

## GENETIC DISTANCE AND ITS RELATION TO THE PERFORMANCE OF INTRAHIRSUTUM F<sub>1</sub> HYBRIDS

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(Received 22 November 2000; accepted 7 May 2002)

Present study was initiated to determine as how far genetic distance is important in the expression of heterosis in some cotton leaf curl virus resistant and other intrahirsutum F<sub>1</sub> hybrids. Three sets of hybrids were developed: 1) highly adapted Cotton Research Institute Sakrand (CRIS) lines crossed with exotic lines, 2) CRIS lines crossed with Cotton Research Institute Multan (CIM) lines, 3) the CRIS lines crossed with CRIS lines. For seed cotton yield, number of bolls formed and fibre length, the hybrids developed from exotic lines expressed more percent of heterosis than hybrids obtained from the crosses of CRIS with CIM or CRIS with CRIS lines that suggested that genetic distance is very important in the expression of heterosis for these traits. The average better parent heterosis of Exotic, CIM, and CRIS hybrids respectively were; 10.6, 42.2 and 22.8 for seed cotton yield, 77.1, 44.3 and 25.2% for number of bolls and 5.8, 4.8 and 4.6% for fiber length. In respect to lint%, all the three sets of hybrids expressed negative mean heterosis whereas for seed index, CRIS x CIM hybrids expressed mean heterosis of 13.5% against 4.7% of CRIS x Exotics and 3.3% of CRIS x CRIS hybrids. Considering the performance of individual hybrids, CRIS-121 x CP-15/2 which gave maximum yield of 146.5 also produced highest bolls of 52.1, whereas hybrid CRIS-168 x CIM-443 ginned maximum of 38.8% lint also gave highest seed index of 7.8 gm and for fibre length, CRIS-121 x CIM-443 produced longer fibre of 29.2 mm.

**Key words:** Genetic distance, F<sub>1</sub> hybrids, Heterosis, *Gossypium hirsutum* L.

### Introduction

Genetic distance can simply be defined as the lines of similar or different origin. Cotton leaf curl virus (CLCV) disease appeared in Punjab Province of Pakistan, long ago but its severity was noticed during 1992-93 when it has hit about 40% of the cotton area and declined cotton production by 2 to 3 million bales (The Pakistan Cotton Grower 1997). This alarming situation warranted cotton breeders to avail two options, 1) to screen the gene pool and make the crosses between CLCV resistant exotic germplasm and high yielding adapted lines and follow selection and testing the material to develop CLCV resistant varieties, 2) to develop CLCV resistant F<sub>1</sub> hybrids. Of course, the long term and practical solution to this problem is to develop CLCV resistant varieties that could take at least 10-12 years of time. On the other hand, development of CLCV resistant F<sub>1</sub> hybrid takes only one year. This paper however reports the amount of heterosis expressed in some CLCV resistant and other intrahirsutum F<sub>1</sub> hybrids.

For development of F<sub>1</sub> hybrid, an understanding about the genetic basis of heterosis is very important. It is believed that manifestation of heterosis largely depends on genetic divergence of parental lines (Hallauer and Miranda 1986). The two parental lines that manifest relatively more heterosis are considered genetically diverse than two parental lines that ex-

press little or no heterosis in the crosses. Thus establishing heterotic patterns among inbreds have an important implication for developing F<sub>1</sub> hybrids. Though, heterosis has been observed and used in many crop species, specially in maize but genetic basis of observed heterosis is still conjectural (Shull 1908). Several hypothesis have been proposed to account for this phenomena but most of them can be included in one or two of these hypothesis; 1) physiologic stimulation, allelic interaction, overdominant or heterozygosity theory by Shull (1908). Accumulation of dominant growth factors or dominant theory proposed by (Bruce 1910). Both theories have been extensively discussed but proving one over the other is still ambiguous and questionable.

Plant breeders believed that no matter whether heterosis was due to allelic interaction or accumulation of dominant genes, yet genetic diversity is very essential for obtaining maximum heterosis in F<sub>1</sub> hybrids. Richey (1922) pointed out that the greatest amount of heterosis was present in lines of extreme types. Similar reports of (Moll *et al* 1962) also supported the concept of genetic divergence for the expression of heterosis in F<sub>1</sub> hybrids. However in an other study, (Moll *et al* 1965) noted that degree of heterosis manifested in most genetically diverse crosses was lesser than that resulting from crossing less genetically diverse hybrids. Many other workers (Akber

*et al* 1993; Singh *et al* 1993; Ansari 1994; Carvalho *et al* 1994 and Lakho *et al* 2001) also indicated that significant amount of intraspecific heterosis for seed cotton yield, staple length, and number of bolls, lint% and seed index. Present studies were therefore intended to determine as how far genetic diversity is important for the expression of heterosis in  $F_1$  hybrids.

### Materials and Methods

Three sets of hybrids were developed, in first set, the varieties evolved at Cotton Research Institute Sakrand (CRIS) were crossed to CLCV resistant exotic lines, in the second set, the varieties of CRIS were crossed to the CLCV resistant varieties developed at Central Cotton Research Institute, Multan (CIM), and in the third set, the CLCV susceptible varieties of CRIS were crossed with each other. In total 14  $F_1$  hybrids, 5 hybrids in each of the first and second sets and 4 hybrids in the third set were developed. All the hybrids were field planted in a randomized complete block design with four replications. The plot size was 10.0 x 35.0 feet where row to row and plant to plant distances were kept at 2.5' and 9.0" respectively. Ten plants of each of the hybrids in each repeat were randomly tagged for taking the observations. Thus, 40 plants of each hybrid were used for recording the data on seed cotton yield per plant (gm), number of bolls, ginning outturn (%), fibre length (mm) using fibrograph machine, and seed index (gm) to determine the differences among the parents and hybrids. The data were subjected to analysis of variance following (Gomez and Gomez 1984). Useful heterosis as defined by Fehr (1987) was calculated as the percentage increase (+) or decrease (-) of  $F_1$  hybrid over better parent.

### Results and Discussion

In cotton breeding and genetics, very little effort has yet been put to determine whether to consider inbreds of close or diverse pedigrees for the maximum expression of heterosis in  $F_1$  hybrids of cotton. In earlier maize breeding programmes, hybrid performances however were predicted from the pedigree of parents where more diverse parents were expected to manifest more heterosis than those that had close pedigree. To answer this dilemma, cotton lines of similar and different origins were crossed and their  $F_1$  hybrids performance was studied. The results from analysis of variance revealed significant differences between parents and hybrids for all the traits except lint percent. It was noted that the averages of the hybrids were quite higher than the averages of the parents Table 1, except lint% where the differences were not striking. In the hybrids where CRIS varieties when crossed with CLCV resistant exotics, gave on an average increased values for all the traits against the hybrids developed by the

crosses of CRIS varieties with CIM varieties or among the CRIS varieties. Regarding yield, the hybrids developed from CRIS x Exotics averaged 121.9 against 104.6 and 90.7 gm of hybrids obtained from the crosses of CRIS x CIM and CRIS x CRIS varieties respectively. The numbers of boll set by the above hybrids were 44.0, 37.0 and 33.5. There were no apparent mean differences in the hybrids for lint% and fibre length. For seed index, the CRIS x CIM hybrids gave mean seed index of 7.3 gm as compared to 6.4 gm of CRIS x Exotics and 6.7 gm of CRIS x CRIS hybrids.

The useful heterosis in three sets of hybrids is presented in Table 2. On an average, the hybrids developed from the crosses of CRIS x Exotics gave 70.6% yield heterosis against 47.2 and 22.8% of CRIS x CIM and CRIS x CRIS hybrids respectively. The maximum yield heterosis of 89.4% was also manifested by the hybrid CRIS-233 x LRA-5166 and the next in the rank was hybrid CRIS-134 x LRA-5166 (84.7%) which is also from the same group of hybrids. The minimum of 15.3% of heterosis, however was expressed by the hybrid of close origin, CRIS-134 x CRIS-121. The trend of heterosis in number of bolls set was very similar to yield in that, the hybrids of diverse origin i.e., CRIS with Exotic expressed more heterosis than the hybrids of CRIS x CIM and CRIS x CRIS.

The former group of hybrids, on an average, gave 77.1% heterosis in number of bolls against 44.3 and 25.2% of two later groups of hybrids respectively. It is generally observed that heterosis of yield and bolls were complementary to each other in that, the hybrids, which expressed more yield heterosis, also expressed increased heterosis in number of bolls. This further suggests that these both traits are positively correlated with each other. In present study, higher percent of heterosis in the hybrids of Exotic x CIM crosses and less in CRIS x CRIS crosses is according to the theories of heterosis and expectations. Nevertheless, one could still argue that why CRIS x CIM hybrids did not express higher or even equal heterosis to that of CRIS x Exotics when CRIS and CIM inbreds possess two properties over the exotics. One is that, both types (CRIS and CIM) of inbreds are highly adapted and second is that, they belong to different origin or pedigree. From the results, it appears that highly adapted lines in our case may possess less number of heterozygous locus or say less number of dominant factors as compared to the exotics. Therefore, exotics are expected to express more heterosis in the crosses than adopted lines. The CIM lines though are of distant pedigree, even then it is suspected that since they are adapted lines therefore, their pedigree may not be as diverse as the exotics used in the present study. Tunio *et al.* (2001) while performing intraspecific crosses of CRIS lines to CLCV resistant exotic lines observed a maximum of 113.7% useful

heterosis in seed cotton yield, 60.45% in bolls per plant and 6.57 in lint%, whereas (Chang *et al* 2001) observed 68.0% useful heterosis in seed cotton yield, 46.5% in bolls per plant and 7.2 in lint% in intraspecific crosses of CRIS x CRIS lines. These results are in close agreement with our findings that the genetically diverse parents express more heterosis than closely related parents.

Majority of crosses in all the three types of hybrids, manifested negative heterosis for lint% suggesting that non-additive genes are controlling this trait. Therefore, heterosis is

not important for lint % and this trait can be improved through hybridization and selection in segregating generations. Several researchers (Salam and Khan 1969; Mirza and Khan 1984) also reported similar findings that dominant genes control the lint% in cotton. Baloch *et al* (1991) noted high level of discrepancy in observed and expected inbreeding depression in  $F_2$  and explained that dominant genes are controlling this trait. The mean heterosis (5.8%) of exotic hybrids for fibre length was higher than both CIM (4.8%) and CRIS (4.6%) hybrids, suggesting that genetic diversity is important for

**Table 1**  
Parental and hybrid performance for some quantitative traits of *Gossypium hirsutum* L

Parents/ hybrids and parentages			Characters				
			Seed cotton yield (gm)	Bolls per plant	Lint (%)	Fibre length (mm)	Seed index (gm)
1.	CRIS-134	(NIAB-78 x St-3)	60.8	22.5	34.3	26.5	6.0
2.	CRIS-233	(CIM-240 x CRIS-121)	75.5	25.2	36.0	27.0	5.9
3.	CRIS-241	(CRIS-7A x CRIS-130)	58.7	20.9	37.5	27.1	5.7
4.	CRIS-121	(B-909 x NIAB-78)	85.4	30.5	36.2	27.0	6.8
5.	CRIS-168	(K-68/9 x NIAB-78)	77.0	29.6	36.7	27.5	7.0
6.	LRA-5166	(Exotic line from India)	50.7	18.8	37.5	26.5	5.8
7.	CP-15/2	(Exotic line from India)	57.5	21.4	37.0	27.5	6.5
8.	CIM-448	(492/87 x CP-15/2)	48.3	15.2	38.0	28.0	6.5
9.	CIM-443	(CIM-109 x LRA-5166)	55.2	22.1	38.5	27.5	5.8
	<b>Mean</b>		<b>63.2</b>	<b>22.9</b>	<b>36.9</b>	<b>27.2</b>	<b>6.2</b>
Crosses between CRIS x Exotic lines (CLCV resistant)							
1.	CRIS-134 x LRA-5166		112.3	43.7	35.5	29.1	6.2
2.	CRIS-233 x LRA-5166		143.3	49.4	37.7	28.8	6.2
3.	CRIS-233 x CP-15/2		121.5	41.9	34.6	28.4	6.9
4.	CRIS-241 x LRA-5166		86.0	33.1	38.3	28.2	5.7
5.	CRIS-121 x CP-15/2		146.5	52.1	37.8	28.9	7.2
	<b>Mean</b>		<b>121.9</b>	<b>44.0</b>	<b>36.8</b>	<b>28.7</b>	<b>6.4</b>
Crosses between CRIS x CIM (CLCV resistant adapted lines)							
1.	CRIS-134 x CIM-448		110.7	36.0	35.2	29.0	7.5
2.	CRIS-34 x CIM-443		81.4	31.3	36.2	29.1	6.7
3.	CRIS-168 x CIM-443		93.6	33.4	38.8	29.0	7.8
4.	CRIS-233 x CIM-443		132.0	47.0	36.1	28.3	7.0
5.	CRIS-121 x CIM-443		105.4	37.5	37.5	29.2	7.5
	<b>Mean</b>		<b>104.6</b>	<b>37.0</b>	<b>36.8</b>	<b>28.9</b>	<b>7.3</b>
Crosses between CRIS x CRIS lines							
1.	CRIS-134 x CRIS-233		89.7	32.0	38.1	28.5	6.6
2.	CRIS-233 x CRIS-241		79.9	30.7	37.6	28.0	6.2
3.	CRIS-241 x CRIS-121		98.5	35.7	34.9	28.7	6.9
4.	CRIS-121 x CRIS-168		94.8	35.6	34.7	28.4	6.9
	<b>Mean</b>		<b>90.7</b>	<b>33.5</b>	<b>36.3</b>	<b>28.4</b>	<b>6.7</b>
	<b>LSD (0.05)</b>		<b>30.5</b>	<b>13.7</b>	<b>ns</b>	<b>1.3</b>	<b>1.2</b>

**Table 2**  
Genetic distance and percentage of useful heterosis expressed in cotton leaf curl virus resistant intrahirsutum F<sub>1</sub> hybrids for some quantitative traits in cotton, *Gossypium hirsutum* L.

Hybrids	Useful heterosis expressed in percentage				
	Seed cotton yield (gm)	Bolls per plant	Lint (%)	Fibre length (mm)	Seed index (gm)
Crosses with exotics					
1. CRIS-134 x LRA-5166	84.7	94.2	-5.0	9.8	3.3
2. CRIS-233 x LRA-5166	89.4	96.0	0.5	6.7	5.1
3. CRIS-233 x CP-15/2	60.9	66.3	-6.5	3.3	6.2
4. CRIS-241 x LRA-5166	46.5	58.4	2.1	4.1	-1.7
5. CRIS-121 x CP-15/2	71.5	70.8	2.2	5.1	6.0
<b>Mean heterosis</b>	<b>70.6</b>	<b>77.1</b>	<b>-3.4</b>	<b>5.8</b>	<b>4.7</b>
Crosses with CIM lines					
1. CRIS-134 x CIM-448	82.1	60.0	-7.4	3.6	15.4
2. CRIS-134 x CIM-443	33.9	39.1	-6.0	5.8	11.6
3. CRIS-168 x CIM-443	21.6	12.8	0.8	5.5	11.4
4. CRIS-233 x CIM-443	74.8	86.5	-6.2	2.9	18.6
5. CRIS-121 x CIM-443	23.4	22.9	-2.6	6.2	10.3
<b>Mean heterosis</b>	<b>47.2</b>	<b>44.3</b>	<b>-5.4</b>	<b>4.8</b>	<b>13.5</b>
Crosses between CRIS lines					
1. CRIS-134 x CRIS-233	18.8	27.0	5.8	5.6	10.0
2. CRIS-134 x CRIS-241	31.4	36.4	0.3	3.3	3.3
3. CRIS-134 x CRIS-121	15.3	17.0	-3.6	6.3	1.5
4. CRIS-134 x CRIS-168	23.1	20.3	-5.4	3.3	-1.4
<b>Mean heterosis</b>	<b>22.8</b>	<b>25.2</b>	<b>-1.5</b>	<b>4.6</b>	<b>3.4</b>

maximum exploitation of heterosis in fibre length. The mean difference between CIM x CRIS and CRIS x CRIS hybrids, however were not so prominent. The positive heterosis in fibre length suggested that dominant genes pre-dominantly control this trait and hybrid crop development is suitable for fibre length in cotton. Baloch *et al* (1991) reported more percent of heterosis in interspecific hybrids than intraspecific hybrids for fibre length.

Surprisingly for seed index, the hybrids obtained from the crosses of exotic lines expressed heterosis of 4.7% as compared to hybrids obtained from the crosses of CRIS x CIM lines (13.5). The CRIS x CRIS hybrids, however expressed minimum heterosis of .3%. These results, thus suggested that if seed index is an important trait in cotton, the crosses between adapted lines of different origin may be preferred over exotic lines.

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