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GENETIC DIVERSITY AMONG UPLAND COTTON GENOTYPES FOR QUALITY AND YIELD RELATED TRAITS

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Fifty upland cotton genotypes were canvassed by Linkage Cluster (LCA) and Principal Component (PCA) analyses to identify the major characters which account for the variation in yield contributing traits. At maturity, data on number of bolls per plant, number of seed per boll, seed cotton yield, seed index, lint index, boll size, ginning out turn, fibre length, fibre strength, fibre fineness, fibre uniformity and fibre elongation was recorded. The first four PCs with Eigen value >1 contributed 64.8 % variability among the cotton accessions. In PC_1 and PC_3 the genotypes possess good yield and fibre traits whereas in PC_2 the genotypes have desired yield components. Results of LCA agreed with that of PCA ordination on axis II and I. Three groups of genotypes were revealed**.** Seed per boll and boll per plant showed highest heritability 99% as compared to other traits. Genetic advance for seed cotton yield was recorded as highest 46.64 followed by seed per boll 16.37. The predicting genotypes from particular groups or clusters may be selected and exploited to improve yield potential and fibre quality of the cotton crop.

Keywords: *Gossypium hirsutum* L., genetic diversity, multivariate analysis, PCA, LCA

INTRODUCTION

Upland cotton, *Gossypium hirsutum* L, is the world's leading fibre producing crop and is grown in more than 80 countries of the world (Dutt *et al*., 2004). It covered an area of 2879 thousand hectares with the production of 13.0 million bales in Pakistan. It contributes raw material to the textile industry, such as cotton lint as an export item, crude oil and cotton seed cake to oil and livestock industry, respectively (Ali, 2009). It accounts for 7.0 percent of value added in agriculture and 1.5 percent of GDP (Anonymous, 2013).

Four kinds of cotton are cultivated globally which includes two diploids *G. herbaceum* and *G. arboreum*, and two New World tetraploids *G. hirsutum* and *G. barbadense* species. Cultivated cotton genotypes have narrow genetic base (Abdukarimov *et al.,* 2003; McCarty *et al.*, 2005). To broaden the genetic base through hybrid breeding program, the genetic divergence among available germplasm is prerequisite. Genetic variation among different cotton genotypes for morphological and fibre quality traits was studied for their improvement (Alishah, 2001; Jian-bian *et al*., 2004; Jiehua, 1988; Li *et al*., 2005). Principal component analysis and linkage cluster analysis was accomplished by the researchers to find the similarity among the genotypes for the traits and their placement into different clusters (Brown, 1991; Jian *et al.*, 2006; Qiaoling and Zhe, 2011). Keeping in view, the study was under taken to run a multivariate analysis approaches viz, PCA, LCA along with the heritability estimates on the cotton genotypes, which will enable us to classify the available germplasm into distinct clusters on the basis of their yield and fibre quality attributes. The information thus obtained will be helpful to develop an effective cotton hybrid breeding program.

MATERIALS AND METHODS

The regionally adapted 50 diverse cotton varieties/lines were planted in the field during May, 2012 in two replications following randomized complete block design for genetic divergence studies. Seeds of each line were spaced 30 cm within the row and 75 cm apart from the other row. All recommended agronomic and plant protection measure were adopted form sowing till harvest to crop. Genotypes were evaluated for number of bolls per plant (NB), number of seed per boll (S/B), seed cotton yield (SCY), seed index (SI), lint index (LI), boll size (BS), ginning out turn (GOT) from five randomly selected plants from each replication. Fibre parameters including fibre length (FL), fibre strength (FS), fibre fineness (FF), fibre uniformity (FU) and fibre elongation (FE) were measured by Spin lab HVI-900 from the Department of Fibre Technology, University of Agriculture Faisalabad, Pakistan. Standard descriptors for cotton were used to measure the traits at appropriate growth stages. The data of these traits was subjected to the analysis of variance for all the characters by following Steel *et al.,* 1997. The average data was analyzed by numerical taxonomic techniques using the procedure of cluster and principal component analysis (Rashid *et al.*, 2008). Data matrix for yield attributing traits 10 × 25 and fibre quality parameters 10 × 25 were prepared for the analysis. The data matrices were standardized to make the variable traits unit less for computing PCA and LCA by using computer program MINITAB 13.2 (Minitab, Paris, France). LCA summarized the position of genotypes in the dendrogram. The character loading was used to calculate the accession component scores. The first two components were extracted for a two dimensional ordinations of accessions.

RESULTS AND DISCUSSION

The analysis of variance for means indicated that the differences among the genotypes were highly significant for all the characters studied. Similar significant mean squares results for earliness in cotton genotypes were also canvassed (Shakeel *et al.*, 2011). To discern patterns of variation, PCA was performed on all variables simultaneously. Eigen values well representing the variation accounted for principal components and eigenvectors indicating the correlation among principal components and original data sets (Table 2).

Table 1. List of 50 Upland cotton genotypes used in the study

Sr.	Accession	Sr.	Accession
1	ACALA 1517-77	26	ACALA-SJ4
2	ALLEPO-45	27	ALLEPO-41
3	BH-118	28	BH-123
4	BH-160	29	BH-162
5	CIM-448	30	CEDIX
6	CIM-496	31	CRIS-220
7	COCKER-307	32	CIM-443
8	COCKER-310	33	CIM-446
9	COCKER-IMPROVED	34	CIM-482
10	CRIS-402	35	CRIS-134
11	DPL-26	36	DNH-29
12	FH-1000	37	FH-113
13	FH-682	38	FH-114
14	FH-87	39	FH-942
15	LRA-5166	40	MNH-700
16	MNH-147	41	MNH-786
17	MNH-552	42	MS-95
18	MNH-93	43	NIAB-86
19	MS-84	44	NIAB-KARSHIMA
20	NIAB-78	45	SLH-257
21	OKRA-3301	46	SLH-41
22	QUALANDARI	47	TH-41-83
23	RH-112	48	VH-141
24	STONEVILLE-731	49	VH-142
25	VH-53	50	VH-161

Out of 10, four PCs exhibited > 1 Eigen value. The PC_1 had 23.8 %, PC_2 showed 16.8%, PC_3 exhibited 12.3 % and PC_4 exhibited 11.9 % variability among the genotypes for the traits under study. Fibre fineness, number of bolls per plant, seed cotton yield and ginning out turn were noted as the characteristics for variability.

The PC_1 exhibited positive effects for GOT, number of bolls per plant, seed cotton yield and fibre length and negative effects for fibre fineness. These findings are in the line with (Taohua and Yichun, 1993). Yield parameters in PC_1 have positive effects. The genotypes in PC_2 exhibited positive effect for lint percentage only and negative effects for fibre fineness, seed cotton yield and number of bolls which depicted variation among cotton genotypes for these traits (Stoilova and Dechev, 2003). Genotypes belonging to PC_2 were erect type and were given weight for fibre fineness and ginning out turn. This suggested that these genotypes might be used for high lint percentage. PC_3 displayed positive effects for lint percentage, number of bolls per plant but negative effect for seed cotton yield which are desired yield parameter. The fibre fineness and fibre strength also in the desired direction (Table 2). Among all the PCs fibre fineness exhibited as the weighted average of the characters. The first three PCs exhibited maximum variation for the traits under study and good cotton improvement may be accomplished through varietal development program.

***Score plot*:** A principal component scatter plot of the cotton accessions depicted that the accessions those were close together were perceived as being similar when rated on the 10 variables. Thus accessions 25-32, 4-29, 18-22, were very close to each other on both PC_1 and PC_2 respectively. The accessions 23, 27, 28, and 50 were rather separated from other accessions. Thus accession 50 was opposite to 31 because one lied in positive region and second lied in negative region (Fig. 1).

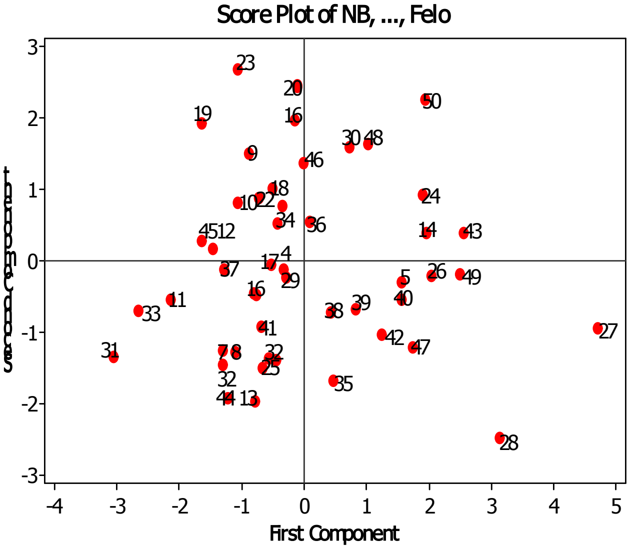

Figure 1. Two dimensional ordinations of 50 germplasm lines of upland cotton.

Biplot: A principal component biplot showed that variables were super imposed on the plot as vectors; relative length of the vector represented the relative proportion of the variability in each variable. The variety which is far away from origin showing more variation and less similarity with other varieties. The number of bolls, seed cotton yield, lint index, seed index, fibre length and fibre strength were well represented while ginning out turn, fibre uniformity exhibited least variability. The quality traits fibre fineness followed by fibre elongation is not in desirable direction (Fig. 2). The variability among the traits under study exhibits the divergence among the genotypes which can be utilized in cotton breeding program effectively.

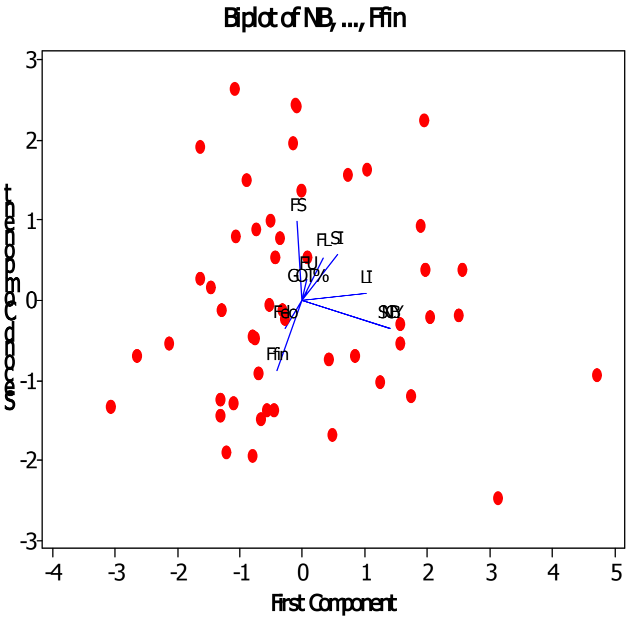

Figure 2. Principal Component's Biplot of 50 upland cotton germplasm.

Analysis of heritability: Genotypic and phenotypic variances, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and broad sense heritability (h^2b) of 17 yield and yield related traits of fifty cotton genotypes are presented in Table 2. GCV ranged from 8.55 to 383.21 among all the traits which were studied. The highest value of GCV (383.21) was observed for seed cotton yield followed by number of bolls per plant (231.38) . PCV ranged from 387.47 to 231.98 among all the traits studied. Number of bolls, seed per boll, seed cotton yield and ginning out turn showed more variation at the phenotypic level (PCV).This indicates that all the genotypes in the study have high genetic potential. This feature is required for hetrosis breeding programme as the index of transmissibility to the next generation (heritability) is in dire need.

Genotypic coefficient of variation (GCV) was maximum for number of bolls and seed cotton yield. Most traits showed high broadsense heritability, ranging from 0.70 for boll size to 0.99 for number of bolls and number of seed per boll. Heritability estimates in broad sense were relatively higher (more than 90%) for all the characters except boll size (0.70). High heritability estimates had been found to be useful in making selection of superior genotypes on the basis of phenotypic performance. Genetic advance value was the highest for seed cotton yield (46.64) preceded by seed per boll (16.37) and number of bolls (15.62) which showed that due to high heritability and genetic advance, the trait which could be further improved is seed cotton yield, number of bolls, number of seeds per boll and lint percentage.

Table 2. Principal Components (PCs) for ten characters in 50 germplasm lines of upland cotton

Variable	PC_1	PC_2	PC_3	PC_4
Eigen value	2.3769	1.6806	1.2711	1.1876
Proportion	0.2380	0.1680	0.1270	0.1190
Cumulative	0.2380	0.4060	0.5330	0.6520

Traits	PC_1	PC_2	PC_3	PC_4
Number of bolls	0.586	-0.210	-0.109	0.029
Seed cotton yield	0.592	-0.212	-0.104	0.061
Ginning out turn	0.031	0.062	0.598	0.313
Lint index	0.430	0.047	0.310	0.085
Seed index	0.236	0.335	0.380	-0.250
Fibre uniformity	0.034	0.152	0.059	0.791
Fibre length	0.140	0.316	-0.412	-0.115
Fibre strength	-0.030	0.587	-0.020	0.148
Fibre elongation	-0.113	-0.216	0.430	0.408
Fine fineness	-0.172	-0.528	-0.145	0.007

Ward's linkage cluster analysis: The letters 1-50 corresponded to the genotypes as exhibited in the dendrogram (Fig. 3). Three major clusters i.e., I, II and III were formed by using the Wards linkage. May *et al.* (1995) reported that cluster analysis identified groups of cotton cultivars those were more closely related. Menezes-Sobrino (1999) conducted a study to characterize 89 garlic germplasm of Brazil and found 13 clusters. Similarly, Baxevanos *et al.* (2008) found the interrelationship and repeatability of seven indices estimated from commercial cotton (*Gossypium hirsutum* L.) varieties and placed them into different clusters. In the current study cluster-I consisted of two sub clusters i.e., Ia and Ib, respectively. Sub cluster Ia further portioned into Ic and Id and sub cluster Ic consisted of 15 genotypes whereas sub-cluster Id exhibited 12 genotypes and sub cluster Ib consisted of 5 genotypes, whereas Cluster-II is partitioned into two sub-clusters IIa, IIb. Sub-cluster IIa composed of 11 cotton genotypes whereas sub-cluster IIb consists of 5 genotypes. Cluster III was composed of 2 genotypes.

Table 3. Estimation of parameters of genetic variability and heritability for yield and fibre quality parameters in 50 genotypes of upland cotton

Traits	Mean ± S. E	GV	PV	EV	GCV	ECV	PCV	$h^2_{(BS)}$	GA
NB	23.38± 1.12	125.17	125.82	0.65	231.38	16.73	231.98	0.99	15.62
S/B	33.22± 0.60	2.03	2.04	1.12	203.71	18.37	204.54	0.99	16.37
BS	3.33±0.031	0.08	0.12	0.035	8.55	1.02	18.64	0.70	0.33
SCY	77.27± 3.38	1134.74	1160.11	25.37	383.21	57.30	387.47	0.97	46.64
GOT%	36.66± 0.46	21.05	22.98	1.93	75.77	22.99	95.98	0.91	6.14
LI	4.57± 0.11	1.12	1.16	0.04	49.65	9.70	50.59	0.96	1.49
SI	7.71±0.12	1.41	1.47	0.06	42.87	8.95	43.80	0.95	1.63
FU	50.63±0.41	17.56	17.33	0.19	58.56	6.10	58.68	0.98	5.80
FS	25.52±0.26	6.66	7.13	0.47	51.09	13.47	52.87	0.93	3.49
FL	28.27±0.22	4.6	4.9	0.26	40.72	9.90	41.86	0.94	2.90
FE	10.70±0.17	3.19	3.24	0.05	54.64	6.58	55.08	0.98	2.50
FF	5.3 ± 0.065	0.41	0.45	0.04	27.91	8.70	29.26	0.90	0.85

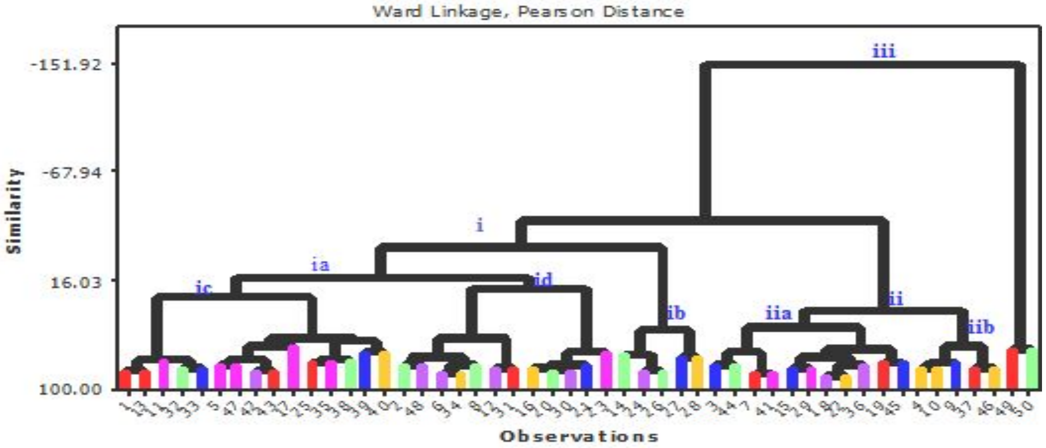

Figure 3. Dendrogram of 50 genotypes of upland cotton

Accessions DPL-6 and QUALANDARI showed 92.02% similarity in sub-cluster IIa whereas, genotypes COKER-307 and FH-113showed 87.15% similarity. The BH-160 75 had 34% level of similarity with both COKER-307 and FH-113 in sub cluster Ib. Similarly in sub cluster Ia, FH-87 and LRA-5166 showed 86.68% similarity with other varieties i.e. STONEVILLE-731, VH-61, VH-141 (Fig. 3). Rana and Bhat (2005) observed that average genetic similarity was 74% in 41 *Gossypium hirsutum* cultivars. (Brown, 1991; Menezes-Sobrino, 1999) reported that cluster analysis has the singular efficacy and ability to identify crop accessions with highest level of similarity using dendrogram. Ghafoor *et al*. (2001) and Rashid (2008) showed multivariate analyses to be a valid system to deal with germplasm collection.

***Conclusion*:** Agronomical traits are expected to provide a general representation of variety relationship according to their growing environment. Their classifications into different clusters predict the selection of genotypes to design a breeding program. Varieties diverse in nature may be used to transfer the desired gene for cotton yield improvement against different ambiances. The genotypes in the positive ordination i.e., 14, 24, 30, 43, 46, 48 and 50 may be used for heterosis breeding program because in score plot analysis the traits away from the ordination are mostly present.

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