

## **Analysis of Genetic diversity in Genetically Modified and Non-Modified Cotton (*Gossypium hirsutum* L.,) Genotypes**

<sup>1</sup>A.A.Kaleri, <sup>2</sup>S.Y. Rajput, <sup>3</sup>G.A.Kaleri, <sup>4</sup>M.K.Kaleri <sup>5</sup>J.A.Marri

<sup>1</sup>(Department of Plant Breeding and Genetics, S.A.U Tandojam Pakistan)

<sup>2</sup>(Cotton Section Agriculture Research Institute Tandojam)

<sup>3</sup>(Directorate, Agriculture Research Institute of Tandojam)

<sup>4</sup>(Department of Biotechnology, S.A.U Tandojam)

<sup>5</sup>(Department of Plant Breeding and Genetics, S.A.U Tandojam)

---

**Abstract:** The main purpose of present research work was to analyze the genetic diversity in 24 Bt and non-Bt cotton genotypes for yield and fiber traits including plant height (cm), first sympodial node number, first effective boll node number, sympodial branches plant<sup>-1</sup>, bolls plant<sup>-1</sup>, boll weight (g), seed index (g), micronaire value (µg/inch), staple length (mm), ginning outturn % and seed cotton yield plant<sup>-1</sup> (g). Results exhibited that genotypes differed significantly at  $P \leq 0.01$  for all the studied traits. In cluster analysis, all 24 genotypes were divided into five small clusters, indicating the existence of wider genetic diversity among the tested genotypes. Cluster number four consisted of four genotypes, this cluster can be characterized as having more number of bolls plant<sup>-1</sup> and seed cotton yield plant<sup>-1</sup>, hence the genotypes of this group may be proved promising result in producing higher seed cotton yield plant<sup>-1</sup>. With regards to genetic distance, out of the 276 pairs of comparisons, some pairs exposed greater genetic distance while couple of pairs revealed very narrow genetic distance; consequently, these pairs can further be utilized in heterosis and backcross breeding programs in cotton crop respectively. From PCA analysis, eleven components were isolated from the eleven studied characters. The first, second and third components explained 25.4, 19.7, 15.1% of total variation, respectively. The cumulative percent of variance accounted of 60.03% in the first three components, demonstrating a significantly high variability that can be exploited for further breeding programs in cotton crop.

**Keywords:** Cotton, Genetic Diversity, Seed Cotton Yield, Fiber Traits Cluster analysis, PCA analysis.

---

### **I. Introduction**

Cotton is termed as white gold due to its importance significantly contribution to the national economy by providing raw materials to the local textile industries and as an export item. Pakistan is the fourth largest cotton producer and exporter in the world, it accounts about 6.9% in Agriculture and about 1.4% in GDP. For increasing the production potential of cotton varieties it is important to understand the relationship among different characters (McCarty et al., 2008). The analysis of correlation coefficient deals with the extent of association between several plant traits and finds out the component traits which help in selection for the enhancement in yield and improvement of fiber quality. Genetic variability is the key to the success and serves as blood to any breeding program for crop improvement. Genetic diversity of cultivated cottons is declining due to repeated use of the same elite germplasm as parental material. The genetic diversity depends on the number and the diversity of the original ancestors involved in the development of a germplasm pool. There are many sources of cotton germplasm representing a range of genetic diversity, but the germplasm is not well utilized for increasing the genetic variability which can be available for cotton improvement (Bowman et al., 1996). Broader sense variability increase the chances of selection for a specific genotype, due to this reason heritability is a good indicator to transfer the required traits from parents to their off spring.

Keeping in view to above mentioned facts, that current study was aimed to assess the genetic variability for yield and fiber traits in Bt and non-Bt cotton genotypes using various statistical approaches so that the promising genotypes could be identified for development of improved cotton varieties.

### **II. Material And Methods**

An experiment was conducted in an Experimental area Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam. The genetic materials consisted of 24 Bt and Non-Bt cotton, *Gossypium hirsutum* L., genotypes, viz. BT-555, SGA-1, Lalazar, S-1-815, MNH-886, CIM-496, FH-113, CIM-534, BT-886, FH-901, BT-905, CRIS-494, IR-3701, IR-1524, CRIS-134, CRIS-342, BT-142, BT-703, Tarzan-1, Neelam-121, AA-804, MG-6, NIAB-78, and CRIS-121 sown in Randomized Complete Block Design with four replications, Seedlings are thinned before first irrigation to maintain plant to plant distance 30 cm, while row to row distance was kept 75 cm. All the recommended cultural and agronomic practices were adopted uniformly throughout the growing period. Data were collected for plant height (cm), bolls plant<sup>-1</sup>, sympodial

branch plant<sup>-1</sup>, 1<sup>st</sup> effective boll node number, 1<sup>st</sup> sympodial node number, boll weight (g), ginning outturn percentage (GOT%), seed index (100-seed weight, g), staple length (mm), micronaire value (µg/inch) and seed cotton yield plant<sup>-1</sup> (g).

Data were evaluated for their mean performance, analysis of variance, heritability analysis, principal analysis component, cluster analysis, genetic distance and traits diversity analysis. The recorded data was analyzed through different computer program such as Statistix 8.1 software, Poptene computer software and NTSys-pc software. The results of each analysis are given in their respective headings.

### III. Experimental Results

The present study was carried out to assess the genetic diversity among 24 Bt and non Bt cotton genotypes. The analysis of variance, mean comparisons, correlation and principal component analysis were derived through Statistix v. 8.1 computer software. Genetic distance and cluster analysis were obtained with the help of SPSS v. 17 computer software. Heritability analysis was carried out as suggested by Allard (1960). The analysis of variance for all the characters is given in Table-1. The obtained results revealed that genotypes differed significantly at P ≤ 0.01 probability level for plant height, first sympodial node number, first effective boll node number, sympodial branches plant<sup>-1</sup>, bolls plant<sup>-1</sup>, boll weight, seed index, staple length, micronaire value, gining outturn % and seed cotton yield plant<sup>-1</sup>, indicating the existence of considerable genetic diversity among the genotypes for studied traits.

**Table1. Mean performance of Bt and non-Bt cotton genotypes for various traits**

Genotypes	Plant height (cm)	First sympodial node number	First effective boll node number	Sympodial branches plant <sup>-1</sup>	Bolls plant <sup>-1</sup>	Boll weight (g)	Seed index (100 seed wt, g)	Micronaire value (µg/inch)	Staple length (mm)	Gining outturn percentage	Seed cotton yield plant <sup>-1</sup> (g)
CRIS-134	87.65	5.60	10.40	15.30	35.00	2.61	6.95	3.36	27.68	36.40	91.08
AA-802	75.15	5.15	11.25	16.50	29.65	3.27	7.4	3.46	28.13	38.55	98.35
NIAB-78	96.50	4.75	11.05	16.15	35.75	2.98	7.42	3.44	28.31	34.45	105.63
CIM-496	106.75	5.30	9.75	26.90	43.55	3.11	7.45	3.33	27.48	31.80	134.22
IR-3701	88.80	5.60	9.40	17.75	29.30	3.14	7.85	4.25	28.66	43.70	88.11
IR-1524	82.75	5.40	10.60	26.00	38.40	3.37	7.80	3.38	28.42	34.00	129.64
CIM-534	90.55	5.70	9.95	15.15	33.80	2.75	7.40	3.33	29.40	33.30	93.25
FH-113	101.75	4.90	9.40	31.65	43.55	3.15	7.15	3.42	29.10	44.15	137.5
MG-6	91.65	5.10	9.90	23.55	35.95	3.06	6.90	3.40	27.19	32.75	110.69
BT-555	96.15	4.65	9.95	19.55	29.85	3.51	6.90	3.42	28.02	35.75	98.72
BT-886	86.55	4.75	9.85	26.25	25.30	2.71	6.93	4.19	29.12	44.90	68.37
SGA-1	77.55	5.00	9.45	15.70	30.50	3.14	6.40	3.36	29.82	34.06	95.56
FH-901	85.70	5.20	9.20	17.95	29.15	3.04	6.15	4.27	26.81	43.40	89.38
BT-703	111.45	5.55	9.40	21.20	28.70	2.87	5.80	4.26	27.72	41.85	82.46
LALAZAR	89.95	5.50	8.85	28.00	30.60	3.15	6.30	4.36	26.75	32.35	96.38
BT-905	83.80	4.80	10.05	17.30	26.85	3.11	6.25	3.39	28.16	39.30	83.99
TARZAN1	73.85	4.60	10.05	25.20	29.25	3.22	6.15	3.46	26.72	36.00	94.06
S#1-815	95.50	4.90	10.35	31.95	49.90	3.08	6.15	3.39	27.47	31.30	153.65
CRIS-342	113.65	5.10	9.55	27.30	31.40	3.08	6.45	3.44	28.15	33.10	96.98
CRIS-494	89.95	6.95	9.65	18.80	25.65	3.55	7.10	3.51	26.83	38.85	90.86
Neelam121	84.40	6.25	10.40	24.55	38.10	3.52	5.50	3.57	26.88	35.60	133.86
CIM-598	102.55	7.70	9.45	31.35	28.65	3.54	7.55	3.55	27.26	34.55	101.56
MNH-886	91.85	7.95	10.90	23.80	40.10	3.58	7.20	3.46	29.06	44.25	143.2
BT-142	80.40	5.70	8.95	24.30	32.05	3.45	6.60	4.33	25.46	39.00	110.51
LSD (0.5%)	2.357	0.504	0.951	1.899	2.111	0.246	0.556	0.166	1.135	1.443	11.00

#### 3.1 Mean performance of genotypes

The data regarding mean performance of genotypes is given in Table-1. The data revealed that genotype CRIS-342 produced tallest plants of 113.65 cm while Tarzan-1 recorded the shortest plants measuring of 73.85 cm as compared to the rest of the genotypes. In case of first sympodial node number, the genotype MNH-886 showed maximum value (7.95), however, the minimum value (4.6) was recorded in Tarzan-1 genotypes. With regard to first effective boll node number the maximum value was recorded in genotype AA-802 (11.25) while genotypes Lalazar showed minimum value of 8.85 among rest of the genotypes. For

sympodial branches plant<sup>-1</sup>, S#-1-815 produced the highest number of sympodial branches plant<sup>-1</sup> (31.95), whereas CIM-534 produced the lowest number of sympodial branches plant<sup>-1</sup> (15.15). With respect to bolls plant<sup>-1</sup>, the variety S#-1-815 set maximum number of bolls plant<sup>-1</sup> (49.9) against other genotypes, while minimum (25.3) number of bolls plant<sup>-1</sup> were obtained from BT-886. MNH-886 weighed bigger bolls of 3.58 g, while the smaller bolls were observed in variety CRIS-134 (2.61 g). The variety IR-3701 gave higher seed index (7.85 g); however, the variety Neelam-121 gave the lower seed index (5.50 g). The maximum micronaire value was observed in Lalazar of (4.36) while minimum value was observed in genotype CIM-496 & CIM-534 (3.33). In case of staple length SGA-1 measured the longer staple length of 29.82mm, while the shorter staple length (25.46, mm) was recorded in BT-142. With regards to ginning outturn %, the maximum (GOT %) was observed in BT-886 of 44.9, while the lowest value was observed in S#1-815 that was 31.3. The variety S#-1-815 produced maximum seed cotton yield plant<sup>-1</sup> (153.65 g), whereas the variety BT-703 gave the lowest seed cotton yield plant<sup>-1</sup> (82.46 g). In general, varieties S#-1-815 displayed better performance in terms of sympodial branches plant<sup>-1</sup>, bolls plant<sup>-1</sup> and seed cotton yield plant<sup>-1</sup>.

### 3.2 Heritability Analysis

The heritability of a trait within a population is the proportion of observable differences in a trait between individuals within a population that is due to genetic differences. Factors including genetics, environment and random chances can all contribute to the variation between individuals in their observable characteristics. Heritability measures the fraction of phenotype variability that can be attributed to genetic variation (Raj et al., 2008 Heritability estimates are helpful in deciding the characters to be considered while making selection. High heritability estimates ( $h^2$  b.s.) were observed for plant height ( $h^2=97.55\%$ ), 1<sup>st</sup> sympodial node number ( $h^2=85.70\%$ ), sympodial branches plant<sup>-1</sup> ( $h^2=94.32$ ), bolls plant<sup>-1</sup> ( $h^2=94.50\%$ ), seed index ( $h^2 =71.18\%$ ), boll weight ( $h^2=69.07$ ), micronaire value ( $h^2=92.07$ ), staple length ( $h^2=60.66$ ), ginning outturn % ( $h^2=94.85$ ) and seed cotton yield plant<sup>-1</sup> ( $h^2=88.45\%$ ), whereas moderate heritability was also found for 1<sup>st</sup> effective boll node number ( $h^2=45.35$ ).

**Table 2. Heritability estimates for various traits in Bt and non-Bt cotton**

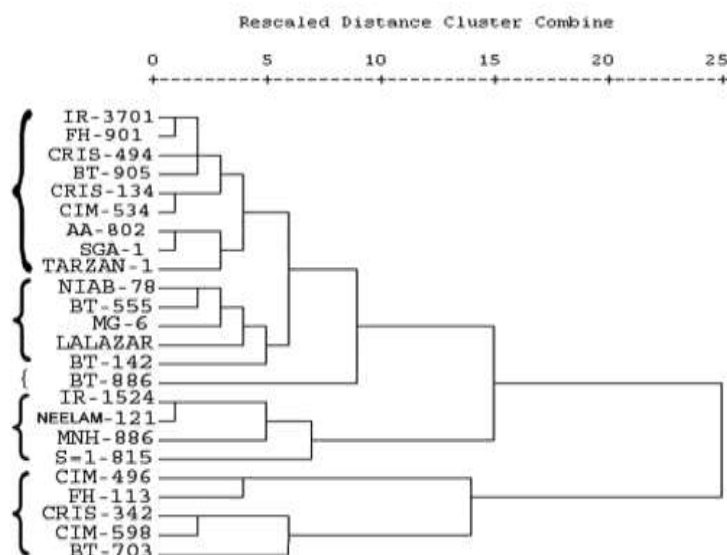
Characters	Genotypic variance ( $\delta^2g$ )	Phenotypic variance ( $\delta^2p$ )	Heritability % (Broad sense)
Plant height	111.218	114.01	97.55
1 <sup>st</sup> sympodial node #	0.764	0.891	85.70
1 <sup>st</sup> effective boll node #	0.288	0.635	45.35
Sympodial branches plant	30.107	31.92	94.32
Bolls plant <sup>-1</sup>	38.529	40.769	94.50
Boll weight	0.067	0.097	69.07
Seed index	0.383	0.538	71.18
Micronaire value	0.151	0.164	92.07
Staple length	0.998	1.645	60.66
GOT%	19.277	20.323	94.85
Seed cotton yield plant <sup>-1</sup>	466.28	527.13	88.4

### 3.3 Cluster Analysis

Cluster analysis is the most widely used technique for classifying environments or genotypes into homogeneous groups. It operates on a matrix of dissimilarity (or similarity) indexes for all possible pairs of genotypes or pairs of environments, depending on which is being clustered (Ghaderi et al., 1980). Cluster analysis was carried out to know the patterns of groupings of genotypes. The dendrogram was produced from the UPGMA clustering method of genotypes based on Euclidean distances. A dendrogram tree was achieved from cluster analysis of 24 Bt and non-Bt cotton genotypes on the basis of 11 fiber and yield traits as illustrated in Fig. 1. According to grouping, cotton genotypes divided into 5 different clusters. In first cluster there were total nine genotypes including IR-3701, FH-901, CRIS-494, BT-905, CRIS-134, CIM-534, AA-802, SGA-1 and Tarzan-1, while second cluster was composed of five Bt cotton genotypes such as NIAB-78, BT-555, MG-6,

Lalazar and BT-142. Third cluster possessed only one genotype, namely, BT-886 where as fourth cluster consisted of four genotypes out of twenty four Bt and non-Bt cotton genotypes such as IR-1524, NEELAM-121, MNH-886 and S-1-815. Fifth cluster comprised of five genotypes, namely, CIM-496, FH-113, CRIS-342, CIM-598 and BT-703. The cluster analysis divided the 24 Bt and non-Bt cotton genotypes into 5 small clusters, demonstrating the presence of greater genetic diversity among the tested genotypes. On the basis of obtained results, it is recommended that the genotypes clumped together into group four, showing desirable gene combinations for seed cotton yield plant<sup>-1</sup>, offering that these Bt and non Bt- cotton genotypes could be exploited in future breeding programs in order to improve seed cotton yield.

**Figure1. Tree diagram of 24 upland cotton genotypes for 11 characters using hierarchical cluster analysis (Ward's method)**



Xian et al. (2012) also reported similar results of genetic diversity analysis; he divided 38 cotton genotypes into two groups with similar genetic background, the same breeding unit and the same type varieties. Another research conducted by Esmail et al. (2008) indicated that cluster analysis based on Euclidean distance using yield characters grouped the 21 cotton genotypes into two main groups. Cluster “A” and “B” composed of eleven and ten genotypes, respectively. Moreover, Mugheri (2015) also reported the higher number of clusters while studying genetic diversity on Bt-cotton genotypes, indicating the greater genetic diversity for variety of agronomic and yield traits based on cluster analysis in a group of Bt cotton genotypes.

### 3.4 Genetic Distance Analysis

The data matrix of tested characters formed the basis of Euclidean genetic distance calculations. Genetics distance values for all 276 pair wise comparisons of the 24 Bt and non-Bt cotton genotypes is presented in Table 3. The estimated genetic distance values ranged from 3.89 to 112.881. The greater genetic distance of 112.88 was observed between S-1-815 and BT-703 genotypes, followed by BT-886 and FH-113 (104.35), CRIS-342 and S-1-815(103.20), BT-886 and CIM-496 (103.11). However, the narrow genetic distance of 3.89 was found between FH-901 and IR-3701, followed by CIM-534 and CRIS-134 (5.57), Neelam-121 and IR-1524 (5.81), CIM-598 and CRIS-342 (7.79), CRIS-494 and FH-901 (8.01). The positive and negative loading shows the presence of positive and negative correlation trends between the components and the variables. Therefore, the mentioned characters (Table 6) which load high positively and negatively contributed more to the diversity and they were the ones that most differentiated the clusters Ahmad et al. (2005).

With regards to genetic distance, it ranged from 3.899 to 112.881. Among the 276 pairs of comparisons from genetic distance, some pairs of comparisons (S#1-815/BT-703, BT-886/FH-113, CRIS-342/S-1-815 and BT-886/CIM-496) exposed greater genetic distance. Of the particular note, these pairs can further be utilized in heterosis breeding programs in cotton crop because these pairs contain a range of genes for various traits. On the other hand, some pairs of comparisons (FH-901/IR-3701, CIM-534/CRIS-134, Neelam-121/IR-1524, CIM-598/CRIS-342 and CRIS-494/FH-901) established narrow genetic distance. Consequently, these pairs of genotypes could be proved trustworthy breeding materials for backcross breeding.

**Table 5. Genetic distance among 24 Bt and non-Bt cotton genotypes**

Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	
1. CRIS-124	.00																								
2. AA-802	15.42	.00																							
3. NIAS-78	14.88	23.20	.00																						
4. CIM-496	29.39	76.61	91.72	.00																					
5. IS-3701	10.19	17.20	21.82	92.86	.00																				
6. IS-1554	40.07	24.74	29.70	72.42	64.50	.000																			
7. CIM-434	4.57	17.20	12.74	91.14	21.24	28.85	.000																		
8. IS-112	91.85	78.78	92.88	14.29	94.23	72.48	92.88	.000																	
9. MS-6	21.41	22.90	10.24	84.92	28.25	21.60	19.11	86.99	.000																
10. BT-555	15.64	21.49	9.90	94.63	15.23	25.91	10.05	96.64	15.20	.000															
11. BT-886	28.65	24.19	42.11	105.11	22.49	82.23	20.82	104.25	45.25	22.89	.000														
12. SCA-1	12.29	6.00	22.19	79.46	14.10	27.00	12.62	82.23	22.74	19.73	22.52	.000													
13. IS-901	10.08	14.75	22.48	89.85	2.99	42.12	12.18	91.28	25.92	14.60	22.46	14.00	.000												
14. BT-702	77.28	66.21	88.80	55.22	77.40	84.21	80.60	58.05	85.56	84.75	76.41	67.98	74.49	.000											
15. LALAZAR	15.62	19.81	17.75	88.67	17.70	24.91	14.22	90.86	15.91	12.28	21.26	18.12	17.55	80.10	.000										
16. BT-905	12.29	17.29	27.62	91.46	8.83	48.64	15.25	92.58	20.98	20.54	18.54	15.04	8.41	72.20	19.94	.000									
17. YAZGAN-1	18.55	10.27	27.89	76.11	19.22	27.29	20.46	78.25	25.24	24.20	20.41	11.46	14.95	62.22	17.00	17.42	.000								
18. S-1-815	66.22	66.04	52.22	87.65	70.84	20.02	64.60	87.70	68.11	59.89	89.90	65.71	70.28	112.88	60.20	76.28	66.52	.000							
19. CRIS-142	77.28	65.22	86.20	39.95	78.73	78.42	80.00	64.22	81.42	85.64	81.05	67.11	75.72	17.58	78.05	74.24	62.20	102.20	.000						
20. CRIS-494	11.10	17.01	20.14	92.87	7.24	42.72	10.92	94.82	22.88	12.22	24.69	15.25	8.01	78.67	14.20	9.88	18.44	49.22	79.18	.000					
21. NIELAM-121	45.21	28.22	21.82	74.25	47.28	4.81	61.95	75.25	24.50	28.50	67.06	40.42	64.21	89.88	28.27	22.12	41.58	24.66	82.26	45.75	.000				
22. CIM-496	79.65	64.98	87.74	24.79	80.85	78.10	82.19	60.40	82.26	84.96	82.75	69.26	77.82	22.83	79.21	74.73	42.80	101.92	7.79	80.97	81.59	.000			
23. IS-886	45.71	49.96	40.69	82.71	56.57	19.96	52.27	81.74	25.68	47.77	76.79	42.69	55.95	101.66	50.02	62.72	54.19	21.11	94.02	55.78	18.87	82.85	.000		
24. BT-142	22.74	14.10	19.90	75.21	25.14	21.06	22.95	74.42	12.64	21.49	42.55	19.01	22.26	74.70	18.62	28.89	18.11	49.83	70.80	22.91	24.54	71.41	24.41	.000	

### 3.5 PCA Analysis

Principal component analysis (PCA) was carried out on the basis of correlation between fiber and yield traits. Eleven components were extracted from the eleven studied traits (Table-3) by PCA analysis. The first three components revealed more than one Eigen value while rest of the six components showed lower Eigen values than one. The first, second and third principal component accounted for 25.4, 19.7, and 15.1% of total variation, respectively. The cumulative percent of variance accounted 60.03% of total variation in the first three components. In the current study, PCA was carried out on the basis of correlation for fiber and yield traits. Eleven components were isolated from the eleven studied characters by PCA analysis. The first five components showed more than one Eigen value whereas rest of the six components exhibited lower Eigen values than one. The first, second, third, fourth, and fifth components explained 25.4, 19.7, 15.1, 12.6 and 9.1% of total variation, respectively. The cumulative percent of variance accounted of 81.90% in the first five components, demonstrating a significantly high variability that can be exploited for further breeding programs in cotton. The preservation and utilization of genetic resources could be made by partitioning the total variance into its components. It also provides a chance for exploitation of suitable germplasm in crop improvement for particular plant traits (Pecetti et al., 1996). PCA is an influential tool to obtain parental lines for successful breeding programs (Nazir et al., 2013).

**Table 4. Vector loading and explained percentage variances by the 11 PCs**

Characters	Eigenvectors										
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Plant height	-0.188	0.107	-0.17	-0.60	-0.36	-0.429	-0.110	-0.342	0.2811	0.1840	0.0269
1st sympodial node #	-0.108	0.355	0.479	0.006	-0.29	-0.456	0.082	0.3249	0.3000	-0.364	-0.026
1st effective boll node #	-0.196	-0.388	0.347	0.232	0.233	-0.376	0.041	-0.539	0.3184	0.2132	-0.024
Sympodial branches plant <sup>-1</sup>	-0.359	0.339	-0.19	-0.21	0.033	0.395	-0.171	-0.258	0.6398	-0.080	-0.038
Bolls plant <sup>-1</sup>	-0.524	-0.083	-0.04	-0.14	0.339	-0.033	0.251	0.2057	-0.213	-0.115	-0.642
Boll weight	-0.209	0.356	0.324	0.387	-0.17	0.181	-0.478	-0.094	-0.320	0.3212	-0.257
Seed index	-0.084	-0.214	0.476	-0.22	-0.40	0.510	0.461	-0.141	-0.088	0.0366	0.0282
Micronaire value	0.250	0.453	0.160	-0.20	0.344	-0.047	0.356	0.1155	0.1069	0.6246	-0.014
GOT %	0.2959	0.190	0.361	-0.29	0.451	0.086	-0.183	-0.353	-0.255	-0.475	-0.007
Staple length	0.0265	-0.416	0.285	-0.43	0.089	0.066	-0.532	0.4299	0.1822	0.2184	-0.179
Seed cotton yield plant <sup>-1</sup>	-0.555	0.077	0.096	0.018	0.283	0.025	0.026	0.1537	-0.232	0.0062	0.7183
Eigenvalues	2.7992	2.165	1.662	1.318	1.001	0.587	0.486	0.3763	0.3121	0.2228	0.0022
Percent of variance	25.4	19.7	15.1	12.6	9.1	5.4	4.4	3.4	2.8	2.0	0.0
Cumulative% of variance	25.4	45.1	60.3	72.8	81.9	87.3	91.7	95.1	98.0	100.0	100.0

### IV. Conclusions

Highly significant differences were observed among Bt and Non-Bt cotton genotypes evaluated for all the 11 studied traits. The results of current study show that genetic diversity among the tested Bt and Non-Bt cotton genotypes was present. Parents from divergent clusters can be used for hybridization in order to isolate useful recombinants in the segregating generations. This information might be used in the genetics and breeding programs for improvement of upland cotton genotypes.

### References

- [1]. Ahmad, I.A. and A.A. Khan. 2005. A modified mini-prep method for economical and rapid extraction of genomic DNA in plants. *Plant Mol Bio.*, 22: 89-89.
- [2]. Allard, R.W. 1960. *Principles of Plant Breeding*. John Wiley and Sons Inc. USA.
- [3]. Beer, S.C., E. Souze and M.E. Sorrels. 1995. Prediction of genotype performance from ancestral relationship in oat. *Crop Sci.*, 35: 69-73.
- [4]. Becelaere, G., E.L. Lumbbers, A.H. Paterson and P.W. Chee. 2005. Pedigree-vs.DNA marker-based genetic similarity estimates in cotton. *Crop Sci.*, 45(6): 2281-2287.
- [5]. Boopathi, N.M., I. Ravikesavan, K. Iyanar and S. Muthuraman. 2008. Genetic diversity analysis in (*Gossypium barbadense* L.) accessions. *J. Cotton Res. Develop.*, 22(2):135-138.
- [6]. Bowman, D.T., O.L. May and D.S. Calhoun. 1996. Genetic base of upland cotton cultivars. *Crop Sci.*, 36: 577-581.
- [7]. Cowen, N.M. and K.J. Frey. 1987. Relationships between genealogical distance and breeding behaviour in oat (*Avena sativa* L.). *Euphytica*, 36:413-424.
- [8]. Esmail, R.M., J.F. Zhang and A.M. Abdel-Hamid. 2008. Genetic diversity in elite cotton germplasm lines using field performance and RAPD markers. *World J. Agric. Sci.*, 4: 369-375.

- [9]. Ghaderi, A. Everson., EH. 1980. Classification of environments and genotypes in wheat. *Crop Sci.* 20:707-710.
- [10]. McCarty, J., J. Wu and J. Jenkins, (2008) Genetic association of cotton yield with its component traits in derived primitive accessions crossed by elite upland cultivars using the conditional ADAA genetic model. *Euphytica*, Vol. (161): 337-352.
- [11]. Mugheri, M.A. 2015. Genetic variability analysis of some agronomical traits in BT cotton genotypes (*Gossypium hirsutum* L.). MSc thesis submitted through department of Plant Breeding and Genetics to Sindh Agriculture Univ. Tando Jam.
- [12]. Nazir, A., J. Farooq, A. Mahmood, M. Shahid, and M. Riaz. 2013. Estimation of genetic diversity for CLCuV, earliness and fiber quality traits using various statistical procedures in different crosses of *Gossypium hirsutum* L. *Vestnik Orel Gau.* 43(4):2-9.
- [13]. Pecetti, L., P. Annicchiaro, and A.B. Damania. 1996. Geographic variation in tetraploid wheat (*Triticum turgidum* spp. *Turgidum* convar. *Durum*) landraces from two provinces in Ethiopia. *Genet. Resour. Crop. Evol.*, 43: 395-407.
- [14]. Raj, A., V. Oudenaarden and A. Alexander. 2008. Nature, nurture, or chance: Stochastic gene expression and its consequences. *Cell*, 135 (2): 216–226.
- [15]. Salahuddini, S., S. Abro, A. Rehman and K. Iqbal. 2010. Correlation analysis of seed cotton yield with some quantitative traits in upland cotton (*Gossypium hirsutum* L.). *Pak. J. Bot.*, 42(6): 3799-3805.
- [16]. Tang, S. and W. Yang. 2012. Status and analysis of cotton fiber quality distribution in china and suggestions. *Cotton Sci.*, 18: 386–390.
- [17]. Xian, T. A., X.Y.Li, J.D. Wang, J.Y. Zheng, H. Sha, T.X. Jiang, L.K. Duo and M. Mo. 2012. Genetic diversities of upland cotton varieties in south Xinjiang. *Cotton Sci.*, 22(6): 603-610.