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## Genetic Variation and Combining Ability for Yield and Fiber Traits among Cotton F<sub>1</sub> Hybrid Population

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**Abstract:** The experiment was conducted to detect genetic variation and genetic effects associated with cultivars. Seven varieties of upland cotton (*G. hirsutum* L) representing a broad array were crossed in all possible combinations in diallel fashion, the parents and F<sub>1</sub> progenies were sown in replicated experiment. Hayman diallel cross analysis was employed to investigate the nature of action and interaction of genes involved in the inheritance of character while the Griffing techniques was used to estimate general and specific combining ability of parents and genetic components of the variance for traits under study. Diallel analysis revealed that all the characters were polygenetically inherited and exhibited the greater part of genetic variation is due to dominant effect for all traits as  $(H_i/D)^{1/2}$  value is more than one and the dominant gene effect H<sub>1</sub>, H<sub>2</sub> is also significant for all traits under study. The H<sub>1</sub> value is almost equal to H<sub>2</sub> for all the traits, which indicate the occurrence of equal gene frequency at all loci. The ratio H<sub>1</sub>/4H<sub>1</sub> is also nearly equal 0.25 for all traits except for node of first fruiting branch, seed cotton yield and staple length, which reflected that positive and negative alleles are equally distributed among the parents for all traits. Significant estimates for General Combining Ability (GCA) and Specific Combining Ability (SCA) effect is significant for all traits but GCA mean square were smaller than SCA indicating dominant gene action for the traits under study and it is possible that hybrid vigour for these traits can be utilized. From the GCA value, it is estimated that LRA-5166 is the best combination for NFB, boll number and monopodial branches while FH-945 is best combiner for plant height, number of nodes/plant, staple length. From SCA effect it is observed that cross FH-901 X MNH554, LRA5166 X FH-945 were good cross combination for selecting the genotypes having lower NFB and M.B values, in segregating generation while the cross combination LRA5166 X CIM499 has the reasonable SCA effect for seed cotton yield, GOT% which indicated that the progenies of this cross should be used for improving yield, yield components with early maturing traits like less monopodial branches and lower value of NFB. The estimate of heritability broadsense (H<sub>b,s</sub>) and narrow sense (H<sub>n,s</sub>) indicated that the main portion of genetic variation among the population under study was due to dominant gene effect.

**Key words:** Cotton, genetic components, combining ability, diallel

### INTRODUCTION

New cotton cultivars continue to be developed that are earlier in maturity and higher in yield, however major improvements in fiber quality have not generally been associated with cultivars developed in breeding programs in the Pakistan.

Agronomic practices and environmental conditions influence the development of cotton fiber but the genotype of the cultivars also exert major influences on the fiber quality<sup>[1]</sup>. Cotton has been modified over many decades of breeding and selection to improve yield. In the identification of cotton from perennial to an annual growth habit plant breeders have selected a growth habit

of the cotton plant that reduces the no. of lateral monopodial branches that are found before sympodial fruiting branches are formed, resulting in an earlier onset of flowering<sup>[2]</sup>.

The primary limitation of use of F<sub>1</sub> hybrid is the expense of producing F<sub>1</sub> seed. However interest in hybrid cotton production is increasing among public programs and private seed companies. Information about combining ability and genetic variation among cotton varieties and their hybrids is essential to develop a best hybrid.

Wild cotton sp. have been used for improving the fiber traits like fineness and strength<sup>[3-5]</sup> but also have undesirable traits such as low lint % age or short fiber. Lee *et al.*<sup>[6]</sup> stated that estimates of GCA effects as a main

facts for significance for lint percentage and boll weight. Significant GCA by location interactions and SCA main effects also present for seed cotton yield. In a diallel study among six inbred lines, El-Adel and Miller<sup>[7]</sup> found that GCA of F<sub>1</sub> owes to be more important than SCA for lint yield and components of yield with the exception of lint yield.

A systematic approach for the depiction of the parents and crosses superior for the traits under investigation is helpful for plant breeder to choose the efficient method of selection for isolation of superior genotypes among the offsprings of hybrid progenies under investigation; for this purpose combining ability analysis was attempted in this study. By diallel analysis, the kind and relative magnitude of genetic variability among the group of varieties strains can be determined.

Baloch *et al.*<sup>[8]</sup> studied combining ability and genetic parameters for yield and fiber traits in upland cotton and results showed that proportion of variance due to GCA was higher than SCA for seed cotton yield, lint % age and staple length which suggested that these traits are predominantly controlled by additive gene. Kumaron *et al.*<sup>[9]</sup> carried out genetic analysis of seed cotton yield, days to first flower and bolls/plant in cotton and observed additive dominant gene action for these traits. High values for broad sense heritability estimates for these traits were noted. Subhan *et al.*<sup>[10]</sup> observed significant difference among hybrids and their parents in upland cotton for no. of bolls/plant and lint % age and showed additive type of gene influence, while, over-dominance type of gene action for seed cotton yield/plant was observed.

The objective of this research was to measure agronomic and fiber properties and to detect genetic variation and genetic effects associated with cultivars.

## MATERIALS AND METHODS

Seven cotton genotypes were selected as parents on their agronomic performance and fiber properties and crossed in half-diallel mating design in 2003-04. The Parents were as follows, LRA-5166, CIDEX, CIM-499, CIM-446, FH-901, MNH-554 and FH-945. Crosses and parents were arranged in a Randomized Complete Block Design with three replications at Cotton Research Station, Multan, 2004-05. All agronomic practices were used equal for each replication. The sowing was done by dibbling three seeds per hill to ensure uniform stand, later thinned to one per hill. The row to row distance was kept 75 cm and plant to plant was 30 cm. The inputs such as irrigation, fertilizer and other cultural practices were adopted as recommended by department. The pest control measure were managed on an optimal fashion.

The data of plant height, no. of nodes per plant, node of first fruiting branch, no. of boll, monopodial branches,

boll weight and seed cotton yield from ten guarded plant was taken in from parents as well as their hybrids. The seed cotton sample of each variety was taken in laboratory and ginned by roller machine. From lint weight, GOT% was computed and staple length was measured by fibrograph. All data of parents and their F<sub>1</sub> hybrids were statistical analyzed<sup>[11]</sup>.

An extended additive-dominance model proposed<sup>[12-14]</sup> be used to estimate the genetic component of variation and combining ability.

## RESULTS AND DISCUSSION

Analysis of variance of plant height, total no. of nodes/plant, node of first fruiting branch, monopodial branches per plant, no. of bolls/plant, boll weight, yield, ginning out turn and staple length indicated that significant differences existed among all genotypes. i.e. parents and their F<sub>1</sub> hybrids for all these traits (Table 1). The inferences regarding inheritance pattern can be made from the value of D, H<sub>1</sub>, H<sub>2</sub> and F components of genetic variation presented in Table 5. It is evident from Table 5 that variation due to additive component is significant for monopodial branches/plant, seed cotton yield, GOT% and staple length and non-significant exist for plant height, total no. of nodes/plant, NFB and no. of bolls/Plant. The dominant gene effect H<sub>1</sub> and H<sub>2</sub> is significant for all traits under study. The additive gene effect (D) is significant only for MB, seed cotton yield, GOT% and staple length, while for all other traits to be studied were found non-significant. The dominant gene effect (H<sub>1</sub> and H<sub>2</sub>) is larger than additive component (D) for all traits, which indicated that the greater portion of genetic variation is due to dominant gene effects. Since H<sub>1</sub> value was almost equal to H<sub>2</sub> for all traits under study which indicated the occurrence of equal gene frequency at all loci. The positive and significant value of (F) for no. of nodes/plant, monopodial branches/ plant, boll weight, seed cotton yield and staple length showed that dominant and recessive genes are in equal proportions in the parents which were also supported by the estimate of ratio  $[\{4D H_1\} + F] - [\{4D H_2\} - F]$ . The degree of dominance  $(H_1/D)^{1/2}$  showed that the greater part of genetic variation was due to dominant effect (Higher degree of dominance) for all traits under study. The ratio  $(H_2/4H_1)$  is nearly equal to 0.25 for all traits except for NFB, seed cotton yield and staple length which indicated that positive and negative alleles were distributed equally among the parents for these traits while unequal distribution was predicted for NFB, seed cotton yield and staple length as their value is not equal 0.25. The non-significant value of h<sup>2</sup> for MB, seed cotton yield, GOT% and staple length showed the absence of overall dominance effect of heterozygous loci. The results indicated that mean square for GCA was

**Table 1: Mean Squares of analysis of variance of character**

SOV	DF	Height (cm)	Node	NFB	MB	Boll (No.)	Boll (wt.)	Yield (kg ha <sup>-1</sup> )	GOT (%)	SL
Block	2	72.54	0.028	0.372	0.065	45.35	0.032	62.973	1.512	0.72
Genotype	27	995.38*	22.3901*	1.674*	4.13*	651.40*	1.591*	2314.14*	29.064*	2.29*
Error	54	32.74	2.1142	0.220	0.211	16.167	0.026	25.29	1.879	0.20

\* = Significant at 5%, \*\* = Significant at 1%, PH = Plant Height, GOT % = Ginning Outturn, NFB = Node of First Fruiting Branch, SL = Staple Length, MB = Monopodia Branches, Boll Wt. = Boll Weight

**Table 2: Means Squares for combining ability analysis in 7x7 diallel analysis in cotton**

SOV	DF	Height (cm)	Node	NFB	MB	Boll (No.)	Boll (wt.)	Yield (kg ha <sup>-1</sup> )	GOT (%)	SL
GCA	6	866.88**	19.60**	1.49**	2.67**	587.27**	0.908**	1974.87**	52.99**	0.589**
SCA	21	1032.09**	23.18**	1.72**	9.26**	669.73**	1.786**	3623.11**	22.22**	1.27**
Error	54	32.74	2.11	0.22	0.21	16.16	0.026	25.29	1.87	0.200

\* = Significant at 5%, \*\* = Significant at 1%

**Table 3: Predicted general combining ability effects for yield and fiber properties of nine parents**

Genotype	Height (cm)	Node	NFB	MB	Boll (No.)	Boll (wt.)	Yield (kg ha <sup>-1</sup> )	GOT (%)	SL
LRA-5166	-6.206	-0.457	-0.286	0.584	6.373	-0.016	-3.385	0.583	-0.052
CIDEX	-3.243	0.082	0.225	0.089	-4.404	-0.272	-19.684	-2.553	0.406
CIM-499	-4.132	-0.902	-0.115	-0.166	4.361	0.180	9.620	0.167	-0.164
CIM-446	3.423	-1.015	-0.216	0.540	-5.482	0.131	13.727	-0.125	-0.272
FH-901	-1.947	0.703	-0.063	-0.911	-3.438	0.189	-2.421	-0.175	-0.074
MNH-554	1.681	0.273	0.350	0.455	-0.504	-0.201	-6.522	2.196	0.009
FH-945	10.423	1.323	0.107	-0.591	3.117	-0.011	8.707	-0.094	0.146

**Table 4: Predicted specific combining ability effects for yield and fiber properties of nine parents**

Parents	Height (cm)	Node	NFB	MB	Boll (No.)	Boll (wt.)	Yield (kg ha <sup>-1</sup> )	GOT (%)	SL
P <sub>1</sub> x P <sub>2</sub>	0.42	0.47	0.043	-0.49	27.23	-0.29	32.05	-4.93	-1.23
P <sub>1</sub> x P <sub>3</sub>	-1.34	1.29	0.045	0.16	24.47	-0.21	45.24	4.13	0.99
P <sub>1</sub> x P <sub>4</sub>	10.42	5.07	-0.51	0.12	-9.48	0.80	-7.43	4.96	-0.15
P <sub>1</sub> x P <sub>5</sub>	6.79	2.81	-0.007	0.03	-12.02	-0.15	-0.58	-0.48	-1.25
P <sub>1</sub> x P <sub>6</sub>	-24.16	-4.75	0.17	0.27	17.33	-0.005	19.11	2.21	1.96
P <sub>1</sub> x P <sub>7</sub>	33.75	1.06	-0.17	-0.74	2.11	-1.02	12.25	-2.66	-0.37
P <sub>2</sub> x P <sub>3</sub>	0.68	-1.08	2.03	-0.34	0.65	1.05	-22.09	4.23	0.57
P <sub>2</sub> x P <sub>4</sub>	6.13	-3.16	-0.19	1.82	10.09	-0.28	48.19	-1.0	-0.61
P <sub>2</sub> x P <sub>5</sub>	3.16	1.74	-0.27	0.57	2.45	0.53	-14.95	1.63	-0.58
P <sub>2</sub> x P <sub>6</sub>	-2.46	3.63	1.36	0.20	-3.18	0.42	19.28	-0.05	-0.63
P <sub>2</sub> x P <sub>7</sub>	13.13	-0.14	0.69	0.08	-18.10	0.03	-25.54	-0.93	0.06
P <sub>3</sub> x P <sub>4</sub>	13.68	1.74	-0.81	0.20	-1.97	-0.06	-2.93	0.74	0.45
P <sub>3</sub> x P <sub>5</sub>	-18.27	0.62	0.09	0.49	-0.71	-0.32	11.44	1.52	-0.08
P <sub>3</sub> x P <sub>6</sub>	35.42	1.28	1.007	1.96	19.05	-0.16	-26.28	3.48	0.07
P <sub>3</sub> x P <sub>7</sub>	-8.64	-0.66	-0.50	0.34	0.72	-0.33	23.32	1.81	-0.33
P <sub>4</sub> x P <sub>5</sub>	28.16	0.14	0.09	-0.54	12.82	0.39	-0.26	-0.94	0.12
P <sub>4</sub> x P <sub>6</sub>	-8.79	2.94	-0.65	0.08	-2.8	-0.85	-2.62	-1.22	1.04
P <sub>4</sub> x P <sub>7</sub>	6.79	-0.07	2.25	0.30	11.57	-0.10	-11.25	1.51	-0.19
P <sub>5</sub> x P <sub>6</sub>	0.23	-0.71	-1.47	-0.46	-1.45	-1.44	-18.67	-0.57	-0.68
P <sub>5</sub> x P <sub>7</sub>	3.49	3.67	0.03	1.75	9.92	-0.05	-20.50	-0.63	0.60
P <sub>6</sub> x P <sub>7</sub>	10.53	0.43	-0.64	-0.61	2.99	-0.59	9.29	0.54	0.96

P<sub>1</sub> = LRA-5166, P<sub>2</sub> = CIDEX, P<sub>3</sub> = CIM-499, P<sub>4</sub> = CIM-446, P<sub>5</sub> = FH-901, P<sub>6</sub> = MNH-554, P<sub>7</sub> = FH-945

**Table 5: Genetic components of the traits**

Components	Height (cm)	Node	NFB	M.B	Boll (No.)	Boll (wt.)	Yield	GOT (%)	SL
E	11.38±29.6	0.68±0.9	0.075±0.1	0.069±0.08	5.73±36.07	.009±0.07	8.87±86.2	0.62±1.3	0.073±0.2
D	50.97±83.7	2.934±2.9	0.304±0.3	2.018±0.2*	48.62±102.02	0.483±0.4	1197.26±244.0*	8.30±3.7*	1.36±0.5*
F	11.49±200.9	2.501±6.1	0.72±0.8	0.981±0.5	27.02±244.7	0.85±0.5	1510.44±585.5	6.23±9.0	2.57±1.4
H <sub>1</sub>	1241.37±201.6*	26.93±6.1*	2.44±0.8*	2.83±0.5*	799.52±245.6*	2.30±0.5*	3009.12±587.6*	31.5±9.03*	3.99±1.4*
H <sub>2</sub>	1104.08±177.6*	24.66±5.3*	1.69±0.7	2.52±0.5*	704.1±216.4*	1.78±0.4*	2164.74±517.8*	24.66±7.9*	2.64±1.2
h <sup>2</sup>	65.71±19.3	10.82±3.6*	-1.65±0.5	0.47±0.5	57.19±45.3	3.11±0.3	39.62±347.7	3.02±5.3	0.46±0.8
(H <sub>1</sub> /D) <sup>1/2</sup>	4.93	3.03	2.839	1.186	4.05	2.18	1.58	1.95	1.71
H <sub>2</sub> /4 H <sub>1</sub>	0.22	0.22	0.173	0.223	0.22	0.19	0.18	0.195	0.16
1/2F/[D(H <sub>1</sub> -H <sub>2</sub> )] <sup>1/2</sup>	0.069	0.48	0.755	0.620	0.19	0.85	0.75	0.411	0.95
(4DH <sub>1</sub> ) <sup>1/2</sup> + F/(4D H <sub>1</sub> ) <sup>1/2</sup> - F	1.047	1.32	2.44	1.515	1.14	2.36	2.32	1.47	3.46
H n.s	0.235	0.165	0.251	0.49	0.24	0.14	0.32	0.399	0.084
H b.s	0.97	0.917	0.887	0.95	0.97	0.98	0.98	0.945	0.909

\* = Significant at 5%

smaller than SCA for all traits indicating a dominant gene action (Table 2). From these results it can also be concluded that hybrid vigour for these traits can be utilized in hybrid seed production breeding programme but from the Table 3 it is also evident that the means square values of GCA has minor differences for NFB, boll number and boll weight. So the utilization of hybrid vigour for these traits may not be more fruitful. The highest positive value of GCA for number of bolls per plant and monopodial branches/plant observed for LRA-5166 while FH-945 showed highest value for plant height and number of nodes/plant. The highest GCA value for boll weight, seed cotton yield and GOT% was exhibited by FH-901, CIM-446 and MNH-554, respectively. For earliness in cotton NFB and monopodial branches are the main traits of a genotype that determine its earliness. The highest negative GCA effect for NFB and M.B were observed by LRA-5166 and FH-901, respectively.

The cross  $P_5 \times P_6$ ,  $P_1 \times P_7$  showed the lowest value for SCA effect for NFB and Monopodial branches/plant, (Table 4). So it is suggested that the selection for earliness should be practiced in the progeny of these two crosses and these parents can be used in crossing for incorporating the earliness related traits in new genotypes.

The cross  $P_1 \times P_2$  and  $P_1 \times P_4$  had the highest SCA effects for no. of bolls/plant and no. of nodes/plant, respectively, while  $P_2 \times P_4$  had highest SCA effect for seed cotton yield. Highest SCA effect for GOT% and staple length was observed in cross combination of  $P_1 \times P_4$  and  $P_1 \times P_6$ , respectively (Table 4). The cross  $P_1 \times P_6$  showed highest negative SCA effect for plant height and total no. of nodes/plant which indicated that progeny from this cross should be used for developing genotype with low height/node ratio. The cross  $P_1 \times P_3$  has the reasonable SCA effect for yield, no. of bolls/plant, boll weight, staple length, plant height, NFB and GOT%, which indicated that the progeny of this cross should be used for further selection in segregating generation for improving the seed cotton yield, no. of bolls/plant, staple length, GOT% with short structure and early maturing genotype.

The heritability estimates in broadsense heritability were higher for all traits to be under study but narrow sense heritability was low for all traits except GOT% and seed cotton yield. It indicated that the main portion of genetic variation among the population under study was due to dominant gene effect. So it is recommended that in the segregating generation, breeder should be very careful for selection and pedigree method should be adopted for improving these traits from the population, which are under study.

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