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GENETIC DISTANCE, HERITABILITY AND CORRELATION ANALYSIS FOR YIELD AND FIBRE QUALITY TRAITS IN UPLAND COTTON GENOTYPES

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ABSTRACT

The present research was carried out to determine the genetic distance, heritability and correlation coefficients for yield and fibre quality traits in fifteen upland cotton genotypes. The traits studied were; plant height, sympodial branches plant^{-1}, number of bolls plant^{-1}, boll weight, ginning outturn (%), seed index, seed cotton yield plant^{-1} and staple length. The genetic distance was further supported by statistical procedures like cluster analysis, coefficient of parentage and principal component analysis. The mean squares from analysis of variance revealed that genotypes differed significantly at 5 % probability level for all the traits except that seed index and staple length were non-significant. The mean performance of genotypes suggested that IR-524 produced the tallest plants; Sadori produced the maximum number of sympodial branches plant^{-1}, Sohni formed highest number of bolls plant^{-1}; Tarzan-1 yielded heaviest bolls and gave highest seed cotton yield plant^{-1}; NIA-Ufaq ginned maximum lint % and Chandi-95 recorded highest seed index and measured longest staple length. The correlation coefficient indicated that all the morpho-yield traits were significantly associated with seed cotton yield and with each other suggesting that one or more yield traits can be used as selection criteria to improve the seed cotton yield.

The higher heritability estimates (h^2b.s) were recorded for almost all the studied traits except seed index. Such results revealed that improvement in those traits can be made through direct phenotypic selection. Cluster analysis arranged all the 15 genotypes into four different groups. Cluster third characterized the genotypes as having more number of plants and with higher seed cotton yield plant^{-1}, hence genotypes of this group may prove promising in producing higher seed cotton yield plant^{-1}. While concerning genetic distance, out of 105 pair wise comparisons, some pairs manifested greater genetic distance; consequently, those genotypes can be utilized in heterosis and backcross breeding programmes for the introgression of novel genes. From principal component analysis (PCA), eight components were extracted for studied characters. The first two components accounted for about 99 % variation from total variation, thus the cumulative percent of variance was 99.0 % in first two components. The first two PCAs demonstrated significantly higher variability that can be exploited for further breeding programmes in cotton.

Key words Cotton, genetic distance, heritability, correlation analysis, yield

INTRODUCTION

Pakistan is the fifth largest producer of cotton, the third largest exporter of raw cotton, the fourth largest consumer of cotton, and the largest exporter of cotton yarn in the world. About 1.3 million farmers (out of 5 million) cultivate cotton over 3.0 million hectares, covering 15% of the cultivable land in the country. Cotton and cotton products contribute about 10 % to GDP and 55 % to the foreign exchange earnings of the country. Altogether, 30 to 40 % of the cotton is used for domestic consumption and the remaining is exported as raw cotton, yarn, cloth, and garments (http://edu.par.com.pk/ wiki/cotton). Cotton is the world's most important natural textile fiber and an important source of feed, foodstuff, and oil, with approximate world consumption put at 27 million metric tons per year (Chen *et al.*, 2007). The science of plant breeding has a documented history in cotton improvement to meet the requirement of producers and processors. To meet fibre necessities of the world's growing population, a significant improvement in cotton production has been universally realized (Farooq *et al.*, 2014). In upland cotton breeding programmes, the improvement in lint yield is not only the objective but fibre quality characters like staple length, strength, fineness etc. are also important for textile industry. World demand for cotton is growing at rapid pace, which is greater than the world population growth rate (http://www.cicr. org.in / pdf/ELS/so2.pdf).

Cotton breeders are trying to develop varieties, which could adapt to our adverse varieties those could will adapt our adverse environmental conditions and produce higher yield, higher ginning outturn percentage, better fibre quality and response to higher fertilizer doses along with increased resistance to diseases and insect pests. For breeding programmes, parents must be genetically superior, physiologically efficient, possess good general and specific combining ability so that they could be utilized for both variety development programmes and commercial exploitation of heterosis for hybrid crop development. Cotton improvement programmmes have responded well to the needs of growers and industry such as combining higher seed cotton yield, early maturity and good fibre quality traits. Modern cotton breeders and bioengineers have contributed to achieve these goals (Zia *et al*., 2011). Genetic distance is a measure of the genetic divergence between species or individuals in populations or within species. The populations with similar alleles have low genetic distance, which indicate that they are closely related and have acquired common ancestors. To overcome the threat of this uniformity, it is very important that genetic diversity, available in both the cultivated and its wild progenitors, may be thoroughly utilized to create new genetic complexes for higher yield and tolerance to various biotic and abiotic stresses in cotton (Sanghera *et al.,* 2014).

Cluster analysis presents pattern of relationships between genotypes and hierarchical mutually exclusive grouping in such a way that similar descriptions can mathematically be gathered into same cluster (Aremu, 2005). Cluster analysis is based on four methods namely; unweighted paired group method using centroids (UPGMA), single linkages cluster analysis (SLCA), complete linkage cluster analysis (CLCA) and median linkage cluster analysis (MLCA). From these four methods, UPGMA and UPAMC provide more accurate grouping information for breeding material used in accordance with pedigrees and calculated results and they are more consistent with known heterotic groups than the other clusters (Aremu *et al.*, 2007).

Principal component analysis (PCA) is fractional tool which provides information about parental lines for successful breeding prgrammes (Nazir *et al*., 2013). The purpose of principal component analysis is to reduce the number of observed variables into a relatively smaller number of components; this cannot be effectively achieved by the components which account for less variance than those contributed by individual variables. For this reason, components with eigen values less than 1.0 are viewed as trivial and are therefore not retained. Eigen values are thought to be quantitative assessments which indicate as how much a component represents the data. The higher the eigen values of a component, the more representative it is for the data. Heritability is a genetic probability used in breeding and genetics studies that estimates as how much variation in a phenotypic trait in a population is due to genetic variation among individuals which is transferable from parents to their progenies (Baloch and Baloch, 2004). Correlation is a term that refers to the strength of a relationship between two variables. A strong or high correlation means that two or more variables have a strong relationship with each other. While a weak or low correlation suggests that the variables are less related. Thus correlation coefficient deals with the extent of association between several plant traits and finds out the component traits which may be used as selection criteria for the enhancement in yield and its improvement in fibre quality traits (Baloch *et al*., 2015).

MATERIALS AND METHODS

The field experiments were conducted at Experimental field, Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam Pakistan during kharif season 2015 to determine genetic distance, heritability and correlation coefficients for yield and fibre quality characters. For this purpose, fifteen upland cotton genotypes viz. BT-905, CRIS-494, CRIS-342, SI-815, SGA-1, BT-703, IR-524, Tarzan-1, Sadori, Sindh-1, Shahbaz, Hari Dost, NIA-Ufaq, Sohni and Chandi-95 were studied. The experiment was conducted in randomized complete block design with three replications. The observations were taken on plant height (cm), sympodial branches plant^{-1}, bolls plant^{-1}, boll weight (g), ginning outturn percentage (GOT %), seed index (g), seed cotton yield plant^{-1} (g) and staple length (mm).

Management practices: The land was prepared by two dry plowings with tractor followed by surface leveling. The land preparation operations were carried out for equal distribution of irrigation and fertilizers. The crop was kept clean, and periodical weed control practices were carried out to avoid any possible constraint against the experimental process by weeds as unwanted plants. Thus all cultural practices were performed uniformly in all plots, keeping in view the crop requirements. Drilling was done in straight lines through single manual drill. The experiment was planted on 25th April during 2015. One bag of nitrogen, half bag of phosphorus was applied in the form of urea, Di-ammonium phosphate (DAP) at the time of sowing. After that, one bag of urea at first and another bag of urea were applied at third irrigation. The five irrigations were applied during growth and development of the crop. Weeding is the major cause of lower yields in cotton crop. Thus, weeding and inter-culturing operations were performed as and when required. The crop was kept free from weeds, insect pests, and diseases. Plant protection measures were adopted whenever required. The crop was harvested during 17th September and 4th October, 2015 for first and second picking.

STATISTICAL ANALYSIS: The experimental data were recorded and subjected to analysis of variance under linear models of statistics to observe statistical difference among different traits using computer software Statistix 8.1 version. Furthermore, least significant difference (LSD) test was applied to test the level of significance between mean performances of genotypes (Gomez and Gomez, 1984). While, genetic distance and cluster analysis were performed with the help of SPSS ver. 17 computer software.

RESULTS AND DISCUSSION

The mean squares from analysis of variance for all the studied characters are given in Table1. The obtained results revealed that genotypes differed significantly at P≤0.01 probability level for plant height, sympodial branches plant^{-1}, bolls plant^{-1}, boll weight plant^{-1}, GOT %, seed index, seed cotton yield plant^{-1} and staple length indicating the existence of considerable genetic variability among genotypes for different traits except that seed index and staple length were non-significant. Such results indicated that the studied material is useful as genetic resources for variety development and also can be utilized for further breeding programmes. Significant differences among genotypes were also reported by (Baloch *et al*., 2014a).

Table-1: Mean square from analysis of variance for various yield and fibre traits in upland cotton genotypes

Source of variation	DF	Plant height	Sympodial branches plant^{-1}	Number of bolls plant^{-1}	Boll weight	GOT (%)	Seed index	Seed cotton yield plant^{-1}	Staple length
Replications	2	0.67	1.21	8.54	0.01	1.32	0.004	205.94	6.97
Genotypes	14	322.93**	10.52**	51.44**	0.27**	10.05**	0.45	1604.69**	0.65
Error	28	0.79	0.51	1.95	0.005	1.45	0.22	27.08	0.61

** = Highly significant

Mean performance of genotypes: The mean performance of genotypes revealed that IR-524 produced the tallest plants (134.11cm), followed by Tarzan-1 (133.67 cm) while Sindh-1 recorded the shortest plants (97.55 cm) Table2. Yet the plant height varied from 97.55 to 134.11 cm. In case of sympodial branches plant^{-1}, Sadori produced the maximum number of sympodial branches plant^{-1} (27.00) followed by NIA-Ufaq (26.22), however the lowest number of sympodial branches plant^{-1} were produced by Sindh-1 (20.00). The maximum bolls plant^{-1} were recorded by genotype Sohni (43.88) followed by Tarzan-1 (41.88), while minimum bolls plant^{-1} (29.22) were obtained from Sindh-1. The biggest bolls were weighed by Tarzan-1 (3.91 g) followed by at par boll weights of genotypes Sohni and Chandi-95 (3.72 and 3.71 g) respectively, however smallest bolls were weighed by Sindh-1 (2.85 g). Average of lint % indicated that highest ginning outturn (39.40 %) was given by NIA-Ufaq followed by Sadori (39.17 %), nevertheless lowest ginning outturn was observed in BT-703 (33.75 %). The Chandi-95 gave highest seed index (7.45 g) followed by SGA-1 (7.30 g), nevertheless CRIS-494 gave the lowest value of seed index (6.32 g). The genotype Tarzan-1 produced maximum seed cotton yield plant^{-1} (163.84 g), followed by Sohni (163.50 g), while the lowest seed cotton yield plant^{-1} was recorded by Sindh-1 (83.63 g). The maximum staple length (29.11 mm) was measured by genotype Chandi-95 followed by CRIS-494 (28.78 mm), while lowest yet at par staple length (27.44 mm) was obtained by the BT-703 and SGA-1 genotypes.

Based on overall mean performance of genotypes, though Tarzan-1, Chandi-95 and NIA-Ufaq performed well for couple of traits, yet none of the genotypes was superior for all the traits simultaneously. Islam *et al*. (2013), Farooq *et al*., (2013) Rao *et al*., (2013), assessed different *Gossypium hirsutum* varieties for yield and other economic characters and observed significant variations for boll weight and showed its positive effect on seed cotton yield.

Table- 2: Mean performance of upland cotton genotypes for yield and fibre traits

Genotypes	Plant height (cm)	Sympodial branches plant^{-1}	Bolls plant^{-1}	Boll weight (g)	Ginning outturn (GOT %)	Seed index (g)	Seed cotton yield plant^{-1} (g)	Staple length (mm)
BT-905	124.78	24.00	34.11	3.48	36.21	7.27	118.85	28.00
CRIS-494	121.33	24.66	34.66	3.22	36.62	6.32	111.84	28.78
CRIS-342	123.78	23.77	35.89	3.31	38.33	6.59	118.75	27.88
SI-815	126.00	24.89	37.33	3.38	38.91	6.36	126.46	27.89
SGA-1	113.55	22.89	34.99	3.07	34.55	7.30	107.60	27.44
BT-703	124.44	24.89	41.44	2.94	33.75	6.67	121.97	27.44

IR-524	134.11	23.66	40.33	3.68	37.45	7.04	148.48	28.00
Tarzan-1	133.67	23.22	41.88	3.91	37.81	6.87	163.84	28.22
Sadori	122.67	27.00	41.77	3.46	39.17	7.24	145.88	28.00
Sindh-1	97.55	20.00	29.22	2.85	34.33	6.41	83.63	27.88
Shahbaz	108.55	23.22	36.44	3.17	37.32	6.45	115.67	28.55
Hari Dost	107.11	20.66	33.88	3.27	34.61	7.04	111.00	27.66
NIA-Ufaq	132.33	26.22	41.55	3.51	39.40	7.23	146.01	27.78
Sohni	114.89	25.00	43.88	3.72	36.99	6.76	163.50	28.22
Chandi-95	119.89	25.55	41.11	3.71	37.47	7.45	152.54	29.11
LSD (5%)	1.48	1.19	2.34	0.12	2.01	Ns	8.70	ns

Cluster analysis: A dendrogram was developed from cluster analysis of 15 genotypes based on eight yield and fibre quality traits as illustrated in figure-1. Based on this classification, upland cotton genotypes are arranged in four different clusters. In first cluster, there were five genotypes including BT-905, CRIS-342, CRIS-494, BT-703 and SI-815, while second cluster was composed of Hari Dost, Shahbaz, SGA-1 and Sindh-1, yet third cluster was consisted of IR-524, NIA-Ufaq, Chandi-95 and Sadori genotypes, fourth cluster included Sohni and Tarzan-1 genotypes. Cluster analysis is very important statistical method which reveals the genetic similarity or dissimilarity. According to groups, first cluster can be characterized as medium type plants with longer staple length and the second cluster with relatively shorter plants with higher seed index. Third cluster, genotypes showed more number of bolls plant^{-1}, longer staple length, ginned higher lint % and recorded taller plants, while fourth cluster genotypes weighed bigger bolls and gave highest seed cotton yield per plant. Thus, depending on genetic distance and objectives of cotton breeders, crosses can be made accordingly to achieve the goals like broadening the parentage of varieties and obtain high heterosis when two divergent lines are involved in the development of F_1 hybrids in cotton. Based on obtained results, it is suggested that the genotypes clustered together into group one, possess desirable gene combinations for seed cotton yield plant, offering that such cotton genotypes could be used in future breeding programs to improve seed cotton yield. Esmail *et al.*, (2008) observed that cluster analysis based on Euclidean distance using yield characters grouped 21 cotton genotypes into two main groups. Cluster "A" and "B" composed of eleven and ten genotypes, respectively.

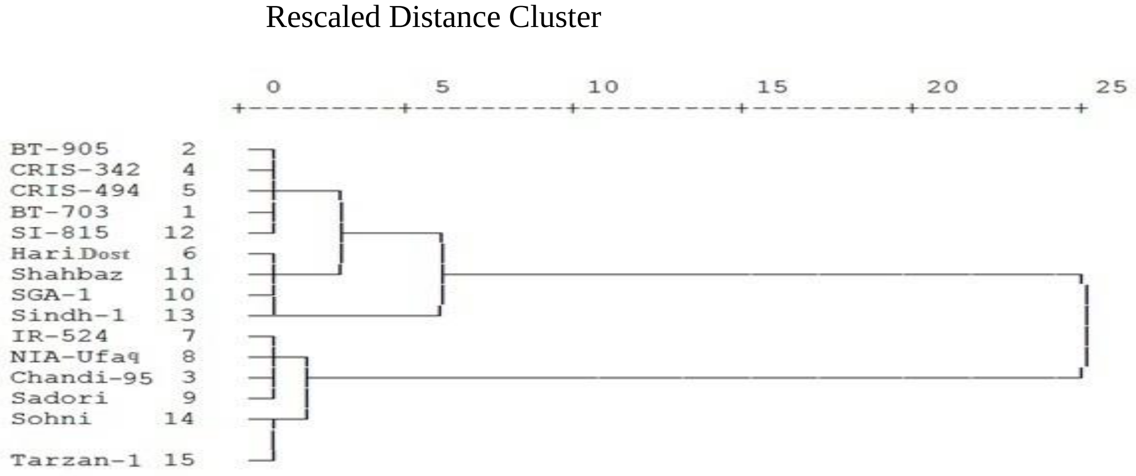

Figure-1: Dendrogram developed for 15 upland cotton genotypes for eight characters by hierarchical clusters analysis (Ward's method)

Genetic distance based on coefficient of parentage: The data matrix of tested characters was formed based on Euclidean genetic distance calculations. Genetic distance values of 105 pair wise comparisons of 15 genotypes are presented in Table 3. The estimated genetic distance values ranged from 3.03 to 89.01. The greater genetic distance of 89.01 was noted between Tarzan-1 and Sindh-1, followed by Sohni and Sindh-1(83.23), Sindh-1 and IR-524 (75.43), Sindh-1 and Chandi-95 (73.70), Sindh-1 and NIA-Ufaq (72.92). However, the narrow genetic distances were found between CRIS-342 and BT-905 (3.03) followed by NIA-Ufaq and IR-524 (4.59), Shahbaz and Hari Dost (6.73) and Sadori and Chandi-95 (7.67) respectively. The greater genetic distance was noted between Tarzan-1 and Sindh-1 which indicated that such genotypes may be utilized in heterosis breeding programme, in cotton. With regards to Nie's Genetic Diversity Index (NGDI), the characters like plant height, sympodial branches plant^{-1} and bolls plant^{-1} exhibited greater genetic diversity, indicating that these genotypes were substantially diverse for such traits. Consequently, this lot of cotton genotypes may prove promising for targeted breeding programmes. Xian *et al.*, (2012) also reported that genetic diversity analysis divided 38 cotton genotypes into two groups from similar genetic background, the same breeding unit and the similar types of varieties.

Table -3: Genetic distance matrix of 15 genotypes of upland cotton

Genotypes	*1	2	3	4	5	6	7	8	9	10	11	12	13	14
BT-703														
BT-905	8.446													
Chandi-95	31.203	34.832												
CRIS-342	8.004	3.039	34.502											
CRIS-494	12.975	7.973	41.270	7.735										
Hari Dost	22.282	19.692	44.447	19.124	15.010									
IR-524	28.525	31.709	14.975	31.803	39.254	46.825								
NIA-Ufaq	25.971	29.414	14.268	29.254	36.715	44.433	4.597							
Sadori	24.692	28.491	7.672	27.991	34.994	39.776	12.404	9.700						
SGA-1	19.277	16.059	46.000	15.670	9.424	7.704	46.174	43.655	40.413					
Shahbaz	18.276	16.789	38.947	15.606	13.557	6.736	41.786	39.074	34.048	10.094				
SI-815	8.155	8.871	27.149	8.250	15.772	25.387	23.745	21.044	20.330	23.243	20.677			
Sindh-1	48.651	45.017	73.709	44.682	37.669	29.385	75.432	72.928	68.829	29.554	34.922	52.486		
Sohni	42.822	46.788	12.436	46.359	52.880	54.239	24.694	24.965	19.610	56.722	48.859	39.274	83.236	
Tarzan-1	43.119	46.553	18.025	46.562	53.972	59.825	15.460	18.216	21.450	60.228	54.609	38.491	89.010	18.991

*1. BT-703, 2. BT-905, 3. Chandi-95, 4. CRIS-342, 5. CRIS-494, 6. Hari Dost, 7. IR-524, 8. NIA-Ufaq, 9. Sadori, 10. SGA-1, 11. Shahbaz, 12. SI-815, 13. Sindh-1, 14. Sohni

Principal component analysis: Eight components were extracted from the eight studied traits by principal components analysis (PCA) Table 4. The first two components revealed higher eigen values while rest of components showed lower eigen values. The first and second components accounted for large amount of variation. The cumulative percent of variances attributable to first two components i.e. PCA1 and PCA2 accounted for 90.6 and 99.0 % of total variation respectively. The first (- .9359) and second (0.311) PCAs were highly associated with GOT %. The third PCA was highly associated with bolls plant^{-1} (0.81) showing large eigen vector. The fourth PCA was highly associated with seed index (0.84). The fifth PCA was highly associated with number of sympodial branches plant^{-1} (0.64). The sixth (0.64) and seventh (0.72) PCAs were greatly associated with seed cotton yield plant^{-1}, while eighth PCA was associated with boll weight (0.99). Principal components analysis (PCA) is a fractional tool to obtain parental lines for successful breeding prgrammes (Nazir *et al.*, 2013). Therefore, the mentioned characters which load either highly positive or highly negative contributes more to the genetic diversity and those are the ones that most differentiated the clusters. As usual, it is customary to choose one variable from identified groups. Elci *et al.*, (2014) also worked-on principal component analysis (PCA) for morphological data in Turkish cotton varieties where PCA indicated the relationships of genotypes in a more meaningful form showing that PCA should be used along with the dendrogram to gain a better understanding of relationships among genotypes.

Table- 4: Vector loading and explained percentage variances by the 8 PCAs

Characters	Eigen vectors							
	PCA-1	PCA-2	PCA-3	PCA-4	PCA-5	PCA-6	PCA-7	PCA-8
Plant height	-0.3084	-0.9465	-0.0450	-0.0797	-0.0057	-0.0192	0.0150	-0.0025
Sympodial branches plant^{-1}	-0.0507	-0.0584	0.5398	0.4793	0.6435	0.0641	-0.2340	-0.0025
Bolls plant^{-1}	-0.1555	0.0366	0.8172	-0.2073	-0.4560	-0.0708	0.2107	0.0791
Boll weight	-0.0110	0.0024	-0.0678	0.0175	0.0465	0.0002	-0.0017	0.9964
Ginning outturn (%)	-0.9359	0.3111	-0.1439	-0.0076	0.0645	0.0106	-0.0420	-0.0238
Seed index	-0.0465	-0.0470	-0.1037	0.8400	-0.5061	0.0751	0.1321	0.0016

Seed cotton yield plant^{-1}	-0.0064	0.0025	-0.0105	-0.0327	0.2339	0.6422	0.7290	-0.0100
Staple length	-0.0051	0.0174	-0.0508	0.1176	0.2466	-0.7565	0.5915	-0.0160
Percent of variance	90.6	8.4	0.5	0.4	0.1	0.0	0.0	0.0
Cumulative percent of variance	90.6	99.0	99.5	99.9	100.0	100.0	100.0	100.0

Heritability estimates in broad sense: The heritability estimates (h^2) in broad sense, genetic variance (σ^2g), phenotypic variance (σ^2p) and environment variance (σ^2e) derived from variance components for various traits are depicted in Table 5. The genetic variance ($\sigma^2g = 107.37$) and the phenotypic variance ($\sigma^2p = 108.15$) with regard to plant height are about equal in expression, which resulted in highest heritability estimates ($h^2 = 99$ %). Thus, high broad sense estimates are attributable to more genetic variance and less environmental variance ($\sigma^2e = 0.78$) for plant height. In case of sympodial branches plant^{-1}, genetic variance ($\sigma^2g = 3.33$) was almost equal to phenotypic variance ($\sigma^2p = 3.83$), thus high heritability estimates ($h^2 = 86.77$ %) was achieved. High broad sense heritability estimate is likely due to less environmental variance ($\sigma^2e = 0.50$) against genetic variance for sympodial branches plant^{-1}. Bolls plant^{-1} expressed modest differences in genetic ($\sigma^2g = 16.49$) and phenotypic variances ($\sigma^2p=18.44$), hence manifested higher heritability estimate ($h^2 = 89.00$ %) for this character. High broad sense estimates resulted due to less environmental variance ($\sigma^2e =1.95$) against higher genetic effects on bolls plant^{-1}. For the boll weight character, the genetic variances ($\sigma^2g = 0.08$) and phenotypic variances ($\sigma^2p=0.085$) were at par in magnitude, which resulted in highest heritability ($h^2=93.78\%$). Higher broad sense heritability estimates could be due to smaller environmental variance ($\sigma^2e = 0.005$) as compared to phenotypic variance for bolls plant^{-1}. For ginning outturn %, the genetic variance ($\sigma^2g = 2.86$) was less than phenotypic variance ($\sigma^2p=4.30$), hence moderate heritability ($h^2=66.51\%$) was reported. While comparing the genetic variance with environmental variance ($\sigma^2e = 1.44$), it seems that genetic variance ($\sigma^2g = 2.86$) was about twice greater than the environmental variance. Such results ended-up in moderate heritability estimates. For seed index, the genetic variance was $\sigma^2g = 0.075$ and phenotypic variance was $\sigma^2p = 0.29$ which indicated that there is a lot of difference in both the variance parameters. Heritability estimates therefore was low (h^2 25.58%), may be due to higher differences between genetic and environmental variances.

Seed cotton yield plant^{-1} manifested higher genetic variance ($\sigma^2g = 525.87$) which was very close to its phenotypic variance ($\sigma^2p = 552.95$), as a consequence, highest heritability ($h^2 = 95.10$ %) was achieved from seed cotton yield plant $^{-1}$. High broad sense estimates indicated that environmental effects ($\sigma^2e = 27.08$) on seed cotton yield plant^{-1} were quite small. Staple length manifested fair amount of genetic variance ($\sigma^2g = 0.39$) as compared to relevant phenotypic variance ($\sigma^2p = 0.624$), as a result high heritability ($h^2 = 62.40$ %) was obtained for staple length. Higher broad sense estimates suggested that environmental effect ($\sigma^2e = 0.234$) on staple length was quite small against genetic variance.

In present studies, high heritability estimates in broad sense were observed for plant height, sympodial branches plant^{-1}, bolls plant^{-1}, boll weight, ginning outturn %, seed cotton yield plant^{-1} and staple length, whereas low heritability was found for only seed index. High heritability values in present studies for these traits indicated that the variation observed in plant traits was mainly under genetic control and less influenced by the environ-mental conditions reflecting the involvement of additive gene action for such traits. Hence, the improvement of traits under study can be made through direct phenotypic selection. Present results are in consonance with those obtained by Abbas *et al*., (2013), Dhivya *et al*., (2014) and Farooq *et al*., (2013).

Table – 5: Heritability estimates for various traits in upland cotton

Characters	**Genotypic variance (σ^2g)**	**Phenotypic variance (σ^2p)**	**Environment variance (σ^2e)**	**Heritability % (b.s.)**
Plant height	107.37	108.15	0.78	99.00
Sympodial plant^{-1}	3.33	3.83	0.50	86.77
Bolls plant^{-1}	16.49	18.44	1.95	89.00
Boll weight	0.08	0.085	0.005	93.78
Ginning outturn (%)	2.86	4.30	1.44	66.51
Seed index	0.075	0.29	0.215	25.58
Seed cotton yield plant^{-1}	525.87	552.95	27.08	95.10
Staple length	0.39	0.624	0.234	62.40

Correlation coefficient (r): Correlation of seed cotton yield, its contributing components and fibre traits are very important for determining suitable selection criteria required for the improvement of seed cotton yields in upland cotton and such data are presented in Table 6. Simple correlation coefficient (r) between seed cotton yield and fibre quality traits of fifteen cotton genotypes revealed that plant height displayed positive correlations with sympodial branches plant^{-1}, bolls plant^{-1}, boll weight, GOT (%) and with seed cotton yield plant^{-1}, while sympodial branches plant^{-1} was significantly and positively correlated with bolls plant^{-1}, boll weight, GOT %, and seed cotton yield plant^{-1}. The correlations of bolls plant^{-1} with boll weight, GOT %, and seed cotton yield plant^{-1} were highly significant and positive. Boll weight also exhibited significant and positive association correlation with GOT %, seed index and seed cotton yield plant^{-1}. Significant and positive relationship between ginning outturn % and seed cotton yield plant^{-1} was also noted. The correlation between seed index and staple length was significant but negatively correlated with each other. Like our results, significant and positive associations between yield and fibre quality traits were already reported by previous researchers like Ashok *et al.*, (2010) and Baloch *et al.*, (2014a).

Table-6: Correlation coefficient (r) between seed cotton yield and fibre traits in upland cotton

Characters	Plant height (cm)	Sympodial branches plant^{-1}	Number of bolls plant^{-1}	Boll weight (g)	Ginning outturn (GOT %)	Seed index (g)	Staple length (mm)
Sympodial branches plant^{-1}	0.6029**						
Bolls plant^{-1}	0.5951**	0.6672**					
Boll weight(g)	0.6041**	0.4185**	0.6308**				
GOT (%)	0.5088**	0.4994**	0.3809*	0.5113**			
Seed index (g)	0.1785^{ns}	0.2041^{ns}	0.2656^{ns}	0.2774*	0.1066^{ns}		
Staple length (mm)	0.014^{ns}	0.0693^{ns}	0.1285^{ns}	0.2337^{ns}	0.1308^{ns}	-0.2804*	
Seed cotton yield plant^{-1} (g)	0.6395**	0.5976**	0.9151**	0.8866**	0.4851**	0.3015^{ns}	0.1952^{ns}

**= Highly significant at 1% probability level, *= Significant at 5% probability level, ns= Non-significant

Conclusion

The results of present study indicated the existence of genetic diversity among the upland cotton genotypes. Higher heritability estimates were found in almost all the characters. Correlation coefficients showed significant and positive associations between major yield and fibre traits with seed cotton yield. Parents from divergent clusters can be used for hybridization programmes to isolate useful recombinants for segregating generations.

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