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Estimates of Gene Effects for Some Quantitative Characters in Upland cotton (*Gossypium hirsutum* L.)

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Abstract: An 8 x 8 diallel analysis study on cotton (*Gossypium hirsutum* L.) was conducted at Faculty of Agriculture, Gomal University, D. I. Khan, during, 1996-99 to determine the type of gene action in the control and expression of some important quantitative characters like seed index and lint index in F_1 and as well as in F_2 generations. The analysis of variance exposed that differences among genotypes for the characters mentioned were highly significant. The Hayman-Jinks model proved to be partial adequate for the characters mentioned in F_1 while completely adequate in the F_2 generations in this manuscript.

Keywords: *Gossypium hirsutum* L., biometric analysis, cultivars, agronomic characters

Introduction

The cotton (*Gossypium hirsutum* L.) being biggest foreign exchange earner in Pakistan, attracts utmost attention of plant breeders to evolve high yield varieties. Consequently, Pakistan has become one of the top cotton producing countries in the world. Abundance of literature is available on practical usefulness of diallel analysis to understand type of gene action and genetic potential of parents in cotton like Singh *et al.* (1985), Raza *et al.* (1990), Murtaza *et al.* (1992), Azhar *et al.* (1994), Busharat *et al.* (1998 a). However results of these studies vary as concluded by Rehman *et al.* (1988), Busharat *et al.* (1998 b) and Subhan *et al.* (2000), depending on genotypes and environmental conditions. This study is aimed to employ diallel cross analysis in understanding breeding utility of eight cotton cultivars for different economic traits.

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 cotton cultivars viz. CYTO 9/91, B-496, SLS-1, Niab-78, NIAB-313/12, B-622 and Niab-78, NIAB-313/12, B-622, NIAB-92 and CYTO-11/91 in a diallel fashion during the months of August and September, 1996. The data of F_1 and F_2 obtained from the crosses and their selfed parents grown in Randomized Complete Block Design with three replications. Each plot comprised single 3-m long row with 30 cm plant to plant and 75 cm row to row distance. The recommended production package was adopted. The data on individual plant basis were recorded at crop maturity and statistically analyzed for seed and lint indices through diallel technique developed by Hayman, (1954a) and applied by Mather and Jinks (1977).

Results and Discussion

The analysis of variance depicted that differences among the genotypes were highly significant for seed index and lint index both in F_1 and F_2 generations. This reflected presence of adequate genetic variability which could be Table exploited in different crossing programs (Table 1). Additive genetic variation seemed to exist for these traits in both the generations as the mean squares due to both male and female parents were highly significant ($P < 0.01$). The interaction differences among male and female parents for seed index and lint index were also significant indicating the presence of non additive heritable genes while the reciprocal differences were recorded as non significant

Table 2a: Analysis of variance of F_1 of diallel data for seed index

S.O.V	d. f	S. S	M.S	F Value
Replications	2	0.9171	0.4586	17.27
Male	7	3.3715	0.4816	18.14**
Female	7	2.6840	0.3835	14.44**
Interaction	49	3.1623	0.0645	02.43**
Error	126	3.3456	0.0266	
Total	191	13.4806		
Reciprocals	28	0.1782	0.0063**	60.24**

NS, non-significant; *, significant ($P < 0.05$) and **, highly significant ($P < 0.01$)

Table 1: Estimates of mean squares and F ratios of different quantitative traits of cotton (*Gossypium hirsutum* L.) in F_1 and F_2 generation.

Trait	Generation	S.O.V.	M.S.	F. Ratio
Seed index	F_1	Replication	0.459	17.27**
		Genotype	0.146	5.51**
		Error	0.027	
Seed index	F_2	Replication	0.917	13.98**
		Genotype	0.109	1.66**
		Error	0.07	
Lint index	F_1	Replication	0.285	34.84**
		Genotype	0.076	9.23**
		Error	0.899	
Lint index	F_2	Replication	1.528	40.71**
		Genotype	0.054	1.4**
		Error	0.038	

**, Highly significant

exposing nothing like maternal effects in F_1 generation. But the interaction and reciprocal differences for the same mentioned characters were noted as non significant depicting absence of non additive heritable genes and maternal effects in F_2 generations (Table 2a, 3a, 4a, 5a). To test the adequacy of additive dominance model of the data, regression analysis was carried out. The analysis of the data (Table 2b and 3b) revealed that the value of regression coefficient b ($b = 0.911 \pm 0.158$, $b = 0.688 \pm 0.129$, $b = 1.021 \pm 0.071$, $b = 0.729 \pm 0.1326$) differed significantly from zero and were none significantly deviated from unity for both the traits i.e., seed index and lint index in both the generations (Table 2b, 3b, 4b, 5b). The results of analysis of variance for arrays showed that $Wr-Vr$ did differ significantly between the arrays in seed and lint indices in their F values which are enough to mold the model partially adequate regarding the characters mentioned in F_1 population. This also indicated the participation of epistacy or multiple allelism in F_1 generation (Table 2c, 3c). The non-significant differences for $Wr+Vr$ indicated the absence of dominance genetic effects, whereas the non-significant differences for $Wr-Vr$ reflected the absence of non-allelic interaction in case of seed and lint indices. The above two tests disclosed that the additive dominance model was fully adequate for the characters mentioned in F_2 population (Table 4c, 5c). The graphic representation of Wr/Vr (Fig.1 and 2) highlighted that Cyto-11/91 and B-622 parents were exposed with maximum dominant genes, while Niab-92 with maximum

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Table 2b: Mean data over replications and reciprocals

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	8.58	8.49	8.68	8.44	8.69	8.66	8.49	8.53	0.0095	0.0146
B-496		8.20	8.33	8.13	8.38	8.38	8.13	8.47	0.0206	0.0404
SLS-1			8.17	8.13	8.31	8.48	8.02	8.43	0.0449	0.0626
Niab-78				7.85	8.35	8.55	8.05	8.32	0.0523	0.0559
Niab-313/12					8.16	8.22	7.99	8.35	0.0409	0.0487
B-622						8.33	8.48	8.42	0.0182	0.0017
Niab-92							7.54	8.37	0.0982	0.0922
Cyto-11/91								8.36	0.0049	0.0139

Regression coefficient (b) = 0.9110± 0.1580, difference of b from zero (b0) = 5.7659**
 different for b from unity (b1) = 0.5631NS NS, non-significant; **, highly significant

Table 2c: Analysis of variance for arrays

Item	d. f	S.S	M.S.	F-Value
Wr + Vr				
Between Array	7	0.0647	0.0092	7.84**
Within Array	16	0.0189	0.0012	
Wr - Vr				
Between Array	7	0.0054	0.0008	3.66*
Within Array	16	0.0034	0.0002	

**, highly significant; *, significant

Table 3a: Analysis of variance of F₁ of diallel data for lint index.

S.O.V	d.f	S. S	M.S.	F Value
Replications	2	0.5699	0.2849	34.84
Male	7	0.9440	0.1349	16.49**
Female	7	0.8666	0.1238	15.14**
Interaction	49	2.9469	0.0601	07.35**
Error	126	1.0306	0.0082	
Total	191	6.3579		
Reciprocals	28	0.2813	0.0100	1.23NS

NS, non-significant, *, significant (P< 0.05) and **, highly significant (P< 0.01)

Table 3b: Mean data over replications and reciprocals.

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	4.06	4.53	4.82	4.85	4.82	4.61	4.69	4.56	0.0656	0.0479
B-496		4.32	4.59	4.63	4.64	4.50	4.53	4.47	0.0104	0.0122
SLS-1			4.48	4.70	4.70	4.68	4.50	4.62	0.0126	0.0019
Niab-78				4.90	4.69	4.84	4.62	4.66	0.0122	0.0122
Niab-313/12					4.49	4.63	4.54	4.65	0.0099	0.0017
B-622						4.43	4.64	4.54	0.0157	0.0177
Niab-92							4.10	4.56	0.0331	0.0168
Cyto-11/91								4.32	0.0121	0.0118

Regression coefficient (b) = 0.6878± 0.1285, difference of b from zero (b0) = 5.3519**
 different for b from unity (b1) = 2.4291 NS, NS, non-significant; **, highly significant

Table 3c: Analysis of variance for arrays

Item	d.f	S.S	M.S.	F-Value
Wr + Vr				
Between Array	7	0.0220	0.00315	18.51**
Within Array	16	0.0027	0.00017	
Wr - Vr				
Between Array	7	0.0014	0.00019	6.07**
Within Array	16	0.0005	0.000032	

**, highly significant

Table 4a: Analysis of variance of F₂ of diallel data for seed index.

S.O.V.	d.f	S.S.	M. S.	F Value
Replications	2	1.8346	0.9173	13.98
Male	7	3.2018	0.4574	6.97**
Female	7	2.7890	0.3984	6.07**
Interaction	49	0.8881	0.0181	0.28 NS
Error	126	8.2647	0.0656	
Total	191	16.9781		
Reciprocals	28	0.2214	0.07.91	0.12NS

NS, non-significant; *, significant (P< 0.05); **, highly significant (P< 0.01)

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Table 4b: Mean data over replications and reciprocals

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	8.50	8.39	8.41	8.38	8.48	8.47	8.25	8.25	0.0086	0.0279
B-496		8.10	8.22	8.06	8.24	8.36	7.95	7.95	0.0248	0.0481
SLS-1			8.27	8.21	8.26	8.39	8.11	8.11	0.0098	0.0298
Niab-78				8.00	8.19	8.33	7.83	7.83	0.0356	0.0589
Niab-313/12					8.25	8.38	8.02	8.02	0.0181	0.0413
B-622						8.42	8.25	8.25	0.0043	0.0182
Niab-92							7.50	7.50	0.0619	0.0790
Cyto-11/91								8.13	0.0135	0.0324

Regression coefficient (b) = 1.0209 ± 0.0713, difference of b from zero (b0) = 14.3093** different for b from unity (b1) = -0.2925NS
 NS, non-significant; **, highly significant

Table 4c: Analysis of variance for arrays

Item	d.f	S.S	M.S.	F-Value
Wr + Vr				
Between Array	7	0.0492	0.0070	1.84**
Within Array	16	0.0612	0.0038	
Wr - Vr				
Between Array	7	0.0229	0.0033	1.59NS
Within Array	16	0.0339	0.0021	

** , highly significant; NS, non-significant

Table 5a: Analysis of variance of F₂ of diallel data for lint index

S.O.V.	d.f	S.S.	M. S.	F Value
Replications	2	3.0555	1.5278	40.71
Male	7	1.2935	0.1848	4.92**
Female	7	1.2001	0.1714	4.57**
Interaction	49	0.9249	0.0189	0.50NS
Error	126	1.0306	0.0375	
Total	191	11.2022		
Reciprocals	28	0.0808	0.0029	0.08NS

NS, non-significant, *, significant (P< 0.05) and **, highly significant (P< 0.01)

Table 5b: Mean data over replications and reciprocals.

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	4.28	4.51	4.68	4.76	4.74	4.49	4.51	4.52	0.0258	0.0237
B-496		4.38	4.60	4.61	4.58	4.51	4.32	4.48	0.0107	0.0189
SLS-1			4.66	4.73	4.66	4.69	4.55	4.63	0.0039	0.0079
Niab-78				4.63	4.69	4.69	4.47	4.70	0.0088	0.0112
Niab-313/12					4.67	4.70	4.49	4.64	0.0064	0.0093
B-622						4.50	4.47	4.47	0.0117	0.0175
Niab-92							4.08	4.41	0.0228	0.0244
Cyto-11/91								4.50	0.0107	0.0175

Regression coefficient (b) = 0.7287 ± 0.1316, difference of b from zero (b0) = 5.5363** different for b from unity (b1) = 2.0615NS
 NS, non-significant; **, highly significant

Table 5c: Analysis of variance for arrays

Item	d.f	S.S	M.S.	F-Value
Wr + Vr				
Between Array	7	0.0077	0.00110	1.29NS
Within Array	16	0.0137	0.00086	
Wr - Vr				
Between Array	7	0.0009	0.00012	0.72NS
Within Array	16	0.0002	0.00018	

NS, non-significant

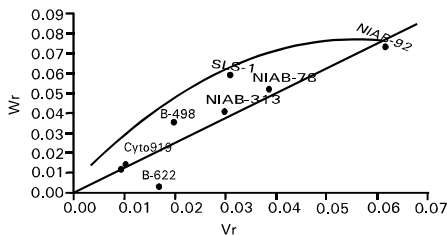


Fig.1: Wr/Vr graph for seed index (F₁)

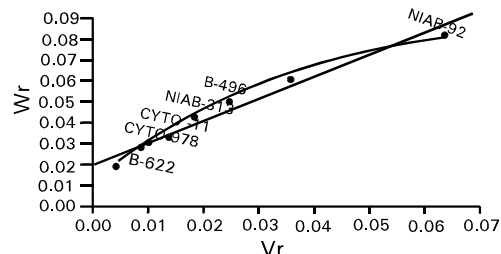


Fig. 2: Wr/Vr graph for seed index (F₂)

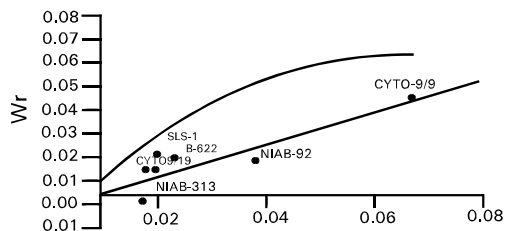


Fig.3: W_r/V_r graph for lint index (F_1)

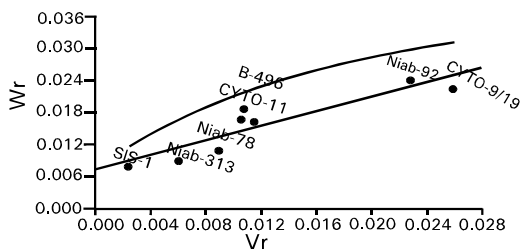


Fig. 4: W_r/V_r graph for lint index (F_2)

recessive genes for seed indices (F_1 , F_2) respectively. In case of lint indices (F_1 , F_2) Niab-313/12 and SLS-1 were recorded with maximum dominant genes, though Cyto-9/91 was noted with maximum recessive genes (Fig. 3 and 4). The regression line cut the W_r axis through the point of intersection thus reflected complete dominance for seed and lint indices in F_1 population (Fig. 1 and 3). Furthermore, the regression line cut W_r axis above the origin, therefore, signified the presence of additive dominance gene action for the characters like seed and lint indices in F_2 population (Fig. 2 and 4). 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 depicted that genes acting additively, were more pronounced than genes acting non-additively. Our results are in confirmative with those of earlier workers, Raza *et al.* (1990), Rehman *et al.* (1993), Azhar *et al.* (1994), Busharat *et al.* (1998a), Busharat *et al.* (1998b), Subhan *et al.* (2000). However finding of some authors, Rehman *et al.* (1988), Azhar and Rana (1993) and Khan *et al.* (1994) don't agree to these observations.

Their differences might largely be attributed to different experimental material with a varied genetic back ground in this respect. The Hayman-Jinks model proved to be partial adequate for seed and lint indices in F_1 generation while both the characters are completely adequate in F_2 generation in this exploration. This type of gene action i.e., additive type with partial dominance, indicates signs for isolation of new hybrids from the lint point of view.

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