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Assessment of Genetic Mechanism in Some Important Quantitative Parameters in Upland Cotton (*Gossypium hirsutum* L.)

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Abstract: Diallel cross analysis of eight parents of cotton (*Gossypium hirsutum* L.) was launched at Faculty of Agriculture, Gomal University, D.I.Khan, during 1996-99. Both additive and non additive effects were observed in case of number of bolls plant^{-1} in F_1 generation, however only additive effects were significant in F_2 generation. Significant additive and non additive effects were observed for boll weight in both the generations. The reciprocal differences were non significant for number of bolls plant^{-1} in both the generations, reflecting the absence of maternal effects or any other departure from simple autosomal inheritance. On the other hand significant reciprocal differences were concluded for boll weight, signifying the presence of maternal effects in F_1 but non significant, suggesting the absence of maternal effects in F_2 generation.

Key words: *Gossypium hirsutum* L., dialle analysis, cultivars, quantitative characters

Introduction

The success in identifying a cotton genotype giving increased seed cotton yield with improved components depends upon availability of genetic variation in breeding population. Thus knowledge about existence of variation in the character to be improved and its genetic basis is fundamental for effective plant improvement. Genetic controlling system of variation in different characters of cotton plant has been studied extensively. The earlier studies of Murtaza *et al*. (1995), Saeed *et al*. (1996), Busharat *et al*. (1998a) and Busharat *et al*. (1998b) showed that additive genetic effects were more imperative in the expression of number of bolls and boll weight. The genetic behavior of some varieties for various quantitative traits varied in different generations under different growing conditions, Gill and Kalsy (1981) and Gumber *et al*. (1983).

Consequently this study was planned to determine genetic basis of some important plant characters so that the potential of the available germplasm is estimated for further improvement under D.I.Khan conditions.

Materials and Methods

Eight local cultivars belonging to Upland cotton, *Gossypium hirsutum* L. viz. CYTO 9/91, B-496, SLS-1, Niab-78, NIAB-313/12, B-622, Niab-78, NIAB-313/12, B-622, NIAB-92 and CYTO-11/91 maintained by selfing were crossed in all possible combinations at Faculty of Agriculture, Gomal University, D.I.Khan during 1996-99. The 56 F_1's along with their parents were grown in Randomized Complete Block Design (RCBD) with three replications. Row to row and plant-to-plant distance were kept as 75 and 30 cm, respectively. F_1 hybrids plants from each cross and parents were self pollinated to raise F_2 progeny. Data were recorded on ten plants from each row on number of bolls plant^{-1} and boll weight in F_1 and F_2 populations. The data were subjected to analysis of variance technique as out lined by Steel and Torrie (1980) for significance of differences among various F_1 and F_2 hybrid populations and their parental lines. Only the significant genotypic differences allow the use of simple additive dominance model as proposed by Mather and Jinks (1971, 77).

Results and Discussion

The results for analysis of variance revealed that mean gentypic differences among the hybrids and their parents in F_1 and F_2 generations, are highly significant for number of bolls plant^{-1} and boll weight. Analysis of variance of number of bolls plant^{-1} and boll weight in both the generations indicated highly significant differences among male and female parents (Table 1). It reflected

the presence of additive genetic variation. The interaction between male and female parents was also found highly significant in number of bolls plant^{-1} and boll weight in F_1 but significant and non significant in F_2 generations. The regression analysis (Table 2, 3, 4 and 5) indicates that the values of coefficient 'b' differed significantly from zero but it was non significantly different from unity for both the characters in both the generations.

The second test was the analysis of variance for Wr + Vr and Wr − Vr arrays. In this case non significant results were found for both Wr + Vr and Wr − Vr arrays in number of bolls plant^{-1} indicating the absence of dominance genetic effects and as well as the absence of non-allelic interaction depicting complete adequacy in case of number of bolls in F_1 generation. While both the Wr + Vr and Wr − Vr reflected the significant variance ratio suggesting the presence of epistasis and thus additive dominance model is modified as partially adequate for boll weight in F_1 population. Like wise non significant Wr− Vr arrays in number of bolls in F_1 exposing the absence of non-allelic interaction while both the Wr + Vr and Wr − Vr reflected the significant variance ratio signifying the presence of epistasis for boll weight in F_2 population (Table 6).

The graphical representation (Fig.1, 2, 3 and 4) showed that maximum dominant genes were possessed by Niab-313/12 and Cyto-9/91 in contrast carried the maximum recessive alleles.

The estimate of components of genetic variation showed that both additive and non-additive genetic effects appeared to be important in the inheritance mechanism of these traits. However after the comparison of these two components, it was represented that genes acting additively, were more marked than genes acting non-additively. Our results are in confirmative with those of earlier workers like, Saeed *et al*. (1996), Busharat *et al*. (1998a), Busharat *et al*. (1998b), Subhan *et al*. (2000) and Subhan *et al*. (2001). However findings of some authors like, Murtaza *et al*. (1995), Khan and Khan (1993), Khan *et al*. (1995), Hassan *et al*. (1999), contradict these findings.

Table 1: Analysis of diallel data for number of bolls and boll weight in F_1 and F_2 populations

Source	F. Ratio of bolls plant^{-1}		F. Ratio of boll weight	
	F_1	F_2	F_1	F_2
Replication	62.16	17.64	18.31	035.28
Male	14.03**	11.09**	48.18**	170.15**
Female	10.98**	11.00**	26.39**	157.78**
Interaction	04.64**	00.54NS	12.92**	005.09**
Resiprocals	00.76NS	00.02NS	01.68**	001.12NS

**, Highly significant (P < 0.01)   NS, non-significant

Table 2: Mean data over replications and reciprocals for number of bolls per plant (F_1 generation)

Parents	Cyto-9/91	B-496	SLS-1	Niab-78	Niab-313/12	B-622	Niab-92	Cyto-11/91	Vr	Wr
Cyto-9/91	2315	29.60	33.39	31.39	35.41	29.74	32.87	28.79	13.8823	7.7938
B-496		26.41	32.88	34.90	35.58	33.89	29.33	30.54	10.1092	4.5600
SLS-1			28.13	34.47	37.59	33.99	30.02	33.86	8.2436	1.0814
Niab-78				28.59	37.14	33.55	29.56	31.87	8.2228	2.1728
Niab-313/12					30.27	36.50	35.53	36.18	5.1267	0.0007
B-622						26.50	29.41	31.01	10.4257	4.5547
Niab-92							27.07	32.16	6.9417	0.3363
Cyto-11/91								24.43	12.1901	6.7795

Regression coefficient (b) = 1.1669 ± 0.0681, difference of b from zero (b_0) = 17.14127**, different for b from unity (b_1) = -2.4514 NS
NS, non-significant   **, highly significant

Table 3: Mean data over replications and reciprocals for boll weight (F_1 generation)

Parents	Cyto-9/91	B-496	SLS-1	Niab-78	Niab-313/12	B-622	Niab-92	Cyto-11/91	Vr	Wr
Cyto-9/91	3.01	3.93	4.27	4.24	4.36	4.01	3.93	3.75	0.1828	0.1197
B-496		3.22	3.89	4.25	4.41	4.00	3.99	3.55	0.1408	0.1066
SLS-1			3.33	4.01	4.23	3.85	4.07	3.82	0.0867	0.0336
Niab-78				3.85	4.36	4.20	4.15	4.07	0.0255	0.0014
Niab-313/12					4.17	4.20	4.22	4.00	0.0176	0.0069
B-622						3.45	3.91	3.78	0.0593	0.0414
Niab-92							3.67	3.85	0.0307	0.0305
Cyto-11/91								3.23	0.0698	0.0682

Regression coefficient (b) =0.1110 ± 0.7337 difference of b from zero (b_0) = 6.6073**, different for b from unity (b_1) =2.3977*
NS, non-significant   **, highly significant

Table 4: Mean data over replications and reciprocals for number of bolls per plant (F_2 generation)

Parents	Cyto-9/91	B-496	SLS-1	Niab-78	Niab-313/12	B-622	Niab-92	Cyto-11/91	Vr	Wr
Cyto-9/91	22.50	24.01	26.65	28.70	28.90	25.08	25.95	23.95	5.2514	5.6244
B496		24.45	27.05	29.05	28.85	25.40	26.18	24.51	3.8918	4.7513
LS-1			27.40	28.80	28.97	26.70	27.15	26.87	0.8488	2.0234
Niab-78				29.34	29.54	28.28	28.38	28.30	0.2305	0.7275
Niab-313/12					29.50	28.85	29.15	28.98	0.0788	0.5808
B-622						25.80	26.13	25.55	1.9298	3.2444
Niab-92							26.40	26.00	1.4830	2.7087
Cyto-11/91								24.40	3.4330	4.4735

Regression coefficient (b) = 0.9757 ± 0.0805, difference of b from zero (b_0) = 12.1072**, different for b from unity (b_1) =0.3016
NS, non-significant   **, highly significant

Table 5: Mean data over replications and reciprocals for boll weight (F_2 generation)

Parents	Cyto-9/91	B-496	SLS-1	Niab-78	Niab-313/12	B-622	Niab-92	Cyto-11/91	Vr	Wr
Cyto-9/91	3.00	3.19	3.15	3.55	3.97	3.19	3.38	3.19	0.09313	0.10498
B-496		3.18	3.20	3.58	3.88	3.22	3.35	3.18	0.06438	0.08593
SLS-1			3.21	3.55	3.93	3.29	3.31	3.19	0.06960	0.08991
Niab-78				3.65	3.93	3.67	3.51	3.61	0.01776	0.03794
Niab-313/12					4.08	3.95	3.82	3.78	0.00867	0.01874
B-622						3.28	3.39	3.23	0.07286	0.09219
Niab-92							3.42	3.30	0.02913	0.05541
Cyto-11/91								3.15	0.05470	0.07788

Regression coefficient (b) = 0.9931 ± 0.0754, difference of b from zero (b_0) = 13.1628**, different for b from unity (b_1) =0.0915
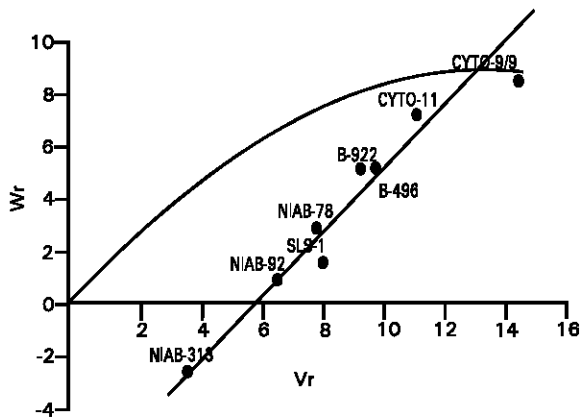NS, non-significant   **, highly significant

Fig. 1: Wr/Vr graph for number of bolls (F_1)
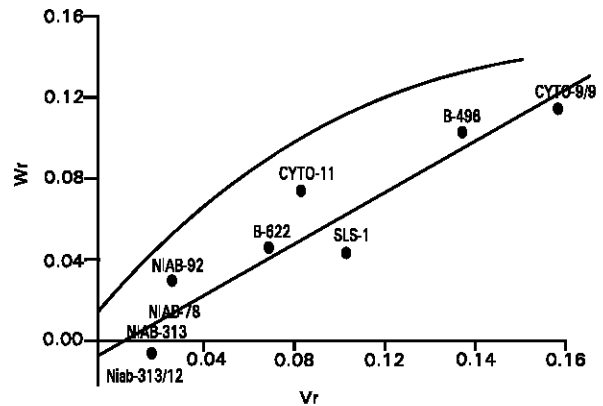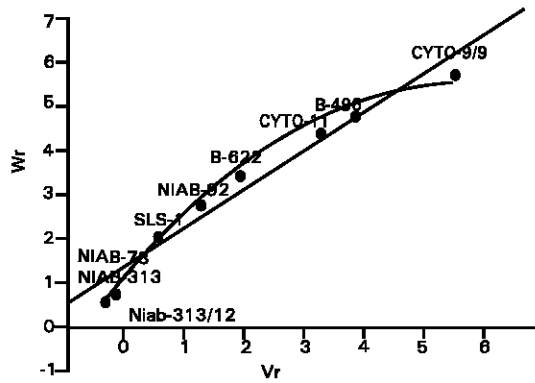

Fig. 2: Wr/Vr graph for bolls weight (F_1)
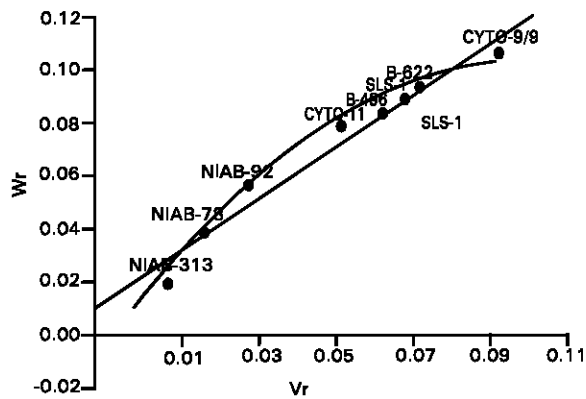
Fig. 3: Wr/Vr graph for number of bolls (F₂)

Fig. 4: Wr/Vr graph for bolls weight (F₁)

Table 6: Analysis of variance for arrays

Source	F. Ratio of bolls plant^{-1}		F. Ratio of boll weight	
	F_1	F_2	F_1	F_2
Wr + Vr Between array Within array	1.24NS	5.24**	19.54**	82.03**
Wr + Vr Between array Within array	0.50NS	0.78NS	04.86*	4.03**

**, Highly significant (P < 0.01)   NS, non-significant

Keeping in view the results of genetic analysis, the Hayman-Jinks model proved to be fully adequate for number of bolls plant^{-1}, while it is partially adequate for boll weight in both the F_1 and F_2 generations in this study. Furthermore over dominance (Heterosis)

style of inheritance was also exposed for both the traits only in F_1 generation. This type of gene action like over dominance in F_1 but additive type with partial dominance in F_2,therefore, strongly suggests that the number of bolls plant^{-1} and boll weight may be made the criteria for selecting high yielding genotypes of cotton under the limits of this exploration.

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