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Assessment of genetic diversity among upland cotton for earliness, fiber quality and yield-related traits using correlation, principal component and cluster analysis

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ABSTRACT

I A field experiment was conducted at Cotton Research Farm, Gazipur in *Kharif* season 2017 with 100 genotypes to evaluate their genetic diversity. The results of the study showed a significant positive link between the number of bolls and seed cotton output, as well as between maturity and boll split. Cluster analysis, Principal Component Analysis (PCA), and correlation were used to categorize the major characters that account for the variation in yield contributing traits. Data were recorded at maturity, bolls plant^{-1}, seed cotton yield, ginning outturn, fiber length and fiber strength. The first four PCs with Eigen value >1 contributed 65.15% variability among the cotton accessions. The genotypes were grouped into ten clusters through multivariate analysis. Cluster III contained a maximum number of genotypes (29) while clusters I (15), II (9), IV (23) and V (13) contained genotypes, cluster VII (4), VI, VIII and X contained genotypes (2) and cluster IX contained only 1 genotype. In all cases, the inter-cluster distances were greater than those of intra-cluster distances, which indicate a wider genetic diversity among the genotypes. Cluster I and IX had the largest inter-cluster distance (35.13), while cluster VI and VIII had the smallest (1.68)-. The results revealed a diverse and close relationship among the genotypes of those clusters. The single boll weight and days to boll split showed a higher contribution to the genetic divergence among 14 characters. Based on genetic diversity results and early-maturity, VII (BC-0451, BC-0456, BC-0491 and BC-0495), VIII (SR-16), IX (BC-0479) and X (BC-0493 and BC-0459) genotypes could be used to develop the short-term cotton variety as following the standard procedure.

Keywords: Cotton (*Gossypium hirsutum L.*), earliness, genetic diversity, GOT, yield.

INTRODUCTION: Cotton is the important cash crop that provides fiber, oil and fuel wood and contributes a major part of income for farmers around the world. More than 150 countries of the world are growing cotton in tropical and subtropical regions (Nawaz et al., 2019 and CEG, 2020). Cotton is classified in the genus *Gossypium*, which according to (Fryxell, 1979) and (Poehlman, 1987) contains 39 species, of which, 33 are diploid and 6 are tetraploid species. There are seven genomes for the diploid species (2n = 2x = 26): A, B, C, D, E, F, and G. The species with the A, B, E, or F genomes are African or Asian in origin and often are referred to as Old World species; the species with the C or G genomes are Australian in origin; the species containing the D genome are New World species, having originated in the Americas. Though primarily found in Mexico, the American diploid species grows wild from Arizona to Peru. The chromosomes of the American diploid species are smaller than the chromosomes of the African and Asian species. Five tetraploid species (2n = 2x = 52) are native to the Americas, while one is found only in Hawaii. They originated as allotetraploids with the AADD genome combination and have 26 small and 26 large chromosomes. Through the use of colchicine to double the chromosome count of the sterile hybrid created by crossing G. arboreum (A genome, 2n = 26) x G. thurberi (D genome, 2n = 26), the origin was experimentally proven. It is possible to cross American tetraploid cottons with the resultant amphidiploid (AADD, 2n = 52) to get fertile hybrid trees. There is a high degree of chromosome homology among most species with the same chromosome number and from the same geographic area. The fact that homology is not complete indicates a certain degree of differentiation in the chromosome complement. Four species of *Gossypium* with spinnable seed fibers, called lint, have been domesticated and form the cultivated cottons. The Gossypium herbaceum species, which originated in the Middle East and may have been the first cotton to be grown, are comprised of two diploid species, G. arboreum L. and G. herbaceum L., and two tetraploid species, G. hirsutum L. and G. barbadense L. It was carried to India, where it became the progenitor of *G. arboreum*. *Gossypium arboreum* is widely cultivated in India, although it is being replaced by *G. hirsutum* introduced from America.

Bangladesh's textile industry uses cotton as its primary raw material. Cotton is a long-duration crop that is cultivated in Bangladesh from July to February as a single crop. Due to the longer duration (6–7 months), cotton can't be fixed in the existing cropping patterns. By increasing the amount of cotton acreage, short duration cotton cultivars would increase production. Earliness characters is a basic breeding objective in upland cotton (Egamberdiev, 1996; Braden and Smith, 2004). Therefore, cotton cultivation is being pushed to the marginal lands only. If the duration of cotton can be reduced to some extent, the crop can be fitted in the three crops based cropping pattern.

Earliness characters in cotton can escape yield losses due to the seasonal threat of biotic and abiotic stresses and also increase economic return by reducing input costs like fertilizer, irrigation and labour (Ali et al., 2003). So, development of short duration cotton varieties is necessary for the interest of the farmers and that it can also increase cotton yield and production. Cotton earliness is a qualitative trait and it depends on its genetic characters (Kassianenko et al., 2003). Earliness in cotton was determined by different plant characteristics. According to (Ahmad et al., 2008 and Baloch et al., 2014) one node decrease in the cotton crop is expected to bring in the cotton crop about 4 to 7 days early. Several other studies reported a strong connection between early maturity and low sympodial branch node numbers with effective boll (Kerby et al., 1990; Kairon and Singh, 1996 and Baloch and Baloch, 2004).

Genetic variation serves as the foundation for the creation of new varieties. A better understanding for the diversity of genetics will help the hybridization program select various parents. Consequently, cotton genotypes must be differentiated by statistical instruments and used in the breeding program. The genotypes of cultivated cotton have a small genetic basis (Abdukarimov et al., 2003 and McCarty et al., 2005). The quantity of genetic differences among available germplasms is an essential and important goal in plant breeding to specialize in the genetic base through the breeding program. For the intelligent utilization of germplasm especially among closely related genotypes, information on genetic diversity is crucial (Govindaraj et al., 2015). The successful breeding program depends on the inclusive knowledge and knowledge of the genetic diversity of the existing germplasm within the élite genetic materials. It allows plant breeders to identify promising genotypes as parental sources which generate diverse populations in order to select and develop enhanced cotton species (Akter et al., 2019).

OBJECTIVE: In light of the above, the current study aimed to assess the genetic diversity of short-duration genotypes of cotton using various early-cotton plant features.

MATERIAL AND METHODS: Plant materials: One hundred cotton genotypes having wider adaptability were examined in the field conditions. The cotton seed were collected from germplasm center, cotton research station, Mahignj, Rangpur, Bangladesh.

Experimental sites: The field experiment was carried out during *Kharif* season in 2017 at the Central Cotton Research, Training and Seed Multiplication Farm, Sreepur, Gazipur, Bangladesh which is geographically situated 24.09^{0}N latitude and 90.26^{0}E longitudes with an elevation of 8.4 meters above the sea level.

Soil status of the experimental fields: The Salna series soil at the experimental site is categorized as Shallow Red-Brown Terrace type, which is based on the order inceptions of soil taxonomy (Brammer, 1978 and FAO, 1988). The loam or clay loam soils that are found over the deeper clay horizons are what define the soils as more or less consistent. The soil's pH is 6.2, with organic matter at

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0.81%, N at 0.40%, K at 0.42 meq, Ca at 1.00 meq, and Mg at 1.50 meq per 100 g. In addition, the soil has 0.55 µg B g-1, 1.92 µg Zn, 31.50 µg P, and 11.60 µg P.

Experimental design: The experiment was run using three replications of the Randomized Complete Block Design (RCBD). The unit plot size was 7.2 m× 1.8 m, where line to line distance was 90 cm and plant to plant distance was 45 cm. Each replication contained 100 genotypes in each plot and a total number of plots were 300. There was 1 m distance between two adjacent plots and 2 m space between two adjacent replications.

Field preparation and seed sowing: The field selected for conducting the experiment was opened at 5 July, 2017 with a tractor and left exposed to the sun for a week. The ground was harrowed, ploughed, and cross-ploughed multiple times within a week, and then laddered to achieve a good soil tilth. Weeds and stubbles were removed. The experimental plot was partitioned into unit blocks and each block into unit plots in accordance with the design of the experiment. The seeds of cotton were defuzzed and treated with Actara @ 5 g kg^{-1} seed and sown @ 2-3 seeds $hill^{-1}$ on 18 July, 2017 in furrows maintaining the row to row spacing of 90 cm and hill to hill spacing of 45 cm. Seeds were placed in pit to a depth of 4-5 cm and then covered with loose soil.

Application of manure and fertilizers: The amount of 260, 266, 316, 100, 22 and 22 kg urea, triple super phosphate, muriate of potash, gypsum, zinc sulphate, magnesium sulphate and borax were applied per hectare of land, respectively. During the last stage of land preparation, all fertilizers were applied, with the exception of urea and muriate of potash. Urea and muriate of potash was applied in basal and three installments at 20, 40 and 60 DAS. Final soil preparation also included the application of 10 t ha^{-1} of well-decomposed cow manure.

Investigation of Agronomic Parameters: For the measurements of the traits, five representative plants were selected randomly from each genotype and later they marked with labels for recognition. Genotypes were estimated for days to 50% squaring (DS), days to 50% flowering (DF), plant height (PH), main stem node of the first fruiting branch (NFB), sympodial branches $plant^{-1}$(PFB), days to boll split (DBS), number of bolls $plant^{-1}$ (NB), single boll weight (SBW), ginning out turn (GOT%), maturity (MD), seed cotton yield (SCY) and also observed lint quality as fiber length (FL), fiber strength(FS) and micronaire were calibrated through Spain lab by using MAGHVI-1401 machine.

Data analysis: The collected data were statistically analyzed; Analysis of variance (ANOVA) for each of the characters was performed with the help of the computer package RStudio. The mean square at the error and phenotypic variance were estimated as Johnson et al. (1955). Mean data for each character were subject to multivariate analysis method viz. Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Canonical Variate Analysis (CVA), and Cluster Analysis (CLSA) were performed using K means clustering. The main components of the correlation matrix and genotypic scores obtained for the first component and subsequent with latent roots greater than uniformity (Jeger et al., 1983). Principal Coordinate Analysis calculated for the inter distances between genotypes (Digby et al., 1989). The clustering was done using hierarchical classification. The computation of average intra-cluster distance for each cluster was calculated by taking possible D^2 values within the members of a cluster obtained from the PCO after the clusters were formed. The formula utilized was $\sum \frac{D2}{n}$, where $\sum D2$ is the sum of distances between all possible combinations (n) of the genotypes included in a cluster. The square root of the average D^2 values represents the distance (D) within the cluster.

RESULTS AND DISCUSSIONS: Analysis of variance (ANOVA): The mean performance of 100 cotton genotypes for different agronomic traits related to seed cotton yield, earliness and lint quality were presented in table 1. The results revealed that the genotypes significantly differ for all the characters studied except GOT%. The results showed significant differences among the genotypes for germination (%), plant height (cm), node number bearing first fruiting branch (NFB), number of primary fruiting branches $plant^{-1}$, Days to 50% squaring, days to 50% flowering, days to boll split, number of bolls $plant^{-1}$, single boll weight (g), days to maturity, fiber length (mm), fiber strength (g tex^{-1}) and seed cotton yield (t ha^{-1}). Cotton earliness is a complex quantitative trait that depends on the interaction between genetic and physiological plant systems with environmental conditions (Kassianenko *et al.*, 2003). The development of early maturing cotton varieties at the moment has become one of the important objectives of cotton breeders because of many reasons, such as short duration cotton cultivars can avoid yield losses that happen due to diseases, insect-pest (particularly bollworms) unfavorable and weather conditions (Singh, 2004). Early maturing cotton cultivars have the advantage of being able to rotate other crops so that wheat can be sowed in a timely way through the cultivation system in different countries (Ali *et al.*, 2003). Delayed cotton maturity also leads to poor quality of fiber (Salam *et al.*, 1993). Moreover, the short duration of cotton genotypes is economical regarding the cost of production because early maturing cultivars evade biotic and abiotic risks (Anderson *et al.*, 1976 and Anjum *et al.*, 2001).

Correlation investigation: The primary statistics of the features showed sufficient variability between 100 cotton genotypes. The data of the simple coefficient of correlation showed positive affiliation between the features analyzed (table 2). The matrix showed positive correlations in sky-blue and negative associations in red. Correlation coefficients are reflected in the color intensity and circle size. In the meantime, the diagram shows the fables color for different associations on the other right of the correlation (figure 1). Boll weight showed a positive relationship with the node number of the first fruiting branch and a positive significant association with seed cotton yield. However, other parameters that demonstrate bolls number was detected to an extreme positive association with seed cotton yield while negative association with GOT. Primary fruiting branches $plant^{-1}$ showed a positive association with bolls $plant^{-1}$ and seed cotton yield while exhibited a negative correlation with NFB. Days to boll split was highly positively associated with maturity and negative with GOT. Days to flowering displayed a strong positive correlation with days to squaring but a negative association with GOT. The study showed a significant negative correlation with cottonseed yield plant-1, a strong positive correlation with the number of bolls plant-1 and cotton seed yield, and a positive significant correlation between the lint index and staple length and fiber strength (Jarwar *et al.*, 2019).

Cluster Analysis for Yield Contributing Traits: The cluster analysis grouped the 100 cotton types into 10 clusters based on various features and variability levels (table 2). Clusters 1-10 comprised 15, 9, 29, 23, 13, 2, 4, 2, 1 and 2 genotypes, respectively. The genotypes in cluster 1 had higher values compared to all other clusters for days to boll split and maturity in this study. Members of clusters 2 and 3 had shown none of any important characters. The members of clusters 4 and 5 showed the highest ginning out turn and maximum days to flowering, respectively but otherwise showed an overall poor performance in terms of days to emergence and seed cotton yield. Cluster 6 consisted of genotypes that had maximum days to squaring and flowering and highest primary fruiting branches $plant^{-1}$. Cluster 7 showed the highest mean values for the number of vegetative branches $plant^{-1}$, minimum boll weight. Cluster 8 showed maximum mean values for secondary fruiting branches $plant^{-1}$. Members of cluster 9 showed the best value for bolls $plant^{-1}$, the highest seed cotton yield but the minimum days to squaring, flowering, boll opening and days to maturity also showed the minimum number of NFB, vegetative branches $plant^{-1}$. In cluster 10 had shown the lowest number of bolls $plant^{-1}$, primary fruiting branches $plant^{-1}$. In order to estimate the genetic variation present among all studied clusters dendrogram (hierarchical cluster) was constructed (figure 2).

Cluster dendrogram showed a wide variation between the genetic variables between genotypes. Based on the cluster and cluster dendrogram analyses, the members of Cluster 9 the genotype BC-0479 are recommended to high yielding earliness cotton genotypes. Those statistical instruments could also be used to identify other potential sources, such as the testing of bread wheat to detect resistance to stem rust in wheat (Nzuve *et al.*, 2012). A lack of connections between various clusters based on agronomic traits and genotype origins in peas (*Pisumsativum*) and mustard (*Brassicajuncea*), respectively, has been noted in Amurrio *et al.* (1995) and Rabbani *et al.* (1998). Similarly, large changes were reported in clusters (Nazir *et al.*, 2013). The large variation between the clusters is of considerable genetic value when it comes to selecting cotton to adapt to CLCuD hit areas. A similar type of results has been reported for germplasm grouping (Ayana and Bekele, 1999 and Grenier *et al.*, 2001).

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CV	DF	GER	PH	NFB	PFB	DS	DF	DBS	NB	SBW	GOT	MD	FL	FS	SCY
Rep	2	685.33	74.86	0.11	30.41	43.01	45.57	101.96	53.17	0.96	1.86	81.50	9.06	23.29	0.18
Gen	99	34.51**	94.49**	0.30**	1.14*	5.14**	6.21*	62.25**	12.23**	0.48**	4.48ns	101.33**	3.96**	1.73**	0.36**
Error	198	5.37	53.70	0.19	0.84	0.67	4.59	39.63	7.33	0.21	4.37	6.61	0.7	0.04	0.06

Table 1: Mean square for various earliness and yield contributing traits in cotton genotypes.
, * indicates significant at 1% and 5% level of significant respectively, ***ns* not significant
CV= Coefficient of variance, DF= Degree of freedom, GER= germination, PH= Plant height at harvest, NFB= Number of node bearing first fruiting branch, PFB= Primary fruiting branches, DS= Days to squaring, DF= Days to flowering, DBS= Days to boll split, NB= Number of boll plant^{-1}, SBW= Single boll weight (g), GOT= ginning out turn, DM= Days to maturity, FL= fiber length, FS= fiber strength and SCY= Seed cotton yield (t ha^{-1}).

Characters	Clusters									
	1	2	3	4	5	6	7	8	9	10
DE	**5.24**	4.83	4.73	**4.00**	4.40	5.00	5.00	4.50	4.00	4.00
GER	80.24	81.78	83.31	89.20	81.50	83.00	**79.00**	83.43	90.00	**95.00**
DS	44.47	43.65	43.35	42.20	44.80	**45.00**	40.00	43.43	**39.00**	41.00
DF	59.94	58.65	58.35	57.20	**60.00**	**60.00**	52.00	58.43	**51.00**	55.00
NB	27.25	26.26	24.35	29.55	26.02	26.74	23.77	25.33	**32.00**	**23.33**
DBS	**112.51**	106.45	104.33	100.87	108.70	107.50	100.00	103.98	**96.67**	100.00
NFB	5.35	4.94	5.21	5.13	4.82	4.70	5.47	5.41	**4.33**	**5.53**
VB	1.59	1.54	1.04	1.16	1.73	1.00	**1.87**	0.78	**0.73**	0.93
PFB	14.16	14.08	13.65	13.85	13.88	**15.44**	13.93	14.42	13.93	**13.00**
SFB	**4.53**	4.33	2.68	2.51	4.43	3.37	3.67	**1.85**	2.83	3.67
BW	5.43	5.64	5.48	**5.82**	4.96	5.42	**4.60**	5.80	5.23	5.73
GOT	**38.89**	39.84	41.12	**41.64**	39.58	41.13	40.90	40.14	41.01	39.13
MD	**193.49**	186.71	182.42	175.47	188.30	185.17	187.33	183.52	**165.00**	177.67
SCY	3.56	3.54	3.11	3.61	**2.99**	3.55	3.30	3.57	**3.87**	3.13

Table 2. Cluster mean for 14 characters in 100 cotton genotypes.
DE= Days to emergence, GP= Germination percentage, DS= Days to squaring, DF= Days to flowering, PHH= Plant height at harvest, NB= Number of bolls plant^{-1}, DBS= Days to bolls split, NFB= Main stem node of first fruiting branch, VB= Vegetative branches plant^{-1}, PFB= Primary fruiting branches plant^{-1}, SFB= Secondary fruiting branches plant^{-1}, BW= Boll weight(g), GOT= Ginning out turn, MD= Days to maturity, SCY= Seed cotton yield (t ha^{-1}).

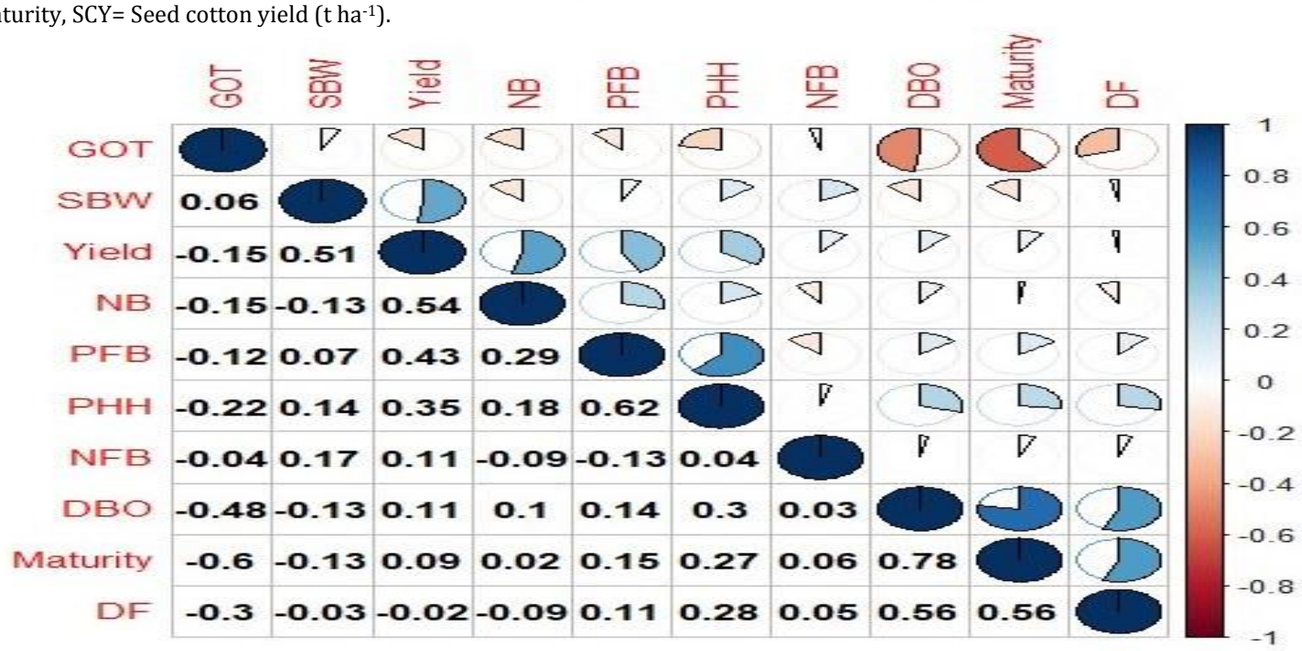

Figure 1: Correlation matrix showing characters correlation with each other. A positive correlation is shown in blue and negative correlations in shown in red color. The color intensiveness and the size of the circle are relatively proportional to the correlation.

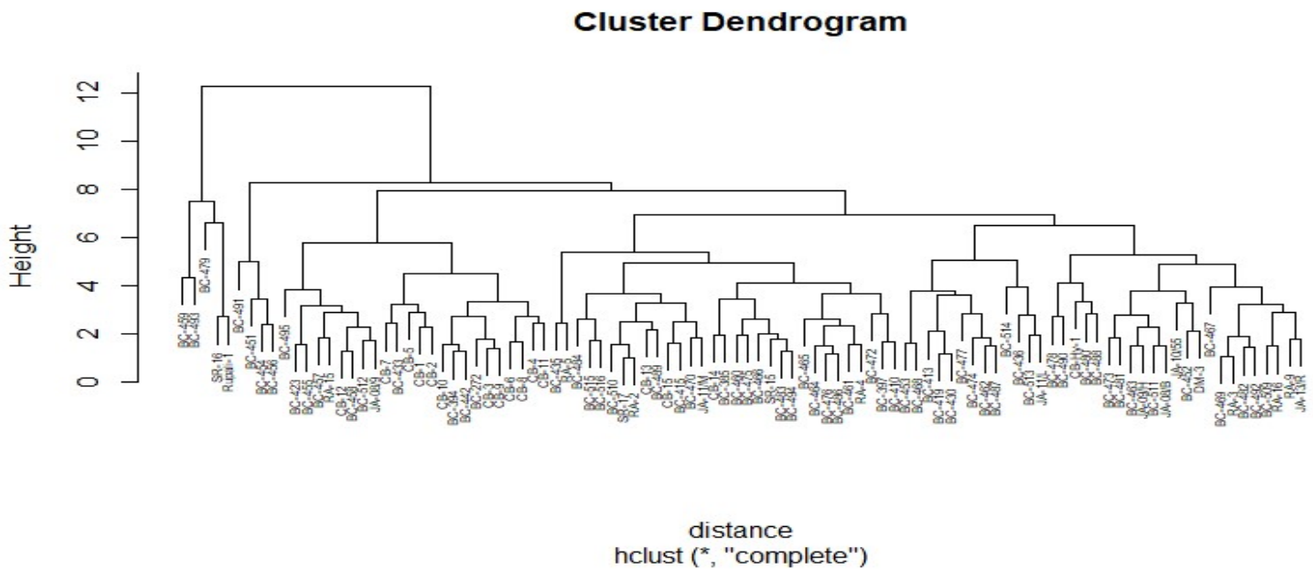

Figure 2: A hierarchical cluster dendrogram showing the position of genotypes within distance in different clusters.

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Principal component analysis (PCA): The principal component analysis (PCA) provided Eigen values and percent for 14 principal component axes in 100 cotton genotypes (table 3). The results showed that, the first four principal components accounted for 65.15 % of the total variation among 14 component axes of the total genotypes, whereas the Eigen values were found as 84.68% in the first seven component axes. As depicted in the PC biplot, the genotypes and variables were placed on the plot as vectors (figure 3).

Principal component axes	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14
Standard deviation	1.99	1.49	1.27	1.15	1.05	0.92	0.88	0.79	0.67	0.60	0.57	0.44	0.39	0.22
Total variance (%)	28.20	15.88	11.60	9.46	7.93	6.04	5.57	4.46	3.16	2.58	2.31	1.38	1.08	0.33
Cumulative variance (%)	28.2	44.09	55.68	65.15	73.08	79.11	84.68	89.15	92.31	94.89	97.20	98.58	99.67	100
Factor loadings by various traits														
Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14
Germination (%)	0.30	0.09	0.11	-0.12	0.05	-0.25	0.63	-0.50	0.25	-0.08	0.29	-0.07	0.05	0.02
Days to squaring	-0.39	-0.19	-0.20	-0.06	0.29	-0.09	0.33	0.14	-0.19	-0.07	-0.02	-0.03	0.12	0.70
Days to flowering	-0.39	-0.16	-0.20	-0.14	0.29	-0.11	0.35	0.14	-0.18	-0.05	0.02	0.05	-0.07	-0.70
Plant height at harvest	-0.26	0.35	0.13	-0.07	0.36	-0.21	-0.29	-0.18	-0.08	0.59	0.34	-0.18	0.06	0.01
Number of bolls	-0.06	0.40	0.00	0.47	-0.30	-0.25	0.30	0.34	-0.11	0.11	0.14	0.06	-0.46	0.06
Days to boll opening	-0.42	-0.06	-0.06	0.05	-0.18	0.03	-0.04	-0.01	0.62	0.08	0.23	0.56	0.14	0.02
NFB	-0.01	0.03	-0.16	-0.53	-0.35	-0.66	-0.26	0.06	-0.11	-0.20	0.06	0.06	-0.04	0.04
Sympodial branches/plant	-0.17	0.43	0.14	0.14	0.40	-0.14	-0.18	-0.27	0.06	-0.54	-0.32	0.22	-0.15	0.02
Boll weight	0.05	0.33	-0.14	-0.60	0.05	0.46	0.13	0.04	0.05	0.13	-0.06	0.16	-0.46	0.11
GOT	0.32	-0.02	-0.16	-0.01	0.45	-0.11	-0.14	0.52	0.45	-0.19	0.28	-0.20	-0.08	0.01
Maturity	-0.43	-0.09	0.01	-0.01	-0.23	0.06	-0.04	-0.16	0.37	-0.12	-0.09	-0.69	-0.31	0.00
Length	0.00	-0.12	0.64	-0.19	0.08	-0.24	0.17	0.29	0.23	0.27	-0.48	0.04	-0.01	0.01
Strength	-0.17	-0.03	0.62	-0.15	-0.07	0.23	-0.02	0.17	-0.22	-0.38	0.54	0.00	0.01	0.01
Yield	-0.10	0.58	-0.08	-0.11	-0.18	0.12	0.17	0.27	0.08	-0.10	-0.13	-0.23	0.63	-0.09

Table 3: Eigen values and percentage of variation for 14 principal component axes in 100 genotypes.

Cluster group	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**7.78**									
II	3.06	**7.10**								
III	4.71	2.46	**6.71**							
IV	8.68	5.57	3.75	**8.98**						
V	12.92	7.00	4.32	4.98	**9.08**					
VI	9.35	3.44	2.45	2.06	2.85	**6.49**				
VII	15.43	9.28	7.94	7.52	4.64	5.00	**11.74**			
VIII	11.29	5.68	2.87	1.74	3.33	**1.68**	3.49	**6.83**		
IX	**35.13**	29.49	25.20	23.31	19.27	23.82	16.52	20.40	**0.00**	
X	22.16	16.35	12.65	10.87	6.81	10.88	5.03	8.77	9.94	**9.26**

Table 4: Average intra and inter cluster distances (D2) values for 100 cotton genotypes.

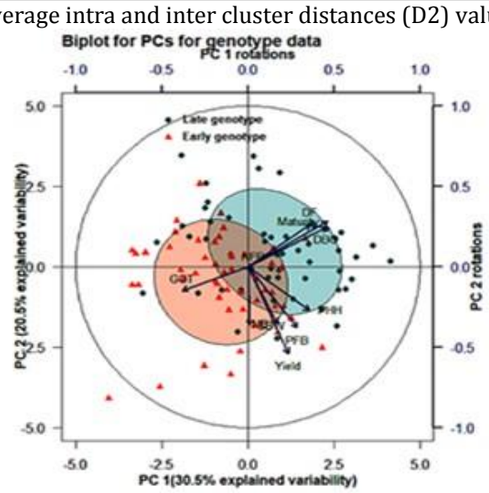

Figure 3: Biplot between PC1 and PC2 showed involvement of different traits in variability.

GP= Germination (%), NFB= Node number of first fruiting branches, PH= Plant height, DF= Days to flowering, NB= Number of bolls plant^{-1}, DBS= Days to boll split, SBW= Single boll weight, GOT= Ginning out turn percentage.

The respective variable distances from PC1 (30.5%) and PC2 (20.5%) elaborated the contribution of different variables towards variability. The early characteristics and yield of the biplot showed the maximum contribution to variability. The biplot showed the extent to which parameters are correlated. Days to flowering, days to boll split, maturity and yield showed a positive correlation with each other while the negative correlation with GOT. While pant height, primary fruiting branches plant^{-1}, NFB and single boll weights were correlated with each other. As illustrated in the biplot and score plot (figures 3), the genotypes BC-0459, BC-0479, BC-0495, CB-hybrid-1 and Rupali-1 have good potential for, days to first square, days to the first flower and days to first boll split. Principal components accounted for 65.15 % of the total variation of the total genotypes, whereas the Eigenvalues were found as 84.68% in the first seven component axes. The respective variable distances from PC1 (30.5%) and PC2 (20.5%) elaborated the contribution of different variables towards variability. Saeed *et al.* (2014) reported that the main contribution of the first two components in different cotton strains.

Canonical variate analysis (CVA): Table 4 displays the intra- and inter-cluster distances (D2) values for 100 cotton genotypes organized into 10 clusters. The greater distance between inter and intra cluster, greater the variability between genotypes and within the class and vice versa. The results obtained from the present study indicated that the inter-cluster distances were larger than intra-cluster distances in all cases, suggested wider genetic diversity among the genotypes of different groups. The Maximum inter-cluster distance was observed between cluster I and IX (35.13) followed by cluster II and IX (29.49) and III and IX (25.20). The maximum inter-cluster distance indicated that the genotypes in these clusters were far diverse than those of other clusters. The minimum inter-cluster distance was observed between clusters VI and VIII (1.68) indicating a close relation distance among the genotypes of those clusters. The highest intra-cluster distance was found in cluster VII (11.74) followed by cluster X (9.26). The lowest intra-cluster distance was noticed for cluster IX (0.0). These results revealed that the genotype in cluster IX (BC-0479) was distantly related and this genotype could be used in a varietal performance. The Maximum inter-cluster distance was observed between cluster I and IX (35.13) and minimum inter-cluster distance was observed between clusters VI and VIII (1.68) indicating a close relation distance among the genotypes of those clusters. The highest intra-cluster distance was found in cluster VII (11.74) and the lowest intra-cluster distance was noticed for cluster IX (0.0). These results revealed that the genotype in cluster IX (BC-0479) was distantly related and this genotype could be used in a varietal performance. Similarly, a result was found by Ali *et al.* (2012) and they suggested that the genotypes belonging to the distant clusters could be used in the hybridization program for obtaining a wide spectrum of variation among the segregates.

CONCLUSIONS: The study examined the short-term genetic divergence of 100 upland cotton genotypes, yield-related characteristics, and seed cotton yield based on field performance. Cluster analysis assisted in identifying superior genotypes for future use in the breeding effort, while principal component analysis revealed that 10 components played a significant impact in overall diversity. Based on cluster analysis, cluster I had the greatest number of varieties (15), cluster II had nine genotypes, and cluster

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III had the highest number of genotypes (29). In contrast, clusters IV, V, VI, and X had 23 genotypes, cluster VII had 4 genotypes, and cluster IX had only 1 genotype. Between clusters I and IX (35.13) and VI and VIII (1.68), the greatest and lowest inter-cluster distances, respectively, were measured. Genetic diversity study suggests that the genotypes from cluster VII (BC-0451, BC-0456, BC-0491 and BC-0495), VIII (SR-16), IX (BC-0479), and X (BC-0493 and BC-0459) could be employed in accordance with standards.

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