Estimation of genetic parameters for quantitative and qualitative traits in cotton cultivars (*Gossypium hirsutum* L. *& Gossypium barbadense* L.) and new scaling test of additive– dominance model

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Abstract

A complete diallel cross of nine cotton genotypes (*Gossypium hirsutum* L. *& Gossypium barbadense* L.) viz Delinter, Sindose-80, Omoumi, Bulgare-539, Termez-14, Red leaf (Native species), B-557, Brown fiber and Siokra-324 having diverse genetic origins was conducted over two years to determine the potential for the improvement of yield, its components, oil and fiber quality traits by means of genetic analysis, combining ability, heritability and heterotic effects. The detailed studies were based on F_1 generations where crossed seeds in the first year were used for F_1 generation in the second year. The successful hybrids were recognized and distinguished by morphological markers such as flower color, spot position and their colors in petal, fiber color, seed linter, leaf color and their shapes. Analysis of variance for Simple Square Lattice Design (SSLD) showed highly significant differences (P ≤ 0.01) among various genotypes which allowed genetic analysis by Griffing, Hayman and Hayman-Jinks, method. Additive- dominance model and related correlation (Wr, Vr) were adequate for majority of the traits and partially adequate for some traits. Majority of the traits were influenced by non-additive gene action in F_1 generation. These results are encouraging for practical improvement through hybrid breeding programs and the contributions of additive genes through selection method. Significant variation for general combining ability (GCA) effects, specific combining ability (SCA) effects ($P ≤ 0.05$) and high narrow sense heritability indicates the potential for improvement through selection. On the other hand, over-dominance gene action, low and moderate rate of narrow-sense heritability for some traits suggests that improvements should be made utilizing a combination and hybrid breeding approach.

Key words: Cotton, Hybrid, Genetics.

Introduction

Modern genetics can be traced to the rediscovery of Gregor Mendel's research in the early 1900s. Mendel recognized that organisms have two copies of each gene (alleles) and that one allele is contributed by each parent to the offspring. This phenomenon is observed in diploid organisms, those which have two sets of each chromosome in the genome. Mendel also concluded that alleles display dominance and recessiveness. However, today we recognize that other types of alleleic

interaction can exist in which alleles are additive (the heterozygote value is the average of the two homozygotes), incomplete dominant (the heterozygote value lies closer to one of the two homozygotes), or overdominant (the heterozygote value exceeds either of the two homozygotes), as well as dominant. Linkage is a key genetic phenomenon impacting plant breeding. Linkage violates Mendelian independent assortment due to the arrangement of genes on chromosomes therefore every gene on a chromosome is inherited together. Many traits are said to be linked because the genes controlling them lie close together on a chromosome and therefore have a higher random probability of being transmitted together to the progeny.

Many other genetic phenomena influence expression of traits. First, multiple alleles can exist for each gene in a population. Each individual may possess only two copies but those copies can differ among individuals (e.g., leaf shape in Upland cotton, *G. hirsutum* L.). Second, epistasis is a phenomenon in which the expression of one gene is affected by the genotype of a gene at a separate locus (e.g., expression of AA, Aa, and aa depends on the genotype at locus B). Third, pleiotropy is a phenomenon in which single gene can affect multiple traits. Fourth, heterosis is a phenomenon in which progeny between unrelated parents perform better than what would be expected based on the average performance of the parents; this is the phenomenon which has led to hybrid seed production for yield improvement in cotton and other crops and can be the result of combinations of the previous genetic phenomena. Finally, environment is a crucial modifier of gene expression (Ragsdale 2003).

Cotton, as a commercial crop, has played a vital role in agriculture, industrial development, and employment generation. This most important cash crop, besides providing raw material (fiber) for textile industry, also provides food in the form of oil and cotton seed cake for human and animal consumption. It also earns a huge amount of foreign exchange through the export of its raw materials as well as its finished products. Due to its undisputed importance, cotton has attracted maximum attention of geneticists and plant breeders and their sustained efforts have led to the evolution of high yielding cultivars for enhancing cotton production in the world. Evolution and utilization of high yielding, stresses tolerant cultivars to have primordial position in the crop production technology package. The research experience has repeatedly established uncontestable importance of transgressive hybridizations, the function of identification of genotypes and putting them to the point of the specific genotypic combinations (Hosseini, 2008).

In view of the pivotal importance of this type of research and its lasting impact upon the future cotton breeding strategies, a research programme is organized to study the genetic basis of different traits

of cotton plant along with combining ability analysis and heterosis in a set of 9×9 complete diallel cross experiment at Botany Department, University of Pune, India during 2004– 2007. Further, this research has three primary objectives: 1) To determine the potential of some quantitative and qualitative traits in screening for yield, oil content and fiber quality across upland and *barbadense* cotton genotypes; 2) To determine the potential to improve mentioned properties by a diallel analysis of nine upland cotton genotypes and 3) To determine the efficiency of correlation between Wr and Vr for epistasis testing instead and along with Wr-Vr ANOVA and *b* (Wr, Vr) regression test and to introduce new test scale for epistasis existence in diallel cross. The all tetraploids (2n = 52) genotypes which have been used in the present research belong to genomic group of $(AD)_1$ and $(AD)_2$ with large and small chromosomes.

Materials and Methods
The results reported in this study pertain to genetic analysis, combining ability and heterosis estimates in Upland cotton (*Gossypium hirsutum* L. & *Gossypium barbadense* L.), conducted at the Research Farm of Botany Department of Pune University (73°, 51'E longitude, 18°, 31' N latitude and altitude 559m) during 2004-2007. Breeding material comprised of nine different *G. hirsutum* L. & *G. barbadense* L. genotypes varied by origin, yield and its components and fiber as well as oil quality traits. The cultivars were Delinter, Sindose-80, Omoumi, Bulgare-539, Termez-14, Red leaf, B-557, Brown fiber and Siokra-324.The brief description of cultivars is presented in Table 1.

Crossing Block
The seeds of the nine diverse genotypes were sown on 12th July 2005, in a non-replicated crossing block by dibbling on a well prepared seed bed. Plants were raised in nine rows, each of 36 meters length, at the spacing of 0.25 and 1.5 meters between plants and rows, respectively. NPK was applied at the rate of 60:60:60. The 1/3 dose of nitrogen and 2/3 dose of phosphorus and potash were applied at sowing time, the remaining nitrogen, phosphorus and potash in two split doses at four-leaf and 25cm of plant height stages. All cultural practices and plant protection were done regularly. The crop was ready for crossing on September 20, 2005. The genotypes were crossed in a complete diallel fashion by hand pollination. Crossing continued up to mid November 2005. All precautionary measures were observed to avoid undesirable contamination of genetic material while selfing and crossing in the crossing block of nine genotypes (Table 2). The ginning was performed with roll-ginning machine and the seeds were kept safely for sowing F_1 experiment in thecoming year.

Table 1. The brief description of cultivars.

Characters	Cultivars				
	Delinter	**Sindose-80**	**Omoumi**	**Bulgare-539**	**Termez-14**
Origin	Iran	Greece	Iran	Bulgaria	Uzbekistan
Oil content (%)	18.7	17.4	21.7	17.13	20.3
Boll Weight (g)	3.7	2.45	1.7	2.7	2.2
Uniformity ratio (%)	47	46	47.5	48	46.5
Staple Length (mm)	24.3	27.5	29.3	24.5	33
Fiber bundle strength (g/tex)	18.4	22.3	25.7	20.1	26.9
Micronaire (g/inch)	4.05	2.6	3.2	3.2	3.05
Earliness (days to flowering)	94.5	78	70	84.5	73

Table 1. Continued.

Characters	Cultivars			
	Red leaf	**B-557**	**Brown fiber**	**Siokra-324**
Origin	Iran	Bulgaria	Iran	Australia
Oil content (%)	18.5	15.9	18.3	16.4
Boll Weight (g)	2.9	2.2	2.5	2.8
Uniformity ratio (%)	43.5	45.5	47.5	48.5
Staple Length (mm)	17.6	26	23.8	27.8
Fiber bundle strength (g/tex)	21.5	19.55	16.95	22.2
Micronaire `(g/inch)	2.75	2.75	3.85	3.15
Earliness (days to flowering)	98	93.5	94	81.5

F_1/Parents Experiment

The 9×9 F_1 complete diallel cross having seventy-two F_1 hybrids along with nine parental cotton were sown on 23th June, 2006, by dibbling on a well prepared seed bed. Each genotype was planted in four rows measuring 6 meters as hill method with conservation of four plants in one hill in a Simple Square Lattice Design (SSLD) with two replications. The row and plant spacing were 80 and 25 cm, respectively. Cultural practices including fertilizer, hoeing, weeding, irrigation and plant protection measures were carried out as recommended for cotton production. The data were subjected to analysis of variance (ANOVA) on the basis of lattice design, using MSTATC, a computer software package. The data were analyzed using dial software(version 1.1) delivered by Mark Burow and James G.Coors and Dial 98 software that had been revised (September, 2006) and delivered by Yasuo Ukai.

Table 2. Crossing block of nine genotypes of cotton (*G.hirsutum* L. & *G.barbadense* L.) during 2005 -2006.

Cultivars	Delinter	Sindose-80	Omoumi	Bulgare-539	Termez-14	Red leaf	B-557	Brown fiber	Siokra-324
Delinter	X11	X12	X13	X14	X15	X16	X17	X18	X19
Sindose-80	X21	X22	X23	X24	X25	X26	X27	X28	X29
Omoumi	X31	X32	X33	X34	X35	X36	X37	X38	X39
Bulgare-539	X41	X42	X43	X44	X45	X46	X47	X48	X49
Termez-14	X51	X52	X53	X54	X55	X56	X57	X58	X59
Red leaf	X61	X62	X63	X64	X65	X66	X67	X68	X69
B-557	X71	X72	X73	X74	X75	X76	X77	X78	X79
Brown fiber	X81	X82	X83	X84	X85	X86	X87	X88	X89
Siokra-324	X91	X92	X93	X94	X95	X96	X97	X98	X99

$X_{ij} = X\male\female$

Morphological Markers

There were more and enough morphological markers for recognition of all successful hybrids such as 1) Petal spot that inherited from parents of Omoumi and Termez-14 and the expression of this marker in crossing with non-petal spot parents was demonstrated from light red petal spot (smaller in size) to dark red petal spots (bigger in size) in the related hybrids (Row & Column 3 and 5 on Fig. 1) and absence of petal spot in non-successful hybrids. 2) Yellowness of petals as marker varies from less yellowness to more yellowness with more yellowness also originated from parents of Omoumi and Termez-14 and their successful hybrids demonstrated a moderate yellowness petals (Row & Column 3 and 5 on Fig. 1) in hybrids. 3) Red color petal marker that originated from Red leaf parent and its hybrids varies from less red petals to more red petals in its related hybrids (Row &

Column 6 on Fig. 1) and absence of red color in non-successful hybrids. 4) Brown fiber marker that was converting from Brown cotton and its crossing with white color parents had light, intermediate and dark brown color fiber (Row & Column 8 on Fig. 4) and absence of brown color in non-successful hybrids. 5) Lint less seed marker that originated from Delinter parent and in its hybrids removing the fiber from seed was easier than non-successful hybrids (Row & Column 1 on Fig. 3). 6) Red leaf marker that originated from genes of Red leaf and its hybrid had intermediate color between green and red color in its successful hybrids (Row & Column 6 on Fig. 2) and green color leaf in non-successful hybrids. 7) Leaf lobbing originated from Siokra-324 parent and those hybrids that had Siokra-324 as one of their parents had leaf lobbing variation from less deeper, intermediate and deeper leaves and consequently without leaf lobbing in non-

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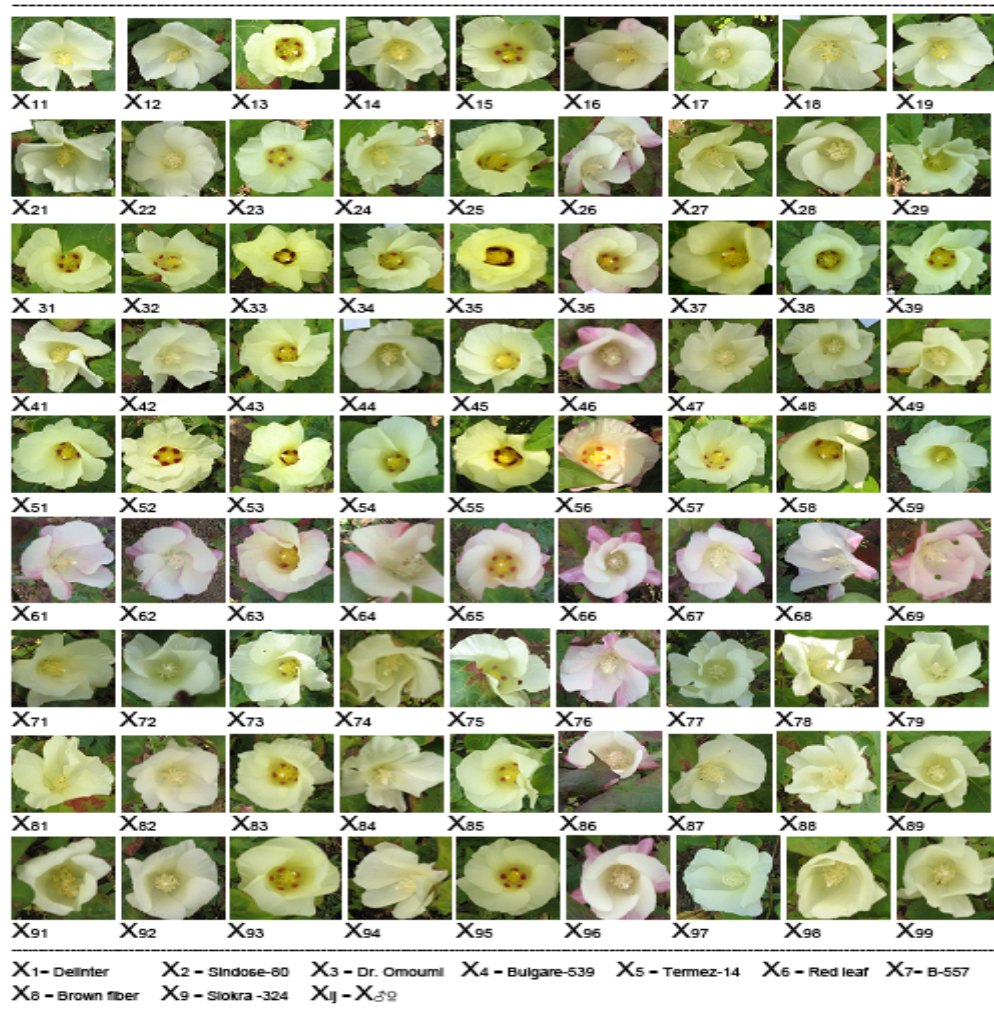successful hybrids (Row & Column 8 on   Fig. 2).

Fig 1. Morphological markers of cotton flower in 9×9 diallel cross.

Results

Analysis of variance in a Simple Square Lattice Design (SSLD) showed highly significant diversity (P ≤ 0.01) among genotypes of the studied traits and those which allowed genetic analysis by Hayman (1954) and Griffing,s (1956) methods (Table 3).

In F1 generation, the analysis of variance of arrays indicated epistasis effects due to the significance of Wr-Vr for uniformity ratio, fiber bundle strength, seed index, seed cotton yield and boll weight; dominance effects due to the significance of Wr+Vr for all traits except boll weight and non-epistasis effects due to the significance of b value for all traits except uniformity. Such results confirmed additive-dominance model for mentioned traits. It was also found that the assumptions of the Hayman-Jinks model are not fulfilled for some traits such as fiber bundle strength, seed index, seed cotton yield and boll weight which

makes the model partially adequate for them and non adequate only for uniformity.

Fig 2. Morphological markers of cotton leaf in 9×9 diallel cross.

Additive- dominance model was adequate for the remaining traits that adequacy of additive-dominance model is with no nonalleleic interaction and independence of gene action for random gene recombination. These results are confirmed with testing of additive-dominance model by means of significant correlation between Wr and Vr that is presented for the first time in this study.

In F_1 generation of uniformity ratio, the regression analysis indicated that regression coefficient (*b*) differed nonsignificantly from zero but significantly from unity.

Fig 3. Morphological markers of cotton seed in 9×9 diallel cross.

The analysis of variance of arrays revealed that Wr+Vr and Wr-Vr were significant, showing existence of dominance with nonallelic interaction and the dependence of genes on random associations in their actions. Also there is non-adequacy of additive-dominance model with nonalleleic interaction and dependent gene action for random gene recombination. It got confirmed by "r" test due to its nonsignificant value indicating non-adequacy of model with

nonalleleic interaction (Table 4) thus the assumptions of the Hayman-Jinks model are not fulfilled which makes the model partially adequate (Jinks, 1954).

Fig 4. Morphological markers of cotton fiber in 9×9 diallel cross.

All the genetic components of variance, the additive (D), dominance (H_1, H_2) and F were significant and h^2 was positive and nonsignificant. The additive component (D) was smaller than dominance components (H_1, H_2) and the mean degree of dominance ($\sqrt{H_1/D}$ = 1.59) was more than 1 indicating non-additive type of gene action and is in increasing position as confirmed by positive and non-significance of h^2(0.028) as well as by the value of Kd/Kd+Kr (0.653). Unequal values of H_1 and H_2 indicating dissimilar distribution of positive and negative genes was also confirmed by the ratio $H_2/4H_1$ (0.203)

which has been showed on Table 5 (Mather1971).

Table 3: Estimation of mean squares and F ratio̓s along with CV% at 80 D.F for analysis of variance for different yield and quality traits of cotton (*G.hirsutum* L. *G.barbadense* L.) in F$_1$ generation during 2006-2007.

Source of Variance	DF	Mean Square					
		Oil Content (%)	Staple Length (mm)	Uniformity Ratio (%)	Micronaire (μg/inch)	Fiber Bundle Strength (g/tex)	Earliness (day)
Replications	1	0.025	0.831	4.840	0.005	4.173	33.802
Treatments							
Unadjusted	80	6.705**	21.255**	5.123**	0.206**	24.587**	124.863**
Adjusted	80	6.705**					
Blocks within Reps (adj.)	16	0.696	0.125	0.353	0.005	0.089	3.677
Error							
Effective	64	0.648					
RCB Design	80	0.649	0.135	0.490	0.006	0.250	5.215
Intra block	64	0.637	0.138	0.524	0.006	0.291	5.599
Relative Efficiency (RCB)		100.5	Less than RCB	Less than RCB	Less than RCB	Less than RCB	Less than RCB
CV%		4.105	1.266	1.493	2.396	2.148	2.907

**. Significant at 0.01 level (2-tailed).
 *. Significant at 0.05 level (2-tailed).

Table 3: Continued.

Source of Variance	DF	Mean Square					
		Lint% (G.O.T)	Seed Index (g)	Seed cotton yield(g)	Boll weight (g)	Bolls/Plant	Plant Height (cm)
Replications	1	5.111	0.155	11.239	0.007	0.747	34.722
Treatments							
Unadjusted	80	44.172**	7.558**	56.518**	0.464**	1.156**	454.878**
Adjusted	80			56.518**	0.464**	1.156**	454.878**
Blocks within Reps (adj.)	16	1.477	0.007	8.156	0.004	0.741	4.056
Error							
Effective	64			3.050	0.002	0.366	3.674
RCB Design	80	4.178	0.009	3.783	0.002	0.412	3.685
Intra block	64	4.853	0.009	2.69	0.002	0.330	3.592
Relative Efficiency (RCB)		Less than RCB	Less than RCB	124.02	106.5	112.46	100.29
CV%		4.749	1.04	7.197	1.584	7.077	1.973

**. Significant at 0.01 level (2-tailed).
*. Significant at 0.05 level (2-tailed).

Table 4: Scaling test of additive-dominance model "*b*" regression analysis, array analysis of variance and correlation (Wr,Vr) for a 9×9 diallel cross experiment of cotton (*G.hirsutum* & *G. barbadense*) in F_1 generation.

Traits	*b* value ± SE	Correlation (Wr, Vr)	Source of variance		D.F	MS	CV%
Oil Content %	(1.016 ± 0.16)**	0.923**	Wr+Vr	Between Arrays	8	8.977**	22.22
				Within Arrays	9	0.7474	
			Wr-Vr	Between Arrays	8	0.356	-75.80
				Within Arrays	9	0.300	
Staple Length (mm)	(0.978 ± 0.093)**	0.97**	Wr+Vr	Between Arrays	8	93.24**	5.48
				Within Arrays	9	0.479	
			Wr-Vr	Between Arrays	8	1.402	-32.42
				Within Arrays	9	0.285	
Uniformity Ratio (%)	(0.053 ± 0.245)	0.081	Wr+Vr	Between Arrays	8	1.833**	29.93
				Within Arrays	9	0.42	
			Wr-Vr	Between Arrays	8	1.532**	-54.17
				Within Arrays	9	0.275	
Micronaire (μg/inch)	(0.925 ± 0.114)**	0.951**	Wr+Vr	Between Arrays	8	0.014**	10.34
				Within Arrays	9	0.0001	
			Wr-Vr	Between Arrays	8	0.0001**	44.83
				Within Arrays	9	0.00001	
Fiber Bundle Strength(g/tex)	(0.786 ± 0.105)**	0.943**	Wr+Vr	Between Arrays	8	67.245**	8.99
				Within Arrays	9	1.681	
			Wr-Vr	Between Arrays	8	2.5**	-229.05
				Within Arrays	9	0.372	
Earliness **(day)**	(0.879 ± 0.091)**	0.965**	Wr+Vr	Between Arrays	8	8408.3**	8.67
				Within Arrays	9	62.35	
			Wr-Vr	Between Arrays	8	193.136	-226.29
				Within Arrays	9	116.802	
Lint% (G.O.T)	(0.781 ± 0.187)**	0.845**	Wr+Vr	Between Arrays	8	546.77**	29.11
				Within Arrays	9	46.908	
			Wr-Vr	Between Arrays	8	48.95	-49.6
				Within Arrays	9	22.823	
Seed index (g)	(0.851± 0.203)**	0.846**	Wr+Vr	Between Arrays	8	7.072**	2.12
				Within Arrays	9	0.007	
			Wr-Vr	Between Arrays	8	0.591**	-4.62
				Within Arrays	9	0.005	
Seed cotton yield(g)	(0.403 ± 0.130)*	0.76**	Wr+Vr	Between Arrays	8	309.62**	16.56
				Within Arrays	9	37.342	
			Wr-Vr	Between Arrays	8	90.161**	-80.52
				Within Arrays	9	16.266	
Boll weight (g)	(0.579 ± 0.227)*	0.692**	Wr+Vr	Between Arrays	8	0.013	40.98
				Within Arrays	9	0.011	
			Wr-Vr	Between Arrays	8	0.004*	-583.66
				Within Arrays	9	0.001	
Bolls/Plant	(0.900 ± 0.151)**	0.914**	Wr+Vr	Between Arrays	8	0.172**	17.69
				Within Arrays	9	0.025	
			Wr-Vr	Between Arrays	8	0.014	-100.33
				Within Arrays	9	0.049	
Plant Height (cm)	(0.873 ± 0.073)**	0.976**	Wr+Vr	Between Arrays	8	49319.2**	11.76
				Within Arrays	9	980.4	
			Wr-Vr	Between Arrays	8	743.82	-49.47
				Within Arrays	9	366.447	

**. Significant at 0.01 level (2-tailed).
*. Significant at 0.05 level (2-tailed).

Table 5. Analysis of variance for various traits in a 9×9 diallel cross of cotton (*G.hirsutum* L. & *G.barbadense* L.) in F_1 generation based on Griffing method I, model mixed-B (due to GCA, SCA and reciprocal effects), Hayman (due to SCA and reciprocal components) and Hayman-Jinks method (estimation of genetic components of variance in F_1 generation).

Source of Variance	DF	Mean Square					
		Oil Content (%)	Staple Length(mm)	Uniformity Ratio (%)	Micronaire (µg/inch)	Fiber Bundle Strength(g/tex)	Earliness (day)
Replications	1	0.025	0.831*	4.840**	0.005	4.173**	33.802*
Treatments	80	6.700**	21.255**	5.123**	0.206**	24.586**	124.863**
GCA(a)	8	40.976**	155.782**	10.326**	0.936**	183.85**	754.694**
SCA(b)	36	4.156**	11.136**	4.712**	0.11**	8.644**	102.638**
b1	1			0.60			
b2	8			3.03**			
b3	27			5.31**			
RECIP	36	1.628**	1.48**	4.354**	0.138**	5.138**	7.126
c	8			5.24**			
d	28			4.27**			
Error(Me)	80	0.324	0.68	0.245	0.003	0.125	2.6
MSGCA/MSSCA		9.86	13.99	2.19	8.51	21.27	7.35
Degree of Dominance(Griffing)		0.88	0.72	4.36	1.13	0.46	1.32
$2\sigma^2 gca/2\ \sigma^2 gca + \sigma^2 sca$		0.53	0.58	0.19	0.47	0.63	0.43
Heritability(ns)(Griffing)		0.49	0.58	0.17	0.45	0.68	0.42
D				2.068**			
H_1				5.174**			
H_2				4.191**			
F				1.999*			
h^2				0.028			
Kd/(kd+kr)				0.653**			
h				0.346			
uv				0.203**			
$\sqrt{H_1/D}$				1.59**			
h^2/H_2				0.0076			
D/D+E)				0.894**			
Heritability(bs)		0.906*	0.992**	0.865**	0.965**	0.99**	0.962**
Heritability (ns)		0.651*	0.754**	0.289**	0.641**	0.82**	0.607**

**. Significant at 0.01 level (2-tailed).
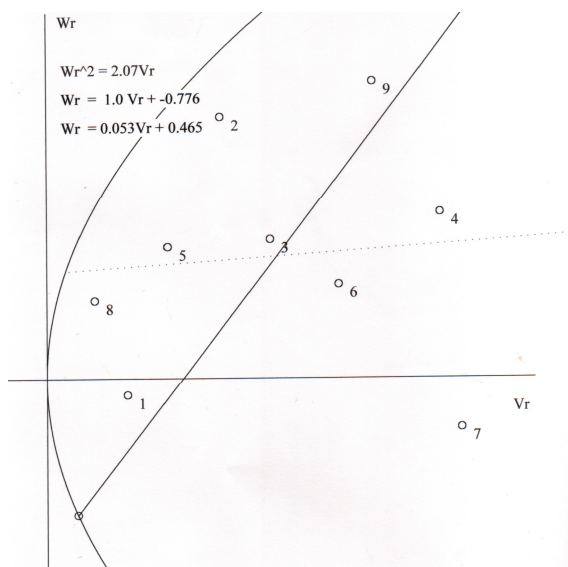 *. Significant at 0.05 level (2-tailed).

Table 5: Continued.

Source of Variance	DF	Mean Square					
		Lint% (G.O.T)	Seed Index (g)	Seed cotton yield (g)	Boll weight (g)	Bolls/Plant	Plant Height (cm)
Replications	1	5.111	0.155**	11.239	0.007	0.747	34.722
Treatments	80	44.172**	7.558**	56.518**	0.464**	1.156**	454.53**
GCA(a)	8	185.31**	42.354**	360.456**	2.69**	8.396**	3637.98**
SCA(b)	36	41.54**	6.034**	38.204**	0.32**	0.68*	199.906**

Table 5: Continued.

RECIP	36	15.436**	1.88**	7.29**	0.114**	0.022	1.722
Error (Me)	80	2.84	0.005	1.89	0.001	0.206	1.842
MSGCA/MSSCA		4.46	7.02	9.43	8.41	12.34	18.20
Degree of Dominance(Griffing)		2.09	1.44	0.98	1.2	0.34	0.55
$2\sigma^2$gca/2 σ^2gca+ σ^2sca		0.32	0.41	0.50	0.45	0.75	0.65
Heritability(ns) (Griffing)		0.30	0.41	0.48	0.45	0.54	0.64
Heritability(bs)		0.902**	0.999**	0.938**	0.912**	0.714**	0.993*
Heritability (ns)		0.466**	0.609**	0.653**	0.647**	0.619**	0.799*

**. Significant at 0.01 level (2-tailed).
*. Significant at 0.05 level (2-tailed).

No	Pr	Wr	Vr	Fr
1	Delinter	-0.074	0.458	0.876
2	Sindose-80	1.145	0.989	0.609
3	Omoumi	0.608	1.272	0.647
4	Bulgare-539	0.723	2.239	0.482
5	Termez-14	0.577	0.689	0.741
6	Red leaf	0.410	1.661	0.618
7	B-557	-0.220	2.361	0.608
8	Brown fiber	0.343	0.272	0.841
9	Siokra-324	1.296	1.855	0.453

Fig 5. Scattering of Parents on Wr/Vr Regression Line and Limitting Parabola for Uniformity Ratio and Their F_1 Fr Values (F_1 Generation).

Low estimates of narrow (0.289) and moderate broad (0.865) and true (0.894) sense heritability were also recorded in F_1 (Table 5). Non- significant positive correlation coefficient (r = 0.108) with b value of 0.07 obtained between Wr+Vr and parental means enunciated that parents containing recessive genes were responsible for increased uniformity ratio, while dominance genes were responsible for decreased uniformity in F_1 generation. The Wr/Vr graph plotted in Fig. 5 and Fr values for F_1 uniformity ratio, show that the regression line (*b*=1) intercepted Wr axis below the origin on negative side which suggested an over-dominance type

of gene action, while regression line ($b=$ 0.053) cuts Wr axis above the origin on positive side which suggested a partial dominance type of gene action. The distribution of array points along the regression line conceive that Delinter (1) and Brown color (8) bearing maximum and positive Fr values and being nearest to the point of origin, had large number of dominant genes, in contrast to the cultivar Bulgare-439 (4) and Siokra (9) being farther and possessing minimum Fr values, had maximum recessive genes.

Mean squares due to GCA and SCA were highly significant for all the traits in F_1 generation by Griffing method indicating the importance of additive and nonadditive effects of genes for genetic controlling of traits. High estimations of MSGCA/MSSCA for all traits and also high narrow-sense heritability for all traits except uniformity ratio (non-adquate trait for additive-dominance model) and lint% by Griffing and Hayman method (differences of heritability between two methods belong to interaction of environment and genetic parameters in Griffing method) displaythe importance of additive effects of genes in genetic control of more traits. This is also confirmed by the degree of dominance estimated near to 1 or less than 1 for some traits. For further improvement and breeding of these traits, selection method should be more efficient. For example, the hybrids of parents manifested the highest oil content because the mean of parents for oil content was 18.282% while the mean of hybrids was 19.77%

and the best crosses with over dominance gene effect for this trait were Omoumi $\times$ Brown fiber (22.95%), Delinter $\times$ Omoumi (22.78%) and Delinter $\times$ Termez-14 (22.495%) indicating 26% increase in oil content (22.95-18.25/18.25$\times$100) which is commercially valuable. For oil content Delinter, Omoumi and Termez-14 were the best general combiner and Sindose-80 $\times$Siokra-324, Termeze-14 $\times$ B-557 and Omoumi $\times$ Brown fiber were the best specific combiner. For other traits including staple length, uniformity, micronaire, fiber bundle strength, earliness, Lint%, seed index, seed cotton yield, boll weight, bolls/plant and plant height the value of their top F_1 hybrids has been increased 7.22mm (34.4-27.18), 3.4%, 1.08 g/inch, 8.08g/tex, -16.72days, 11.69%, 5.62g, 20.6g, 1.96g, 2.15 and 36.06cm in comparison with the mean of their parents respectively.

Heterosis of varying magnitude was found in F_1 generation. Plant height, seed cotton yield and earliness components showed maximum heterosis, while uniformity and micronaire showed low heterosis and the remaining traits showed moderate heterosis. This indicates the higher performance of F_1 hybrids for related traits which is normal from physiological point of view.

Table 6. Top means of parents, hybrids, crosses, GCA, SCA, interaction effects and average heterosis and increased coefficient in F_1 generation.

Traits	Oil Content (%)	Staple Length (mm) (2.5 SL)	Uniformity Ratio (%)	Micronaire (μg/inch)	Fiber Bundle Strength (g/tex)	Earliness (day)
Mean of three top parents	3 = 21.7	5 = 33.1	4 = 48	1 = 4.05	5 = 26.95	3 = 70
	5 = 20.3	3 = 29.35	3 = 47.5	8 = 3.85	3 = 25.7	5 = 73
	1 = 18.7	9 = 27.85	8 = 47.5	9 = 3.15	9 = 22.2	2 = 78
Mean of three top crosses (TC)	8×3 = 22.95	9×5 = 34.4	2×4 = 50	1×8 = 4.25	8×5 = 29.6	3×9 = 68.5
	1×3 = 22.78	6×5 = 34.3	1×9 = 49.5	1×9 = 3.9	7×5 = 29.6	9×3 = 68.5
	1×5 = 22.49	9×3 = 33.9	9×2 = 49.5	8×9 = 3.55	3×2 = 29.5	6×3 = 69
Mean of parents (MP)	18.28	27.18	46.6	3.17	21.52	85.22
Mean of hybrids	19.77	29.26	46.8	3.12	23.51	77.7
LSD (α = 0.05)	1.608	0.731	1.392	0.149	0.995	4.544
LSD (α = 0.01)	2.137	0.970	1.846	0.197	1.320	6.025
Three top GCA	3 = 2	5 = 3.9	5 = 0.61	8 = 0.26	5 = 4.17	3 = -7.6
	5 = 1.46	3 = 3.16	1 = 0.33	1 = 0.20	3 = 3.31	5 = -5.08
	1 = 0.09	9 = -0.44	3 = 0.28	9 = 0.058	9 = -0.31	9 = -3.72
Three top SCA	2×9 = 1.73	1×3 = 2.05	6×7 = 1.8	1×9 = 0.59	5×7 = 2.6	1×2 = -9.69
	5×7 = 1.43	3×7 = 1.9	2×4 = 1.4	2×8 = 0.28	2×3 = 2.1	5×6 = -8.88
	3×8 = 1.26	2×3 = 1.76	3×5 = 1.2	3×5 = 0.21	1×9 = 1.78	3×6 = -8.11
Increased coefficient (TC/MP) %	26	27	7.2	34	38	20
Average heterosis	1.4	2.07	0.187	-0.53	1.98	-7.5
Two top interaction effects	4×8 = -1.27	3×5 = -1.30	2×8 = -3	1×8 = 0.55	5×8 = -3.62	
	8×9 = 1.1	2×7 = 1.17	2×6 = -2.25	5×8 = 0.4	1×5 = -3.02	

Table 6. Continued.

Traits	Lint % (G.O.T)	Seed Index (g)	Seed cotton yield (g)	Boll weight (g)	Bolls/Plant	Plant Height (cm)
Mean of three top parents	8 = 48.98	5 = 9.53	6 = 26.88	1 = 3.72	6 = 9.6	3 = 114
	2 = 45.99	3 = 8.63	1 = 26.84	6 = 2.94	4 = 8.6	5 = 113
	4 = 44.74	6 = 8.42	4 = 22.35	9 = 2.7	7 = 8.1	9 = 91
Mean of three top crosses (TC)	7×1 = 53.2	6×3 = 13.13	4×1 = 40.1	4×1 = 4.55	6×4 = 10.1	3×5 = 121.5
	2×6 = 51.53	7×3 = 12.76	1×4 = 38.34	1×4 = 4.41	6×7 = 10.1	5×3 = 119.5
	7×2 = 50.24	5×6 = 12.62	6×1 = 38.08	7×8 = 4.01	6×1 = 10.1	3×6 = 119.5
Mean of parents (MP)	41.51	7.51	19.50	2.59	7.95	85.44
Mean of hybrids	43.22	9.12	24.86	3.02	8.62	98.61
LSD (α = 0.05)	4.067	0.185	3.489	0.094	1.209	3.829
LSD (α = 0.01)	5.39	0.245	4.636	0.125	1.606	5.088
Three top GCA	1 = 1.66	5 = 1.86	6 = 5.03	1 = 0.53	6 = 1.13	3 = 17.57
	8 = 1.64	3 = 1.78	1 = 4.14	6 = 0.19	4 = 0.37	5 = 16.71
	9 = 1.58	6 = 0.09	4 = 1.9	4 = 0.1	7 = 0.048	9 = 0.24

Table 6. Continued.

Three top SCA	1×7 = 4.97	5×6 = 1.52	1×4 = 8.8	1×4 = 0.87	3×8 = 0.64	5×8 = 10.56
	3×6 = 4.69	3×6 = 1.50	5×9 = 4.2	5×9 = 0.50	3×6 = 0.55	2×5 = 9.45
	3×5 = 4.46	3×7 =1.42	5×7 = 4.2	7×8 = 0.44	1×6 = 0.53	3×4 = 8.34
Increased coefficient (TC/MP) %	28	74	105	76	27	42
Average heterosis	1.7	1.6	5.3	0.43	0.67	13.16
Two top interaction effects	1×6 = -5.07	4×8 = -1.11	7×8 = 6.104	7×8 =0.790		
	3×7 = 3.155	3×4 = -1.02	2×3 = 2.354	2×3 =0.320		

1- Delinter   2- Sindose-80   3 - Omoumi   4-Bulgare-539   5-Termez -14
6 -Red leaf   7-B-557   8- Brown fiber   9- Siokra-324

Discussion

The lint%(G.O.T) was controlled by non-additive genes in F_1 generation, and the results are not in agreement with those reported by Bhatade and Bhale (1983) and McCarty *et al*.(1996) who reported additive type of gene action with partial dominance for inheritance of lint%. The results are in great resemblance with the findings of Kohel (1980) and Avtonomov *et al*. (1981) who determined significant heterosis over mid and also better parents for oil content in F_1 generation. The obtained results are authenticated by the findings of Percy and Turcotte (1992) for improvement of fiber properties in F_1 generation. Related results to micronaire were largely in agreement with the findings of Percy and Turcotte (1992), as they did not notice heterosis for fiber fineness in intra-*hirsutum* and intra-*barbadense* hybrids, although inter-specific crosses of *G.hirsutum* × *G.barbadense* displayed a varying level of heterosis in some studies.

It is concluded that the additive-dominance model was adequate for majority of the traits and partially adequate for some traits. Majority of the traits were influenced by additive genes in F_1 generation. These results are encouraging for practical improvement through hybridization and selection method. Significant variation for genotypic, general combining ability (GCA) effects, and specific combining ability (SCA) effects ($P \leq 0.05$) was identified for all the studies traits and indicates the potential for improvement through selection. In addition for other agronomic traits, it is suggested that improvements should be made through utilizing a backcross approach. We can also produce and use new hybrids that were the best crosses on the basis of our purpose and 12 studied traits commercially. Plant breeders will be able to use data of mean performance, estimation of heterosis, heterobeltiosis, combining ability (GCA and SCA) and interaction effects of all traits while producing new cultivars depending on the annual demand for fiber quality, oil content and other characteristics in F_1

generation. For example, traits including oil content, staple length, uniformity ratio, micronaire, fiber bundle strength, earliness, Lint%, seed index, seed cotton yield, boll weight, bolls/plant and plant height value of their top F_1 hybrids have been increased by 25%, 7.22mm, 3.4%, 1.08 g/inch, 8.08g/tex, -16.72days, 11.69%, 5.62g, 20.6g, 1.96g, 2.15 and 36.06cm respectively in comparison with means of their parents. In seed production programme we can use the best general combiner and the best specific crosses in the view of their interaction effects.

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.Gossypium barbadense L & و روش جدید ارزیابی مدل افزایشی- غالبیت.

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چکیده

تلاقی دآی آلل کاملی بین ۹ ژنوتیپ پنبه (.Gossypium hirsutum L. & Gossypium barbadense L) شامل ارقام دلینته، سیندوز- ۸۰، عمومی، بلغار -۵۳۹، ترمز-۱۴، برگ قرمز (گونه بومی)، ب-۵۵۷، الیاف قهوهای و سای اکرا- ۳۲۴ که دارای تنوع ژنتیکی بالا بودند طی دو سال انجام گرفت. هدف تخمین پتانسیلهای اصلاح صفات عملکرد و اجزای آن، روغن، کیفیت الیاف با استفاده از تجزیه ژنتیکی، قابلیت ترکیبپذیری، وراثتپذیری و اثرات هتروزیس بود. مطالعه و تجزیه واریانس، روی ژنوتیپها و خصوصیات گیاهان نسل اول انجام گرفت جائیکه بذور تلاقی یافته سال اول در سال دوم گیاهان F_1 را بوجود آوردند. هیبریدهای موفق با استفاده از مارکرهای مورفولوژیکی همچون رنگ گل، موقعیت و رنگ لکههای گلبرگ، رنگ الیاف، لینتر بذر، رنگ و شکل برگ تشخیص داده شد. تجزیه واریانس به روش طرح لاتیس مربع ساده (SSLD) اختلاف معنیدار بالائی را بین ژنوتیپهای بکار رفته نشان داد۲ ($P \leq 0.01$) و همین اختلافات واریانس بدست آمده تجزیه واریانس ژنتیکی را با استفاده از روشهای گریفینگ، هیمن و هیمن و جینکز میسر ساخت. مدل افزایشی- غالبیت و همبستگی مربوط به تست اپیستازی (Wr, Vr) برای اکثر صفات کافی و برای برخی صفات نسبتاً کافی بود یعنی بیشتر صفات از عمل ژنهای غیر افزایشی در نسل F_1 متأثر بودند. این نتایج حاکی از بکارگیری اصلاح عملی پنبه از طریق برنامههای اصلاحی هیبریدی و ترکیبی برای عمل غیر افزایشی ژن و روش انتخاب برای صفات متأثر از عمل افزایشی ژن میباشد. تنوع و تفاوتهای معنیدار ژنوتیپها از حیث اثرات قابلیت ترکیبپذیری عمومی (GCA) و خصوصی (SCA) و همچنین وراثتپذیری خصوصی بالا (*P*≤0.05) نشانگر توانایی اصلاح صفات از طریق انتخاب و از طرف دیگر عمل فوق غالبیت ژن، وراثتپذیری متوسط و پایین برای برخی از صفات، روشهای اصلاحی هیبرید و ترکیبی را پیشنهاد می نماید.

کلمات کلیدی: پنبه، هیبرید، ژنتیک.