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Genetics of Yield and Its Components in Upland Cotton (*Gossypium hirsutum* L.)

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Abstract: This study was conducted at Faculty of Agriculture, Gomal University, D. I. Khan, during 1996-99. Eight Upland cotton (*Gossypium hirsutum* L.) varieties were genetically analyzed to explore gene action controlling the phenotypic expression of yield of seed cotton plant[-1] and lint percentage in all the generations. Additive type of gene action with partial dominance was observed for the characters mentioned in both the generations. Over dominance type of gene action was also explored specially for the character like yield of seed cotton plant[-1] under study in F_1 generation, which reflected the manifestation of heterotic effects.

Key words: *Gossypium hirsutum* L., cultivars, cross breeding, additive, over dominance

Introduction

An organized and prosperous hybridization program depends upon an understanding of genetic architecture and inheritance of quantitative characters of prominent cultivars. For such studies various workers have used different methods but method of Hayman (1954a) and Jinks (1954) has most commonly been used. Even though genetic analysis of quantitative characters has widely been reported yet evidences of some partial dissimilarity among research workers have been observed in certain traits. Such divergence could be credited to variation in genetic material, environmental conditions and methods engaged for such studies.

In cotton different authors, Bhatade (1981), Azhar *et al.* (1994), Khan *et al.* (1995), Saeed *et al.* (1996), Ahmad *et al.* (1997), Murtaza *et al.* (1992 b), Busharat *et al.* (1998 b), Busharat *et al.* (1999) and Subhan *et al.* (2001), detected significant additive effects with partial dominance for yield of seed cotton plant[-1] and lint percentage. Others like Rehman *et al.* (1988), Tariq *et al.* (1992) and Khan *et al.* (1993), have reported over dominance type of gene action.

This contradiction in results may be due to different breeding material utilized under different environmental conditions. The current strategy involves high potential commercial varieties being widely used in crossing programs. Such type of studies is expected to provide practical information for scheduling specific and precise breeding programs.

Materials and Methods

All possible F_1 crosses, including reciprocals, were made among eight cultivars of cotton 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. Fifty six crosses and eight parents were sown at Faculty of Agriculture, Gomal University, D.I.Khan, during 1996-99 in Randomized Complete Block Design with three replications. Row to row and plant-to-plant spacing were kept as 75 cm and 30 cm, respectively. F_1 hybrids plants from each cross and parents were self pollinated to raise F_2 progeny. F_2 population was grown during May 1997 in a triplicate progeny row trial employing the said design. The plot size for each cross was 3 x 6 m[2]. The data were recorded on ten randomly selected plants from each entry for two characters viz. yield of seed cotton plant-1 and lint percentage in both the generations. The plot means were used for analysis of variance and where the means were significant, data were further subjected to diallel analysis technique developed by Mather and Jinks (1977).

Results and Discussion

The analysis of variance showed highly significant differences among progenies for yield seed cotton plant[-1] and lint percentage in F_1 and F_2 generations. This indicated presence of adequate genetic variability which could be exploited in different crossing programs (Table 1). There are indications that additive genetic effects were present for lint percentage in both the F_1 and F_2 generations as the mean squares due to male and female items in the basic diallel ANOVA were significant, while interaction and

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
Yield of seed	F_1	Replication	1277.748	28.16**
cotton per plant		Genotype	1286.602	28.36**
		Error	45.368	
Yield of seed	F_2	Replication	588.627	29.65**
cotton per plant		Genotype	567.954	28.61**
		Error	45.368	
Lint percentage	F_1	Replication	15.816	17.59**
		Genotype	1.508	1.68**
		Error	0.899	
Lint percentage	F_2	Replication	3.871	4.88**
		Genotype	1.205	1.52**
		Error	0.793	

**, Highly significant

Table 2a: Analysis of variance of F_1 of diallel data for lint percentage

S.O.V	d.f	S.S	M.S.	F Value
Replications	2	31.63121	5.8156	17.59
Male	7	29.93320	4.2762	04.76**
Female	7	33.26660	4.7524	05.29**
Interaction	49	31.83760	0.6497	00.72 N.S.
Error	126	6431.016	51.03981	
Total	191	38430.4		
Reciprocals	28	2081.132	74.3262	1.4562N.S.

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

Table 2b: Mean data over replications and reciprocals

Parents	Cyto-9/91	B-496	SLS-1	Niab-78	Niab313/12	B-622	Niab-92	Cyto-11/91	Vr	Wr
Cyto-9/91	33.20	34.42	35.70	36.50	35.65	34.75	35.60	34.35	1.0833	1.0065
B-496		34.49	35.53	36.25	35.65	34.45	35.75	34.55	0.5404	0.6403
SLS-1			35.40	36.65	35.60	35.60	35.43	34.90	0.2345	0.2603
Niab-78				36.37	36.00	35.66	36.45	35.92	0.1107	0.0383
Niab-313/12					35.50	35.78	35.97	35.75	0.0312	0.0589
B-622						34.65	35.35	35.05	0.2578	0.3701
Niab-92							35.20	35.53	0.1592	0.1926
Cyto-11/91								34.05	0.4632	0.5727

Regression coefficient (b) = 0.9517 ± 0.0888, difference of b from zero (b0) = 10.7164** different for b from unity (b1) = 0.5443NS 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	5.6892	0.8127	1.61NS
Within Array	16	8.0671	0.5042	
Wr - Vr				
Between Array	7	0.4001	0.0572	0.87NS
Within Array	16	1.0495	6.5592	

NS, non-significant

Table 3a: Analysis of variance of F_2 of diallel data for lint percentage

S.O.V	d.f	S.S	M.S.	F Value
Replications	2	7.7411	3.8705	4.88
Male	7	30.0796	4.2971	5.42**
Female	7	35.3296	5.0471	6.36**
Interaction	49	10.4829	0.2139	0.27 NS
Error	126	99.9516	0.7933	
Total	191	183.5848		
Reciprocals	28	0.71625	0.026	0.032NS

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	33.50	34.95	35.75	36.25	35.90	34.65	35.15	34.55	0.7819	0.8656
B-496		35.10	35.93	36.35	35.75	35.00	35.20	35.00	0.2788	0.4575
SLS-1			36.03	36.55	36.08	35.85	35.92	35.72	0.0984	0.2136
Niab-78				36.67	36.45	36.00	36.28	36.10	0.0497	0.1592
Niab-313/12					36.13	35.95	35.88	35.75	0.0536	0.1638
B-622						34.85	35.15	34.86	0.3061	0.5036
Niab-92							35.26	35.17	0.2027	0.3826
Cyto-11/91								34.87	0.2922	0.5104

Regression coefficient (b) = 0.9663±0.081, difference of b from zero (b0) = 11.9629** different for b from unity (b1) =0.4175NS 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	6.3952	0.9136	5.00**
Within Array	16	2.9248	0.1828	
Wr - Vr				
Between Array	7	1.0650	0.1521	3.54**
Within Array	16	0.6880	0.0430	

**, Highly significant

Table 4a: Analysis of variance of F_1 of diallel data for yield of seed cotton per plant

S.O.V	d.f	S.S	M.S.	F Value	F# Value
Replications	2	2555.495	1277.748	28.16	
Male	7	2426.580	3465.940	76.49**	32.14**
Female	7	1452.250	2074.749	45.73**	19.24**
Interaction	49	4227.090	862.675	19.02**	08.00**
Error	126	5716.334	45.368		
Total	191	89327.74			
Reciprocals	28	3019.568	107.842	2.38**	

NS, non-significant, *, significant (P<0.05) and **, highly significant (P<0.01) #Tested against reciprocal mean square.

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	70.34	116.35	142.65	132.85	154.61	119.29	129.27	108.33	650.6870	399.9338
B-496		84.22	128.22	148.28	156.13	135.57	116.43	108.51	530.2081	314.3373
SLS-1			95.23	138.78	159.11	130.87	122.38	129.56	335.6865	102.5935
Niab-78				161.90	140.93	122.85	129.62	239.2055	52.6724	
Niab-313/12					126.23	153.93	149.89	144.73	126.6368	-92.7632
B-622						92.56	114.98	117.42	353.7529	191.1695
Niab-92							100.35	123.84	197.3983	91.1695
Cyto-11/91								79.19	386.7151	288.2101

Regression coefficient (b) = 0.8782± 0.1256, difference of b from zero (b0) = 6.992** different for b from unity (b1) = 0.9701NS 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	21649.00	30928.70	17.02**
Within Array	16	29080.00	18175.00	
Wr - Vr				
Between Array	7	70958.31	10136.90	02.7*
Within Array	16	60998.88	38120.0	

**, Highly significant and *,significant

Table 5a: Analysis of variance of F_2 of diallel data for yield of seed cotton per plant

S.O.V	d.f	S.S	M.S	F Value
Replications	2	1177.25	588.63	29.65
Male	7	1678.422	397.06	120.74**
Female	7	1569.752	241.97	112.93**
Interaction	49	3307.91	67.51	3.40**
Error	126	01.0306	0.0082	
Total	191	39459.88		
Reciprocals	28	209.52	7.48	0.38NS

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	67.50	77.05	84.10	101.87	114.62	80.01	85.96	76.46	254.3296	255.8188
B-496		77.75	86.61	103.95	111.85	81.81	87.70	77.81	189.2347	215.1624
SLS-1			87.95	102.28	113.89	88.28	89.90	85.73	68.2199	129.2775
Niab-78				107.09	116.14	103.94	99.46	102.17	28.9789	58.2069
Niab-313/12					120.36	113.95	111.50	109.39	18.8968	25.2242
B-622						84.68	88.41	82.55	137.7516	181.8174
Niab-92							90.31	85.81	82.0318	133.3897
Cyto-11/91								76.89	150.2728	190.8038

Regression coefficient (b) $= 0.9882\pm0.0759$, difference of b from zero (bO) $= 13.0197$** different for b from unity (b1) $=0.1546$NS NS, non-significant **, highly significant

Table 5c: Analysis of variance for arrays

S.O.V	d.f	S.S	M.S	F-Value
Wr + Vr				
Between Array	7	45839.50	6547.07	23.56**
Within Array	16	44469.50	2779.34	
Wr - Vr				
Between Array	7	4337.52	619.65	2.77*
Within Array	16	3581.65	223.85	

**, Highly significant and *,significant
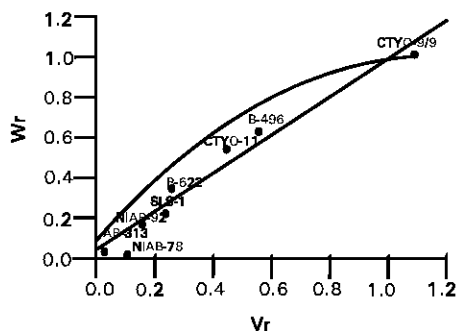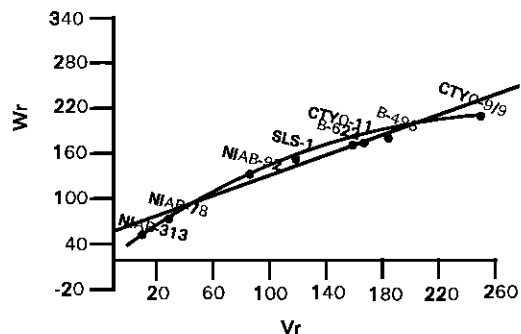

Fig.1: Wr/Wr graph for lint percentage (F_1)

Fig. 2: Wr/Wr graph for lint percentage (F_2)

Fig. 3: Wr/Wr graph for seed cotton yield per plant (F_1)

Fig. 4: Wr/Wr graph for seed cotton yield per plant (F_2)

reciprocal mean squares were concluded as non significant (Table 2 a, 3 a). In so far as the character like seed cotton in F_1 is concerned, all the four items were signif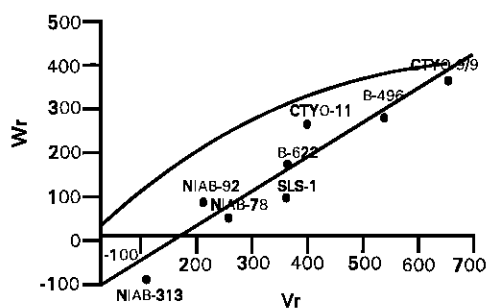icant, consequently, additive genetic effects along with non additive genetic effects and maternal effects were present (Table 4a). Further more, all the three items were exposed as significant while the fourth item like reciprocal was uncovered as non significant depicted thereby both additive and non additive effects but nothing like maternal effects were present in case of yield of seed cotton plant-1 in F_2 generation (Table 5a). The regression coefficients of seed cotton in F_1 (b) $= 0.8782\pm0.1256$, F_2 (b) $= 0.9882 \pm 0.07590$ and as well as of lint percentage in F_1 (b) $= 0.0888\pm0.9517$, F_2 (b) $= 0.9663\pm0.081$, did not differ significantly from unity and of course differed significantly from zero, suggesting the absence of epistasis and revealed the fulfilment of the assumptions for diallel analysis (Table 2b, 3b, 4b, 5b). The non-significant differences for Wr + Vr indicated the absence of dominance genetic effects, whereas the non significant differences for Wr-Vr showed the absence of non allelic interaction and thus additive dominance model is fully adequate in case of lint percentage in F_1
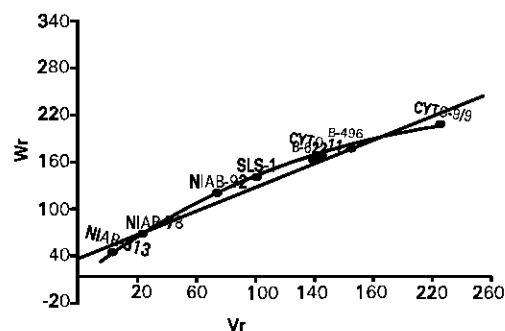
population (Table 2c). While both the Wr + Vr and Wr − Vr reflected the significant variance ratio suggesting the presence of epistasis and thus additive dominance model is molded partially adequate for lint percentage in F_2 population (Table 3c). At the same time as significant variance ratio (Table 4c, 5c) for both the analysis of Wr + Vr and Wr − Vr, were concluded, thus there was present evidence for non allelic interaction which turned the model partially adequate with reference to seed cotton plant^{-1} in both F_1 and F_2 populations.

Graphic position (Fig. 1, 2 and 4) revealed that regression lines for the said characters touched Wr axis above the origin hence signifying thereby additive type of gene action with partial dominance type of gene action except yield of seed cotton plant^{-1} (Fig. 3) in F_1 generation which depicted over dominance type of gene action as the regression line intercepted the Wr axis below the origin. Such type of situation is represented in a diallel analysis when F_1 hybrids score more than either of the parents, which is nothing but the reflection of hybrid vigor or heterotic effects in this connection.

The distribution of array points along the regression line showed that genotypes Niab-313/12 (Fig. 1), Niab-313/12 (Fig. 2) in case of lint percentage while Niab-313/12 (Fig. 3) and Niab-313/12 (Fig. 4) in case of seed cotton contained the maximum number of dominant genes in contrast to Cyto-9/91 in all the characters carried the maximum recessive alleles. Similarly, several workers like Murtaza *et al.* (1992), Azhar *et al.* (1994), Khan *et al.* (1995), Saeed *et al.* (1996), Busharat *et al.* (1998), Busharat *et al.* (1999 b) and Subhan *et al.* (2001) have reported additive type of gene action with partial dominance for these characters. However, findings of some others like, Rehman *et al.* (1988), Tariq *et al.* (1992), Khan and Khan (1993) and Murtaza *et al.* (1995) do not agree with these observations, which might be due to different genotypes used under different agro-ecological factors.

Additive type of gene action with partial dominance was accomplished which discloses beneficial outlines for selection of superior hybrids for the characteristics under study in both the generations. In case of yield of seed cotton^{-1}, over dominance type of gene action was also exposed specially in F_1 generation, which reflected the manifestation of heterotic effects.

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