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Genetic Basis of Variation in Upland Cotton (*Gossypium hirsutum* L.)

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Abstract: An 8x8 diallel analysis study on cotton (*Gossypium hirsutum* L.) was launched at Faculty of Agriculture, Gomal University, D.I.Khan, during, 1996-99 to resolve the type of gene action in the inheritance and expression of some significant quantitative characters like number of seeds boll^{-1} and staple length in F_1 and F_2 populations. The analysis of variance revealed that differences among genotypes for these traits were highly significant. The Hayman-Jinks model proved to be completely adequate in case of staple length in both the populations. Even though it is adequate for number of seeds boll^{-1} in F_1 but partially adequate in F_2 population.

Key words: *Gossypium hirsutum* L., cultivars, agronomic characters, Pakistan

Introduction

In cotton, fantastic genetic potential still awaits exploitation in our commercial varieties. The conclusions of genetic control of various characteristics under different ecological conditions can divulge the prospects for these attributes as a support to recover the attractive cotton plant for future global competition. With the development of diallel cross analysis as a tool for studying quantitative inheritance, it is possible to explore the direct genetic control of the characters.

Turan (1982) and Murtaza *et al.* (1995) observed that genetic control of seeds boll^{-1} was largely accounted for by additive gene effects, nevertheless Singh *et al.* (1985) and Ahmad *et al.* (1991) had accomplished over dominance type of gene action. Similarly, Raza *et al.* (1990), Murtaza *et al.* (1992) Busharat *et al.* (1998), Subhan *et al.* (2000) and Amir *et al.* (2000) concluded significant additive gene effects with partial dominance for staple length. However gene action like over dominance as model of inheritance for staple length were reported by Rehman (1993), Tariq *et al.* (1995) and Ahmad *et al.* (1997).

Materials and Methods

The F_1 and F_2 populations were developed at Faculty of Agriculture, Gomal University, D.I.Khan during 1996-99 by crossing 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. The data on individual plant basis were collected at crop maturity and analyzed for number of seeds boll^{-1} and staple length in F_1 and F_2 populations.

The data recorded were statistically analyzed through diallel technique developed by Hayman (1954a, 1954b) and applied by Mather and Jinks (1977).

Results and Discussion

The results for the analysis of variance revealed that the mean genetic differences among the hybrids and their parents are highly significant for the characters studied like number of seeds boll^{-1} and staple length in F_1 and F_2 populations.

Table 1: Analysis of variance of diallel data for seeds boll^{-1} and staple length in F_1 and F_2 populations

	F. Ratio of seeds boll^{-1}		F. Ratio of staple length	
Source	F_1	F_2	F_1	F_2
Replication	72.59	10.05	19.21	01.94
Male	06.66**	07.87**	03.20**	16.94**
Female	05.31**	07.27**	02.82**	18.02**
Interaction	00.49NS	00.52NS	01.40NS	00.42NS
Resiprocals	00.03NS	00.042NS	00.49NS	00.09NS

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

Additive genetic variation seemed to exist for these traits for both the populations as the mean squares due to both male and female parents were significant (P<0.01). The interaction and reciprocal differences among male and female parents were (P>0.05) non-significant, consequently, confirming that only additive gene action was responsible for heritable variation of these characters. Moreover, the reciprocal differences were found to be (P>0.05) non significant. This revealed that maternal effects were not significant in the inheritance of these characters like seeds boll^{-1} and staple length (Table 1). For that reason, the genotypic differences mentioned above stand excellent and retesting against reciprocal mean square becomes needless. To test the adequacy of additive dominance model for the data set regression analysis was carried out. The analysis of the data (Table 2, 3, 4 and 5) revealed that regression coefficient ($b=0.9431\pm8.7347$), ($b=0.6150\pm0.1590$) deviated significantly from zero but they were non-significantly different from unity for seeds boll^{-1}, staple length in F_1 population and as well as ($b=0.8821\pm0.1270$), ($b=0.9821\pm0.0475$) in F_2 population for the same traits respectively.

The results of analysis of variance for arrays of the traits in study (Table 6) showed that Wr – Vr did differ significantly between the arrays in both the populations except in F_2 (seeds boll^{-1}).

Table 2: Diallel for seeds per boll (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	31.27	31.45	30.85	31.14	31.30	29.88	31.55	31.02	0.2780	0.3399
B-496		30.18	29.80	30.55	30.25	30.10	30.03	29.92	0.2722	0.5181
SLS-1			26.30	28.85	29.10	29.10	29.25	29.55	1.6685	1.7945
Niab-78				29.35	29.75	29.25	29.61	29.60	0.5475	0.9068
Niab-313/12					29.68	29.78	29.93	29.75	0.4018	0.7756
B-622						28.70	29.45	29.56	0.2064	0.4338
Niab-92							29.68	29.77	0.5021	0.7825
Cyto-11/91								29.42	0.2570	0.4730

Regression coefficient (b) = 0.9431 ± 8.7347, difference of b from zero (b_0) = 10.7976**
Different for b from unity (b_1) = 0.6510NS   NS, non-significant   **, highly significant

Table 3: Diallel for staple length (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	26.53	28.33	28.38	28.28	28.23	28.31	28.99	28.79	0.54593	0.36919
B-496		27.09	28.68	28.91	28.49	28.74	28.58	28.11	0.23675	0.22452
SLS-1			27.83	28.88	28.52	28.43	28.89	28.76	0.12056	0.10459
Niab-78				28.95	29.01	28.79	28.89	29.00	0.05487	0.12327
Niab-313/12					27.96	29.03	29.82	28.85	0.33061	0.21572
B-622						27.38	29.07	28.61	0.29099	0.18768
Niab-92							28.38	28.99	0.17691	-0.01446
Cyto-11/91								27.83	0.18029	0.11625

Regression coefficient (b) = 0.6150 ± 0.1590, difference of b from zero (b_0) = 3.8682**
Different for b from unity (b_1) = 2.4220NS NS, non-significant **, highly significant

Table 4: Diallel for seeds per boll (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	30.15	30.05	29.60	29.73	29.75	29.60	29.90	29.75	0.0406	0.2232
B-496		29.09	29.53	28.83	28.93	28.75	29.05	28.83	0.1997	0.0774
SLS-1			25.35	27.95	28.05	27.20	28.05	28.00	1.8035	1.7964
Niab-78				28.50	28.67	28.25	28.45	28.43	0.2759	0.6293
Niab-313/12					28.70	28.15	28.64	28.60	0.2704	0.6295
B-622						27.60	27.90	27.80	0.5517	0.9021
Niab-92							28.50	28.45	0.3914	0.6919
Cyto-11/91								28.30	0.3518	0.6504

Regression coefficient (b) = 0.8821 ± 0.1270, difference of b from zero (b_0) = 6.9447**
Different for b from unity (b_1) =0.9284NS NS, non-significant ** highly significant

Table 5: Diallel for staple length (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	26.57	26.79	27.12	26.97	27.06	26.75	27.95	26.45	0.2144	0.2661
B-496		26.95	27.15	27.10	27.07	26.94	28.05	26.75	0.1672	0.2291
SLS-1			27.20	27.19	27.17	27.05	27.90	26.95	0.0834	0.1571
Niab-78				27.15	27.13	27.09	28.04	27.08	0.1142	0.1739
Niab-313/12					27.10	27.10	28.11	27.04	0.1305	0.1835
B-622						26.90	28.05	26.75	0.1730	0.2307
Niab-92							28.22	27.65	0.0287	0.0805
Cyto-11/91								26.19	0.1930	0.2526

Regression coefficient (b) = 0.9821 ± 0.0475, difference of b from zero (b_0) = 20.6617**
Different for b from unity (b_1) =0.3773NS NS, non-significant **, highly significant

Table 6: Analysis of variance for arrays

	F. Value of seeds $boll^{-1}$		F. Value of staple length	
Source	F_1	F_2	F_1	F_2
Wr + Vr				
Between Array	3.96**	5.78**	1.30NS	1.60NS
Within Array				
Wr - Vr				
Between Array	0.68NS	2.76**	0.30NS	1.59NS
Within Array				

**, Highly significant, NS, non-significant

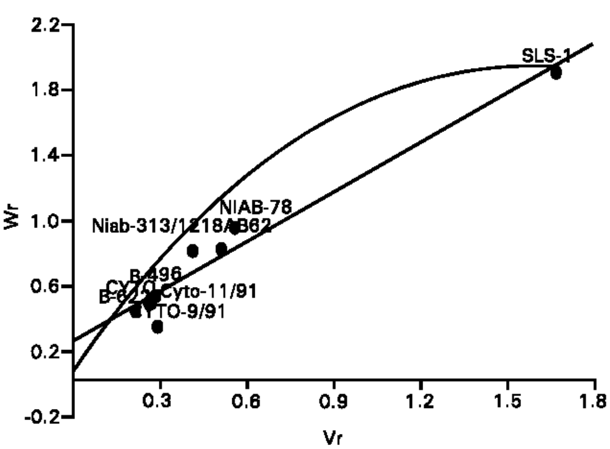

Fig. 1: Wr/ Vr graph for number of seeds per boll (F_1)

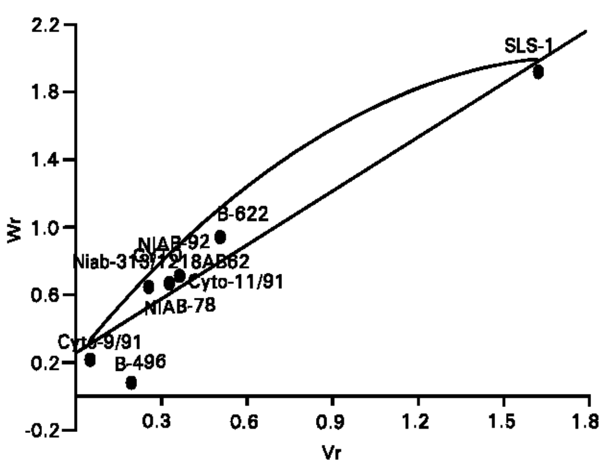

Fig. 2: Wr/ Vr graph for number of seeds per boll (F_2)

The Hayman-Jinks model proved to be completely adequate in case of staple length in both the populations. Although it is adequate for number of seeds $boll^{-1}$in F_1 but partially adequate in F_2 population. From the relatively distribution of array points along the regression line it was exposed that B-622 (F_1) and Cyto-9/91(F_2) possessed the most dominant genes for seeds $boll^{-1}$ while cultivar SLS-1 carried the most recessive genes for this trait in both the populations (Fig. 1 and 2). Furthermore, NIAB-78 (F_1)

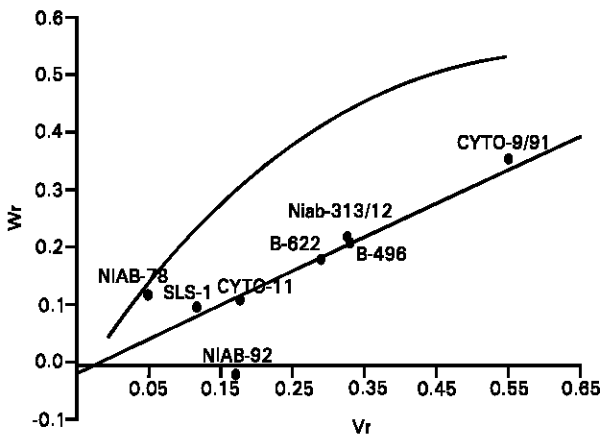

Fig. 3: Wr/ Vr graph for staple length (F_1)

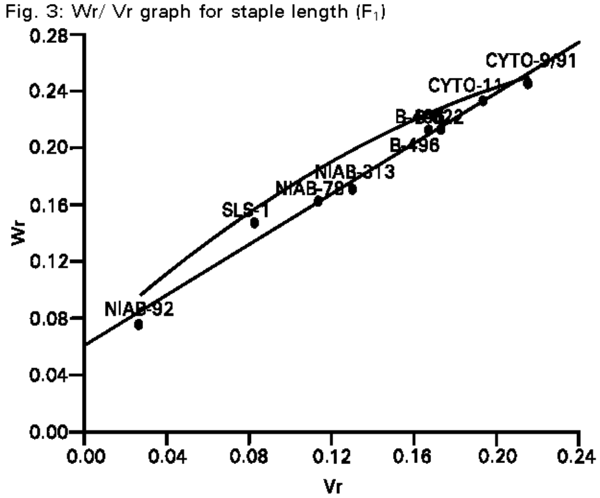

Fig. 4: Wr/Vr graph for staple length (F_2)

and Niab-92 (F_2) contained the maximum dominant genes, whereas Cyto-9/91 possessed the most recessive genes for the trait like staple length in both the populations (Fig. 3 and 4). A perusal of (Fig. 1, 2 and 4) revealed that regression line intercepts the covariance axis above the origin, hence signified additive type of gene action with partial dominance except Fig. 3 in which over dominance was reflected.

These results are in conformity with those of earlier research workers like, Azhar *et al.* (1994), Murtaza (1995), Busharat *et al.* (1998, 1999) and Subhan *et al.* (2000). However findings of some others, over dominance as model for inheritance of staple length and seeds boll^{-1} were reported by Rehman (1993), Tariq *et al.* (1995) and Ahmad *et al.* (1997). This deviation might be due to different varieties with different genetic make up used under different environmental conditions.

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