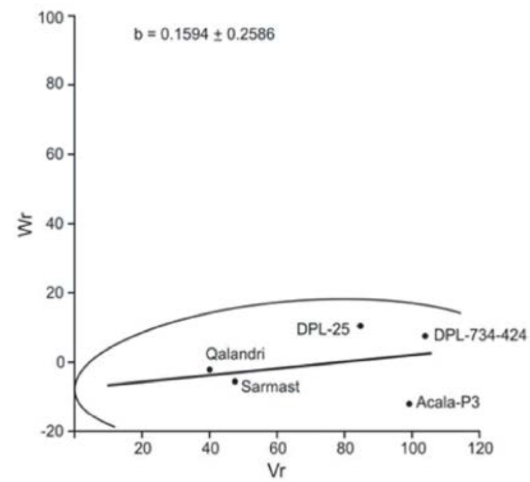

Fig. 3a: Wr/Vr Graph of G.O.T %

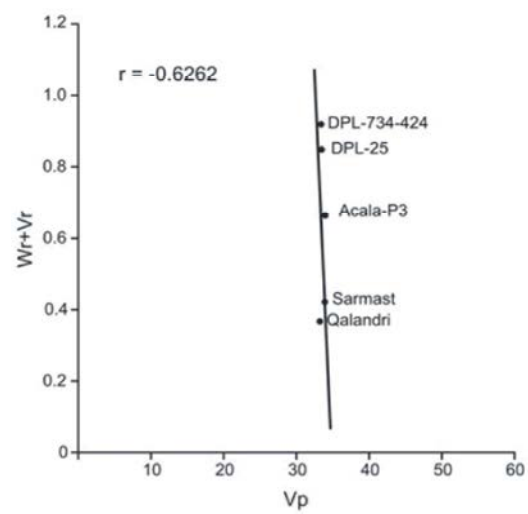

Fig. 3b: Wr+Vr/Vp Graph of G.O.T %

non-significant values of F and h^2 revealed that dominant genes were more frequent than the recessive genes with increasing position of dominant genes. The proportion of $v4DH_1$+ F/$v4DH_1$-F (2.9542) also indicated the excess of dominant genes while the value for h^2/H_2 (0.2429) showed that only one set of genes governed the seed index and the measurement of completely dominant parents was 0.5988. The recorded narrow sense heritability at 5% level of significance was very low indicating low heritability of additive genes.

Data presented in Table 8 revealed that the variety Acala-P_3 had more frequent recessive alleles than other varieties because of its negative sign and the varieties Qalandri, DPL-7340-424 and DPL-25 had the maximum number of dominant genes.

Ginning Outturn Percentage (GOT %): The analysis of genetic variation showed that dominance components (H_1, H_2) and h^2 were highly significant while additive (D), F and E were non-significant for GOT % (Table 7).

Higher values of dominance components as compared to additive component (D=-0.0247) and the ratio vH_1/D displayed over dominance type of gene action for this trait. However, the ratio $H_2/4H_1$ (0.2439) of positive and negative genes showed that they were equal in proportion which was also confirmed by the symmetrical values of dominance components (H_1, H_2). The positive and non-significant value of F and positive and significant h^2 value indicated that dominant genes were more frequent than the recessive with increasing position. The h^2/H_2 ratio (0.9680) exhibited that perhaps one group of genes governed the trait ginning outturn with dominance to some degree and showed the proportion of completely dominant parents (r^2=0.3921). The narrow sense heritability was recorded at 5% level of significance which was negligible indicating no role of additive genes in the control of this trait.

The Table 8 revealed that because of negative values of Frfor Acala-P_3, DPL-25 and DPL-7340-424, they had the maximum amount of recessive genes and positive Fr-values of Qalandri and Sarmast varieties indicated that they had maximum amount of dominant genes. The Wr+Vr/Vp graph also depicted similar results.

DISCUSSION

For plant height, the varieties Acala-P_3 and Qalandri were the best general combiners and could be used as parents in the hybridization program for obtaining best transgressive segregates, as these parents had the preponderant additive genes controlling this character. Amongst the hybrids, the cross Qalandri×Sarmast was the best specific combiner, predominantly controlled by dominant genes, indicating its potential for the development of hybrid cotton. These results are in line with those of Odhano [7], Mehetre *et al.* [8], Laxman and Ganesh [9] and Ansari *et al*. [10] who also obtained significant GCA and SCA variances for plant height. The Wr/Vr graph indicated over dominance type of gene action whereas, negative value of “r” indicated that dominant genes controlled the character plant height. The varieties Qalandri, Sarmast and Acala-P_3 had the maximum dominant genes as indicated by Wr/Vr and Wr+Vr/Vp graph and confirmed by Fr values. These varieties therefore, could be successfully utilized for breeding of hybrid cottons. These results are supported by those of Gul-Hassan *et al*. [11], Mehetre *et al*. [8], Laxman and Ghanesh [9] and Deshpande and Baig [12], who also reported preponderance of dominant genes in the control of this character.

As far as seed index is concerned, DPL-25 proved to be the best general combiner, which could be utilized in the production of pure line varieties. The crosses Qalandri×Acala-P_3 and Acala-P_3×DPL-7340-424 were the best specific combiners for this trait and form the potential material for the development of hybrid cottons. EL-Adl *et al*. [13], Meena *et al*. [14], Zia *et al*. [15], Laxman and Ganesh [9], Mehetre *et al*. [8] and Odhano [7] have also obtained significant general and specific combining ability variances for this trait. The Wr/Vr graph proved the over dominance type of gene action underlying this trait. The negative values of “r” have also indicated that this character was controlled by dominant genes. These results are in agreement with the results of Sayal and sulemani [16] and Subhan *et al.* [17] who also reported over dominance type of gene action for this trait. The results from Wr/Vr and Wr+Vr/Vp graphs and Fr values showed that varieties Qalandri, DPL-7340-424, DPL-25 and Sarmast contained the most dominant genes whereas, the variety Acala-P_3 had the most recessive genes. The former varieties therefore make the most useful material for the development of hybrid cottons.

As regards the GOT%, DPL-25 proved to be the best general combiner followed by Acala-P_3 and DPL-7340-424 showing the highest array means for this trait. Therefore, it is most probable that these varieties when used in the breeding programs 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 Acala-P_3×DPL-7340-424, Sarmast×DPL-25 and Qalandri×DPL-25 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 [18], Mehetre *et al*. [8], Odhano [7] and Anisa *et al*. [19] have also obtained significant GCA and SCA in their material for this trait. The perusal of Wr/Vr graph proved this character to be controlled by over dominance type of gene action, supported by negative "r" value which indicated that this character was controlled by dominant genes. The Wr/Vr graph and Wr+Vr/Vp graph indicated that varieties Qalandri and Sarmast had most of the dominant genes, which is also supported by findings of Fr values for these varieties. These results are in accordance with those reported by Ahmed *et al*. [20], Sayal and Sulemani [16], Ahmed *et al*. [21] and Khan *et al*. [22] who also reported over dominance type of gene action for this character. Abro [23] has also reported complete dominance for the control of this character. These results proved Sarmast and Qalandri as the useful potential material to be exploited in the development of hybrid cottons.

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