

Research Article



Genetic Dissection of Interspecific and Intraspecific Hybrids of Cotton for Morpho-Yield and Fiber Traits using Multivariate Analysis

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Abstract | To estimate level of genetic diversity various cotton genotypes, inter and intraspecific hybrids were assessed for yield, yield contributing and fiber traits using various multivariate analysis such as principle component analysis and linkage cluster analysis. Principle component analysis (PCA) exhibited that first four PC out of nineteen PC, with eigen value >1, contributed about 80.326 % of total variability. Positive contribution towards PC1 was given by seed traits such as lint/seed, seed weight/seed, boll weight, seed index and seed cotton/seed. In biplot analysis, intraspecific hybrids and their parents were present very close to each other while interspecific hybrids, their parent and exotic line were unsimilar and far apart from intraspecific hybrids. Results of linkage cluster analysis (LCA) revealed that among four clusters, performance of genotypes in cluster 3 was superior. PCA and LCA showed that interspecific hybrids showed highest diversity from intraspecific hybrids and concluded that intraspecific hybrids had narrow genetic basis, which can be altered by using interspecific hybrids or exotic lines. These genotypes can be exploited for variety development with enhanced level of diversity, fiber quality and seed cotton yield.

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Introduction

Cotton universally titled as “White Gold” is the principal contributor to oil and fiber industries and major source of foreign exchange earnings in several countries (Khan et al., 2017). Nearly eighty countries are growing cotton to fulfill their fiber and oil demands (Shakeel et al., 2011). China, Pakistan, USA and India are topmost cotton producers and contributing almost 2/3 of world’s cotton land

(Dahab et al., 2013). Bowman et al. (1996) suggested that reduction in fiber and yield parameters in cotton genotypes are due to lower genetic base. Low genetic distance between similar alleles is the major limitation to diversity that urges the breeders to develop high yielding and biotic and abiotic stress resistant complexes by utilizing variation of wild as well as in cultivated progenitors (Sanghera et al., 2014). Genetic diversity in gene pool is a source of exploiting desirable genes for genetic improvement of various important

characters. Therefore, it is necessary to have knowledge about genetic variation for trait (Baloch et al., 2014; Fayyaz et al., 2014). To create enough variations and to get better quality genotypes, it is essential to take advantage of better genotypes in the hybrid breeding programmes (Li et al., 2008). Therefore, diversity among genotypes is conditional to expand genetic makeup through breeding program. Genetic diversity for improvement of different morphological and fiber traits also exists in cotton germplasm was reported. Various studies have been conducted for the enhancement of morphological and fiber traits of cotton genotypes (Alishah, 2001) with diverse genetic makeup in order to develop varieties that could be adaptable to harsh weather conditions with more tolerance to insect pests and diseases. Moreover, exceed to adverse varieties for better fiber traits and high yield and GOT % (Nizamani et al., 2017).

Multivariate statistical techniques like Principle Component Analysis (PCA) and Linkage Cluster Analysis (LCA)—helps the breeders to discover association among genotypes and their various yield linked traits (Brown, 1991; Qiaoling and Zhe, 2011). PCA has an advantage to frame out each genotype to only one group. At each differentiation axis, it also explains the importance of main contributor towards total genetic assortment (Sharma, 2006). Patterns of variations between hybrids disclosed by PCA can be used to utilize genetically and agronomical important genotypes (Isong et al., 2017). For future cotton breeding programs, plant breeders use PCA to evaluate genomic variations. Preservation and characterization of cotton germplasm in various forms viz., better performing breeding lines, wild lines and landraces is quite worthy for evolutionary and genetic process (Haidar et al., 2012). A successful breeding program is necessary for the manipulation of genetic diversity using numerous physiological traits as these traits and the selection procedures are significantly influenced by environment (Ahmad et al., 2012).

The aim of current study is to analyze the variations and genetic diversity in all cotton genotypes and their interspecific and intraspecific hybrids for yield contributing traits by means of PCA and LCA.

Materials and Methods

Planting material

Six parental genotypes CIM-573, Bt.CIM-599, BH-

167, MNH-786, CIM-554 (*G. hirsutum* species) and GIZA-7 (*G. barbadense* species) were crossed with three testers MNH-886, CIM-557 and V4 (exotic cultivar; *G. hirsutum* species) using line × tester mating design to develop interspecific and intraspecific hybrids in greenhouse during 2013.

Field layout

Nine genotypes with their F1 hybrids were evaluated in randomized complete block design using three replications on experimental area of Department of Plant Breeding and Genetics, Faculty of Agricultural Sciences and Technology, Bahauddin Zakariya University, Multan during 2014. Row to row and plant to plant distance was kept 75 cm and 30 cm, respectively.

Data collection

At crop maturity, data for nineteen traits were recorded including number of sympodia/plant, number of monopodia/plant, node of first fruiting branch (NFB), total number of bolls/plant (TBP), total number of nodes/plant (TN), total number of fruiting nodes (FN), boll weight (BW), lint weight/boll (LW), number of seeds/boll (SB), seed index (SI), lint index (LI), ginning out turn (GOT), seed cotton/seed (SCS), seed weight/seed (SWS), lint/seed (LS), seed cotton yield/plant (g/p) (YP), fiber strength (SS), staple length (SL) and micronaire value (Mic). Worley et al. (1974)'s method was used to calculate the seed cotton/seed (SCS), seed weight/seed (SWS), and lint/seed (LS).

Biometrical analysis

The averaged data recorded for all traits was subjected to XL stat software for PCA (Sneath and Sokal, 1973) and SPSS V20 for LCA (Ogunbayo et al., 2005).

Results and Discussion

Principal component analysis (PCA)

PCA is a significant tool to measure the variation among different genotypes for yield contributing traits. In this study, out of total nineteen, first four principle components (PCs) showed eigen value of more than 1 which contributed 80.326% to the total variability (Table 1).

Fruiting nodes, boll weight, lint weight/boll, seed index, lint index, SCS, lint/seed, staple strength, bolls/plant, and yield/plant gave positive contribution

towards PC1 except three parameters (sympods/plant, GOT and micronaire). In PC2 contribution of lint index, staple length, GOT, seeds/boll, sympods/plant, bolls/plant, total nodes/plant, staple strength and yield/plant was positive. Whereas, boll weight, monopods/plant, NFB, fruiting nodes, SCS, lint/seed, SWS and seed index contributed negatively to PC2 (Table 1). Scatter plot showed that genotypes, which were close to each other, resemble each other. While, genotypes apart from each other represented that they were dissimilar. Scatter plot showed grouping of genotypes in four clusters and displayed that genotypes V4 and Giza-7 were quite different from residual genotypes (Figure 1).

Table 1: Principle component analysis for various morpho-yield and fiber traits in cotton genotypes.

	PC1	PC2	PC3	PC4
Eigenvalue	5.756	4.737	2.993	1.776
Variability (%)	30.296	24.93	15.752	9.347
Cumulative variance %	30.296	55.226	70.979	80.326
Factor loadings by different traits				
	PC1	PC2	PC3	PC4
TBP	0.154	-0.025	0.482	0.11
Mono	0.063	-0.306	0.056	0.321
Sym	-0.016	0.22	0.414	-0.205
NFB	0.181	-0.149	0.023	0.343
TN	0.069	0.185	0.455	-0.103
FN	0.101	-0.064	0.171	0.545
BW	0.261	0.31	-0.109	0.117
SB	-0.06	0.409	0.038	0.265
SI	0.352	-0.173	-0.123	0.011
LW	0.127	0.397	-0.142	0.209
LI	0.304	0.168	-0.203	-0.076
GOT	-0.13	0.346	-0.062	0.256
SCS	0.359	-0.124	-0.119	-0.161
LS	0.336	0.123	-0.226	0.009
MIC	-0.004	0.292	-0.191	-0.172
SL	0.275	-0.075	0.269	-0.236
SS	0.238	0.183	0.096	-0.294
SWS	0.366	-0.167	-0.105	0.015
Y/P	0.309	0.123	0.262	0.143

TBP: Bolls/plant; Sym: Sympods/plant; NFB: Nodes of first fruiting branch; TN: Total nodes; FN: fruiting nodes; BW: Boll weight; SB: Seeds/boll; SI: Seed index; LI: Lint index; LW: Lint weight; GOT: Ginning out turn; SCS: Seed cotton/seed; LS: Lint/seed; SWS: Seed weight/seed; Y/P: Yield/plant; SL: Staple length; SS: Staple strength; MIC: micronaire value.

Loading plot showed positive correlation of yield/

plant with fruiting nodes, bolls/plant, NFB, seed index, staple length, boll weight, sympods/plant, total nodes, SCS, SWS, whereas negative correlation with GOT. GOT was positively correlated to micronaire value but negative to staple length. Negative correlation was depicted for GOT, micronaire value and seeds/boll. It expressed that bolls/plant was positively correlated to NFB, monopods/plant, total nodes, seed index, fruiting nodes, lint index, lint weight, staple strength, SWS, SCS and yield/plant (Figure 2).

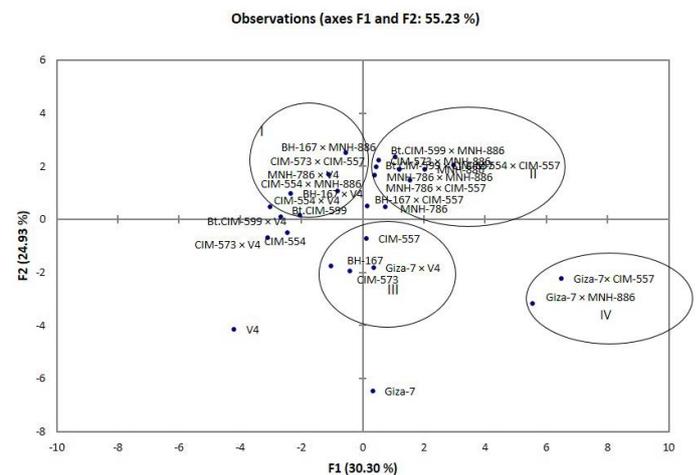


Figure 1: PC scatter plot showing genotypes on first two PCs.

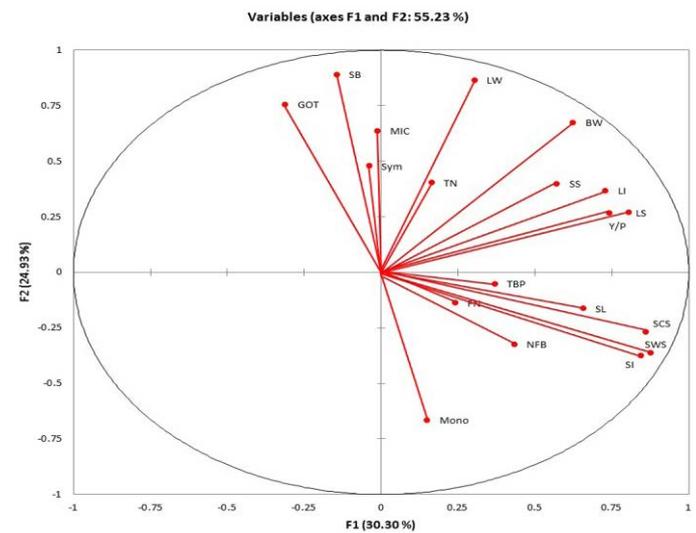


Figure 2: Loading plot of all variables among all the interspecific and intraspecific hybrids of cotton.

Genotype by trait (GT) biplot explains the association of traits with genotypes. In biplot, variable serves as vectors representing variability among genotypes. More distance of vector from the origin showed more variation and vice versa. The biplot analysis in current study showed that genotypes in cluster I were close to the vector traits of sympods and micronaire value. Members of Cluster II showed good performance in terms of boll weight, lint index, lint/seed, staples

strength, yield/plant and total node. Cluster III displayed genotypes in it were good in bolls/plant, staple length and fruiting nodes. Cluster IV showed genotypes have better seed index and SWS traits. Hybrids such as Giza-7 × MNH-886 and Giza-7 × CIM-557 belong to cluster IV and have traits SCS, SWS and seed index, which are better compared to others. Giza-7 was good in monopods/plant. MNH-786 × CIM-557 and CIM-554 × CIM-557 are the members of cluster II are good in yield/plant (Figure 3). Biplot reveals that highest variation is caused by bolls/plant followed by boll weight, total nodes, yield/plant, lint index and sympods/plant, seed index. Thus, PCA's showed that interspecific hybrids were closer to yield and fiber traits vectors.

554 × V4, Bt. CIM 599 × CIM 557, Bt. CIM 599, CIM 573, MNH 786, CIM 554 and Giza 7. LCA depicted that genotypes in Cluster 1 and Cluster 3 are superior in terms of their fruiting nodes, ginning out turn and overall yield performance (Table 2).

Table 2: Cluster analysis of fiber, yield and its contributing traits in cotton.

	Cluster			
	1	2	3	4
TBP	31.44	24.33	41.00	33.45
Mono	1.22	1.56	2.89	4.67
Sym	25.00	19.67	23.78	17.22
NFB	6.33	4.78	8.67	12.11
TN	35.67	28.56	36.11	28.78
FN	57.56	46.44	104.22	103.00
BW	3.32	1.92	2.73	2.01
SB	25.52	15.44	17.19	15.19
SI	7.35	6.13	10.79	9.48
LW	1.41	.61	.95	.74
LI	5.34	4.12	5.49	4.52
GOT	42.46	32.08	34.72	36.83
SCS	.13	.13	.16	.13
LS	5.53	3.93	5.38	4.82
MIC	5.30	4.77	4.50	4.47
SL	26.27	24.47	28.60	24.17
SS	38.27	34.03	40.54	31.93
SWS	.07	.06	.11	.10
YP	104.50	46.56	140.16	67.06

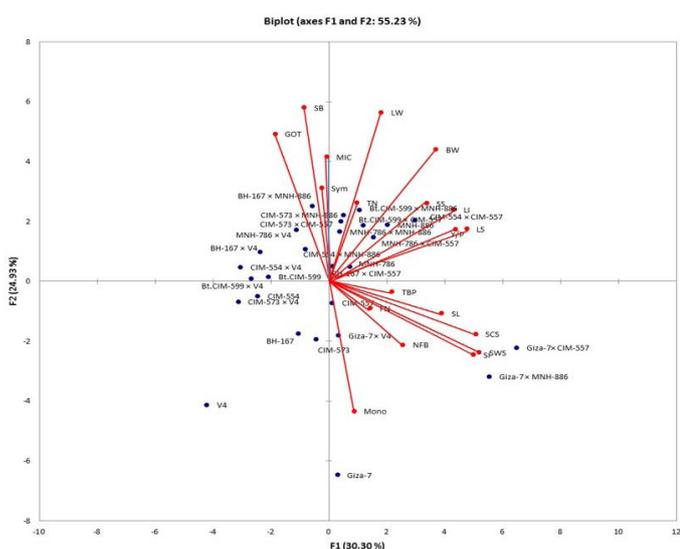


Figure 3: GT biplot for morpho-yield and fiber traits among intraspecific and interspecific hybrids of cotton.

Cluster analysis

Ward's cluster analysis was performed for genetic dissection of different cotton genotypes. A dendrogram from cluster analysis of 27 genotypes based on yield, fiber and morphological traits was drawn (Figure 4). Based on this classification, cotton genotypes were prearranged into four different clusters. In first cluster, there were six genotypes including Bt. CIM 599 × MNH 886, CIM 573 × MNH 886, BH 167 × MNH 886, BH 167 × V4, BH 167 × CIM 557 and CIM 557, while cluster two collected four genotypes named CIM 573 × V4, BH 167, MNH 886 and V4, third cluster was composed of six genotypes i.e., Giza 7 × MNH 886, Giza 7 × V4, CIM 573 × CIM 557, MNH 786 × CIM 557, CIM 554 × CIM 557, Giza 7 × CIM 557 while fourth cluster included eleven genotypes viz, MNH 786 × MNH 886, CIM 554 × MNH 886, Bt. CIM 599 × V4, MNH 786 × V4, CIM

TBP: Bolls/plant; Sym: Sympods/plant; NFB: Nodes of first fruiting branch; TN: Total nodes; FN: fruiting nodes; BW: Boll weight; SB: Seeds/boll; SI: Seed index; LI: Lint index; LW: Lint weight; GOT: Ginning out turn; SCS: Seed cotton/seed; LS: Lint/seed; SWS: Seed weight/seed; YP: Yield/plant; SL: Staple length; SS: Staple strength; MIC: micronaire value.

By splitting the total variation into its components, the conservation and utilization of germplasm could be accomplished (Mugheri et al., 2017). The existence of morpho-yield and fiber traits variation among interspecific and intraspecific hybrids of cotton genotypes was substantiated by PCA. The maintenance and manipulation of genetic resources could be done by partitioning the total variance into its components. It also offers a tool for exploitation of appropriate genotypes in crop improvement for traits of interest (Saeed et al., 2014). The PCA is a potent tool to obtain parental genotypes and their hybrids for a successful breeding program (Akter et al., 2009; Jarwar et al., 2019) through selection of best

genotypes on the basis of mean values of several traits (Malik et al., 2011). In current study, the PC analysis

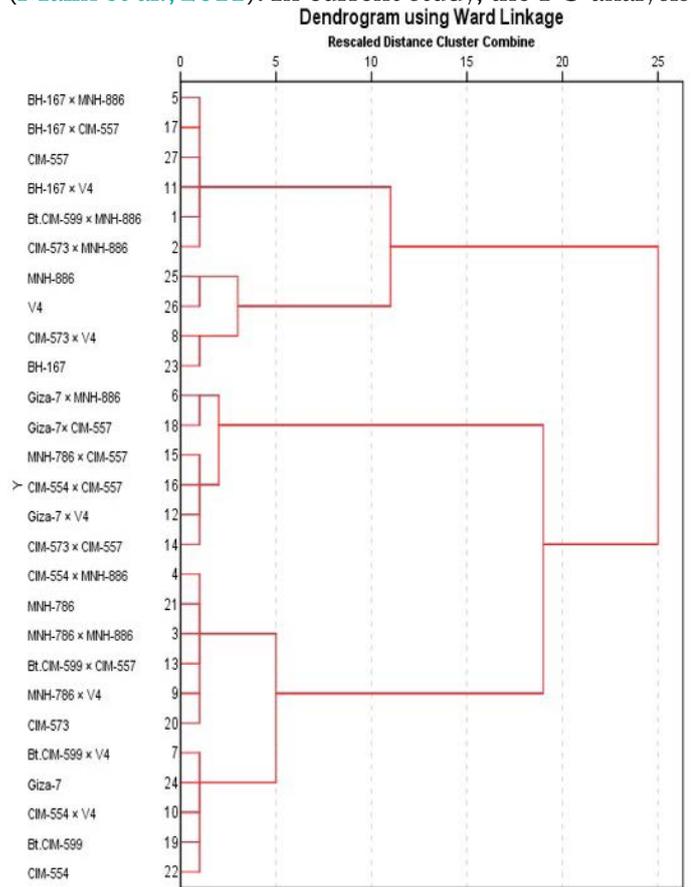


Figure 4: Ward's Linkage Cluster Analysis; dendrogram of interspecific and intraspecific hybrids of cotton

split the total variance into 4 PCs contributing maximum diversity towards germplasm. Significant contribution of first PC to total variability has been reported for various traits (Chozin, 2007; Mujaju and Chakuya, 2008) and followed by PC2 (Nazir et al., 2013). In this experiment, PC1 was mainly due to variations in bolls/plant, seed index, lint index, staple length, staple strength and seed cotton yield. Shakeel et al. (2015) also reported that variation on PC1 was mainly attributed due to staple length and lint index. Whereas, PC2 showed variance due to number of sympodia/plant, boll weight, micronaire value, GOT and yield/plant. Ahmad et al. (2012) also reported positive contribution of seed index to PC1 and GOT, lint index, nodes/plant and micronaire value to PC2. The scatter plot displayed association between four clusters, which showed similarity and variation between different genotypes and hybrids. Significant lack of diversity in Upland cotton is due to wide usage of few genetic sources with narrow genetic base during breeding programs (Iqbal et al., 2001). Enduring cultivars among *G. hirsutum* (CIM-557, CIM-554, CIM-599, BH-167, MNH-

786, MNH-886) showed lower level of genetic diversity. This result favors the findings of Guang and Xiong-Ming (2006) who reported that most of cotton genotypes were developed from some genetic resources. Deficiency of sufficient genetic variation in material used highlighted the requirement to introduce diverse cotton genotypes via hybridization or using exotic lines being a source of genetic diversity (Abdurakhmonov et al., 2008).

GT biplot indicate association among cotton genotypes and their hybrids as well as compare different genotypes on basis of various traits (Yan and Reid, 2008). Genotypes which made longest vectors from origin of biplot showed extreme levels for single or multiple traits depicting that genotype may be good or poor in that trait (Yan and Rajcan, 2002). Results of GT biplot analysis revealed that interspecific hybrids, Giza-7 x MNH-886 and Giza-7 x CIM-557, are good for SCS, SWS, staple length and seed index traits, while CIM-554 x CIM-557 and MNH-786 x CIM-557 are good in yield/plant. Fiber fineness, fiber length and GOT showed positive association depicting that fiber traits can be improved by improving lint percentage (Munir et al., 2016). Results showed that interspecific hybrids had overall good performance and can be further utilize to enhance fiber yield and quality of cotton. PCA indicated genetically diverse and overall good performing interspecific hybrids regarding yield (Isong et al., 2017; Malathi and Rajesh, 2019). Ward's dendrogram was constructed to estimate genetic diversity among various genotypes (Grenier et al., 2000; Nazir et al., 2013). Aliyu and Fawal (2000) stated that cluster analysis has excellent skill to recognize plant genotypes with maximum level of resemblance using dendrogram. In this experiment, twenty-seven genotypes (parental lines and their hybrids) are grouped in four clusters. The cluster 3 of dendrogram showed variation among interspecific hybrids from most of other intraspecific hybrids and parental genotypes. Cluster analysis revealed that members of Cluster 3 comprising on Giza-7 x MNH-886, Giza-7 x V4, CIM-573 x CIM-557, MNH-786 x CIM-557, CIM-554 x CIM-557 and Giza-7 x CIM-557 showed overall good performance for yield/plant, bolls/plant, staple length and staple strength and can be utilized in future breeding programs. These biometrical tools could be utilized for discovery of other latent sources, for example, to discover tolerance against stem rust in wheat (Nzuve et al., 2012), soil acidity in common

beans (Legesse et al., 2013), drought in wheat (Parchin et al., 2013), salt in barley (Allel et al., 2016) and cotton curl virus in cotton (Javed et al., 2017).

Conclusions and Recommendations

Utilization of various biometrical techniques like PCA and LCA, provide information that can be used to discover, classify and select genotypes with diverse genetic makeup. Multivariate approaches made it possible to identify and select genotypes that are good in fiber traits with other morpho-yield parameters linked with enhanced seed cotton yield. Results showed that Giza 7 (*G. barbadense*), V4 (exotic cultivar) and interspecific hybrids in comparison to intraspecific hybrids have better genetic diversity and are better in yield linked traits compared to other studied genotypes. These genotypes can be utilized for selection of better performing genotype with high seed cotton yield and broad genetic makeup.

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Author's Contribution

Sana Munir contributed in conducting experiment and writing draft of manuscript. Muhammad Kamran Qureshi involved in design and concept of experiment and finalizing the draft for publication. Ahmad Naeem Shahzad; analysis and interpretation of data and finalizing the draft. Ismat Nawaz; technical and material support and coordinating the research. Muhammad Shahzad Anjam; analysis and interpretation of data. Sumaira Rasul involved in critical revision of the manuscript and supervising the work. Muhammad Asif Zulfiqar involved in critical revision of the manuscript and finalizing the draft.

Conflict of Interest

The authors declare that there is no conflict of interests.

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