



Assessment of genetic variability in cotton (*Gossypium hirsutum* L.) genotypes

Muhammad Junaid Mari¹, Abdul Wahid Baloch¹, Shah Nawaz Mari¹, Liaquat Ali Bhutto², Naila Gandahi¹ and Amanullah Mari¹

¹Department of Plant Breeding & Genetics, SAU, Tandojam, Sindh-Pakistan

²Agriculture Research Institute, Tandojam, Pakistan

Abstract

The selection of high-yielding cotton lines is critical for the evaluation of phenotypic characteristics. For Cotton Breeders, it is always in preference to select desirable genotypes, based on the diversified characters from the available germplasm. The selected phenotypic diversity can be useful for aiding information in parental selection, adherence to this, a set of 12 advanced cotton lines were evaluated for genetic diversity at Cotton Research Institute, Tandojam during Kharif season in the year of 2020. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications while seven agronomical traits, were included in the experiment. The mean square of genotypes, was differed significantly ($P < 0.05$) for all studied traits, representing that genetic diversity exists in these cotton germplasms and can be used in further utilization. Considering the agronomic performance, the genotype of B-2 was on the top in average values including plant height (174.40 cm), bolls plant⁻¹ (42.067), seed cotton yield plant⁻¹ (139.34 g), GOT% (37.800%), and staple length (28.00 mm), hence indicating its valuable breeding resources for future cotton breeding. A Genetic Distance of 92.683 was found between B5 and B2 genotypes, which is high enough, and revealing that this pair may be used in a hybridization program for vigorous hybrid production and better selection in subsequent generations. The Variance Percentages for the first, second, and third principal components were 42.70, 23.10, and 17.20, respectively. The first three components contributed 83.00 percent of the variation for genotypes, which is high enough for the cotton crop improvements. The cotton genotypes, were divided into three categories, based on phenotypic data. The number of groups obtained, might be beneficial in generating cotton genotypes with a variety of characteristics and diversifying the Cotton Gene Pool.

Keywords: cotton, genetic variations, morphological traits, seed yield.

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Email:

marijunaid7@gmail.com

1. INTRODUCTION

Cotton (*Gossypium hirsutum* L.), commonly known as "White Gold," is a high-value fibre and cash crop that is widely produced to support the national economy by generating large amounts of foreign money¹.

Cotton is one of the most important fibre crops on the planet, and the 50 species that make up the crop have a wide range of phenotypic variation². The upland cotton is the most widely produced fibre crop, being grown in more than 80 nations and areas throughout the world. *G. hirsutum* L, is currently responsible for 95 per cent of global cotton output³. Quantifying genetic divergence among available germplasm is a precondition and a significant aim in plant breeding in order to extend the genetic base through breeding programs. For an effective utilization of germplasm, information on genetic variation, within and among closely related genotypes, is required⁴. A Genetic diversity is desired for key agricultural problems at genetic levels. Although many successful cotton cultivars have been produced from closely related parents, recent yield increases have prompted some to call for more use of alien material⁵. Variation in germplasm collections has been used to identify good genotypes for improving output. Various morphological characteristics, including fibre quality, yield component components, resistance, and seed quality, are used to determine the appropriate genotype⁶. For practical use of plant genetic resources as well as for identifying evolutionary connections, evaluation of germplasm and measurement of genetic diversity are required⁷. The accurate evaluation of the genetic diversity of good *G. hirsutum* L germplasm will give a guide for choosing parents and estimating the degree of inheritance, variation, and level of heterosis, which are critical for achieving breeding goals for cotton geneticists and breeders⁸.

The divided 21 cotton genotypes into four distinct groups. L was the most divergent genotype in a distinct 1 group (A), followed by L in the second group (B). The third cluster (C) had 15 13 genotypes and was split into five sub-clusters, whereas the fourth cluster (D) had 6 genotypes and was split into three sub-clusters. The results of field studies indicated that there was a lot of variation in yield and its components amongst the genotypes that were examined. Principle Components (PC) Analysis was used to examine the results. PC₁ had 23.8 per cent variability, PC₂ had 16.8 per cent, PC₃ had 12.3 per cent, and PC₄ had 11.9 per cent diversity across the genotypes for the characteristics studied. Four of the 10 PCs have more than one Eigenvalue. The genotypes in PC₁ had good yield and fibre characteristics, whereas the genotypes in PC₂ had desirable yield components. Furthermore, PC₃ has both yield and fibre quality characteristics⁹. The genetic diversity in a group of 26 BT-cotton genotypes for seed cotton production and characteristics. The results indicated that genotypes differed substantially by P-0.01 for all characteristics, indicating that there is significant genetic variability among genotypes that needs to be investigated further. All genotypes were split into nine tiny groups for cluster analysis, with cluster one consisting of five genotypes that were classified as high-yielding genotypes. The first three main components accounted for 75.90 per cent of overall variability, which is regarded as high and might be used in future cotton breeding efforts¹⁰. The evaluated genetic diversity in cotton genotypes and found that cluster III had the most genotypes (16) and cluster X had the fewest genotypes (1). (7). In every example, inter-cluster distances were greater than intra-cluster distances, implying that genotypes from other clusters have more genetic variety. Clusters two and five had the greatest and smallest inter-cluster distances, respectively. The genotypes of those clusters were shown to have a diverse and tight connection¹¹. The current study aims to find a superior variety in cotton lines based on diversified characters among the cotton genotypes that will be useful for further breeding programs in order to gain of high-yielding cotton varieties to overcome the low production, it is vastly being noticed that due to low production, the demand for cotton fibre is rising around the world.

2. MATERIALS AND METHODS

2.1 Studied Area

The current field experiment was done at the experimental field of Cotton Research Institute, Tandojam, during kharif season, 2020.

2.2 Samples collection

At maturity, the number of sympodial branches plant⁻¹ was counted from tagged plants. From tagged plants, the total number of opened bolls was counted and recorded as the number of productive bolls plant⁻¹. The seed cotton yield plant⁻¹ (grams) was divided by the number of productive bolls plant⁻¹ to get the boll weight plant⁻¹. Mature bolls were collected in paper bags as they reached maturity, and seed

cotton was stored separately from each plant. When the dew factor had passed, picking began after 10:00 a.m. The weight of seed cotton yield plant⁻¹ was measured with the help of an electronic balance in grams. The lint proportion in a seed cotton sample after ginning is known as ginning outturn. The samples were sun-dried before being ginned using an electric saw gin machine. The length of each plant's fibres was carefully measured in millimetres.

2.3 Experimental setup

The experimental design was put out in a randomized complete block design with three replications. Row-to-row space was 75 cm and plant-to-plant distance was preserved at 30 cm. All the necessary agronomic procedures and plant protection measures were performed to achieve healthy plants. By using a meter scale, the height of the selected plant was measured in (cm) from the surface of the soil to the tip of the main stem. Cotton buds usually arise from the leaf axils. The higher ones are referred to as axillary buds, while the lower ones are referred to as additional axillary buds. The additional axillary bud produces a fruit-bearing sympodial branch.

2.4 Analysis

The acquired data were subjected to an analysis of variance and least significant difference test using statistical computer software (Statistic Ver. 8.1). The SPSS v.21 computer program was used to perform genetic distance, principal component analysis, and cluster analysis.

3. RESULTS AND DISCUSSIONS

Results revealed that traits were significantly differences ($P < 0.05$) for all investigated parameters except seed index.

Table 1 Mean Square obtained from analysis of variances

Genotypes	Replication	Genotype	Error
Plant height	10.57	955.503**	4.53
Sympodial branches plant ⁻¹	3.02	177.46**	2.108
Bolls plant ⁻¹	0.65	157.022**	5.921
Boll weight	0.01	0.44*	0.05
Seed cotton yield plant ⁻¹	27.09	979.02**	38.59
GOT%	0.24	7.44*	0.27
Seed index	0.02	0.91*	0.01
Staple length	0.54	0.23 ^{ns}	0.24

The high and low plant height was recorded as 174.40 cm and 113.53 cm in B1 and B5, respectively, according to observation, the maximum yield decreased with the decrease of plant population and increase in plant height¹². On the same side, the other experiment proposed that additive effects playing a more important role in reducing plant height¹³, which can further facilitate for making diversified varieties in breeding programs. For sympodial branches, maximum sympodial branches were recorded in B8 (40.40) and minimum sympodial branches were recorded in B1 (19.067), followed by B3 (21.267), our findings showed variations in sympodial branches. The experiment was conducted to assess growth and yield performance in a number of varieties, the results showed that the variety having a greater number of sympodial branches performed maximum in yield and had a greater number of bolls and ginning out turn percentage¹⁴. The maximum counted bolls plant⁻¹ (43.80) were found in B11; next in rank was the genotype B2 (42.067), however, minimum bolls plant was set by B4 (25.333), followed by B12 (29.40). The research reported that the quantity of bolls plant⁻¹ is directly proportional to seed cotton yield plant⁻¹¹⁵, The seed

cotton yield tends to have a positive genotypic correlation with bolls plant⁻¹, plant height, boll weight, staple length and strength, earliness, and GOT%, with respect to our findings the variety has a maximum number of bolls can be used for breeding programs. Longer fibre length was measured in B6 (28.13 mm), followed by (27.8 mm) while the minimum was measured in genotype B1 (27.067 mm), followed by (27.8 mm). As far as the seed index is concerned, a higher seed index was obtained in B4 (8.30 g); nonetheless, a lower seed index was achieved in B2 (6.50 g).

Table 2. Mean Performance Analysis

Genotypes	Plant height (cm)	Sympodial branches plant ⁻¹	Bolls plant ⁻¹	Boll weight (g)	Seed cotton yield plant ⁻¹ (g)	GOT%	Seed index (100-seed weight, g)	Staple length (mm)
B1	122.47 de	19.067 f	20.600 e	4.0400 a	97.02 ef	36.773 bc	6.9667 ef	27.067 b
B2	174.40 a	31.867 c	42.067 a	3.3200 b	139.34 a	37.800 a	6.5067 h	28.000 a
B3	124.93 cd	21.267 ef	35.533 b	3.0133 bcd	106.49 de	36.560 c	8.1067 b	27.600 ab
B4	120.13 e	19.400 ef	25.333 d	3.2733 bc	82.05 h	37.493 ab	8.3000 a	27.767 ab
B5	113.53 f	21.800 de	30.867 c	2.7267 de	83.47 gh	36.527 c	7.2267 d	27.600 ab
B6	108.47 g	19.933 ef	30.200 c	2.9300 cde	88.00 fgh	36.913 abc	7.0100 ef	28.133 a
B7	128.07 c	31.067 c	36.600 b	2.5733 e	92.90 fg	37.567 ab	6.8867 fg	27.600 ab
B8	142.13 b	40.400 a	43.200 a	2.9200 cde	125.94 b	37.780 a	6.7733 g	28.000 a
B9	106.33 g	18.867 f	30.000 c	3.0733 bcd	91.71 fgh	37.660 ab	6.8867 fg	27.667 ab
B10	128.53 c	32.667 c	36.467 b	3.0933 bcd	112.21 cd	35.033 d	7.1200 de	27.767 ab
B11	127.33 c	36.800 b	43.800 a	2.7800 de	120.74 bc	33.880 e	7.6000 c	27.933 a
B12	127.47 c	23.800 d	29.400 cd	3.3600 b	98.39 ef	33.140 e	7.7133 c	27.800 ab

The data matrix of tested characters is formed on the basis of Euclidean genetic distance calculations. Genetic distance values for all 66 pairwise comparisons of the 12 upland cotton genotypes. A higher genetic distance was observed between B5 and B2 which was 92.683, followed by B9 and B2 (89.701), B4 and B2 (89.967), B2 and B1 (81.446), B12 and B2 (67.045), B6 and B2 (65.823), B3 and B2 (64.717) and B8 and B5 (60.782), B10 and B2 (59.968), B8 and B6 (57.179), B9 and B8 (56.918), B8 and B1 (54.010), B11 and B2 (51.495), B8 and B4 (51.629). However, the minimum or less genetic distance was observed between B6 and B5 (7.233), followed by B9 and B6 (7.710), B10 and B7 (10.843) and B12 and B7 (11.047), B10 and B3 (11.586), B6 and B4 (11.607) B5 and B4 (12.165) B12 and B3 (13.832), B9 and B5 (13.857), B11 and B10 (14.449) B4 and B1 (14.520) B12 and B10 (14.899) B11 and B8 (15.791). The genotypes with a maximum range of genetic distance have better-predicting characters for some traits, which can be used in breeding for better production of cotton crop¹⁶.

Table 3. Genetic distance between newly evolved cotton genotypes

		Euclidean distance										
	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12
B1	0											
B2	81.446	0										
B3	28.347	64.717	0									
B4	14.52	81.967	22.835	0								
B5	23.15	92.683	30.98	12.165	0							
B6	21.576	89.678	26.72	11.607	7.233	0						
B7	27.177	65.823	13.811	19.654	28.142	25.513	0					
B8	54.01	36.742	33.719	51.629	60.872	57.179	33.135	0				
B9	25.498	89.701	25.351	17.159	13.857	7.71	27.56	56.918	0			
B10	31.528	59.968	11.586	27.11	35.496	31.488	10.843	26.117	31.364	0		
B11	45.57	51.495	22.835	41.352	48.95	44.794	23.428	15.791	43.695	14.449	0	
B12	19.514	67.045	13.832	15.833	26.499	24.326	11.047	37.527	26.657	14.899	28.664	0

The variance percentages for the first, second, and third components were 42.70, 23.10, and 17.20, respectively; the first three components contributed 83.00 percent of the variation for genotypes. Considering the genotypes, coefficients of the first PCA were greatly associated with seed cotton yield plant⁻¹ (0.5131%), followed by sympodial branches plant⁻¹ (0.4931), bolls plant⁻¹ (0.4761%), plant height (0.4519%), however, seed index also associated with PC₁ but in the negative direction (-0.2373%), followed by boll weight (-0.0728%), GOT (-0.0257%), staple length (-0.0222%). While GOT percentage (0.565%) had a great contribution in PC₂, however, plant height (-0.0687) has an association in PC₂, but in a negative direction. On the other, PC₃ had highly contribution to bolls plant⁻¹ (0.3606%). The eigenvalue one criteria, often known as the Kaiser criterion, is the most commonly used criteria for identifying principal components in principal component analysis¹⁷. We can keep and analyse any component with an eigenvalue greater than one using this technique. For all of the attributes, the first three principal components had eigenvalues > 1 and cumulative variability of 83.00 percent. Plant height, sympodial branches plant⁻¹, bolls plant⁻¹, and seed cotton production were all significant characteristics in PC₁, and they all contributed significantly to cumulative variability. Cotton improvement should have received special attention as a result of these characteristics in future breeding efforts¹⁸ and the published previous findings of these characteristics illustrating their contribution to cumulative variability and future cotton improvement initiatives¹⁹.

Table 4. Principal component analysis of various agronomical characters in newly evolved cotton genotypes

Genotypes	Components		
	PC1	PC2	PC3
Plant height	0.4519	-0.0687	-0.3679
Sympodial branches plant ⁻¹	0.4931	-0.0335	0.1321
Bolls plant ⁻¹	0.4761	-0.02	0.3606
Boll weight	-0.0728	-0.2941	-0.7691
Seed cotton yield plant	0.5131	-0.1402	-0.1551
GOT%	-0.0257	0.565	-0.2265
Seed index	-0.2373	-0.4587	0.2169

The analysis of the cluster of twelve cotton genotypes was based on eight morphological traits shown in fig; According to the cluster analysis under study, cotton genotypes split up into three main groups. Cluster one has five genotypes such as B5, B6, B9, B1, and B4; cluster two is comprised of six cotton cultivars including B7, B10, B3, B12, B8, and B11, whereas cluster three solely depends on one genotype (B2), also findings showed diversification and mentioned the result of cluster analysis, studied cultivars into three discrete clusters, according to his result cluster⁻² and cluster⁻³ got optimum values of cotton seed yield and, number of bolls per plant, seed index and staple length²⁰.

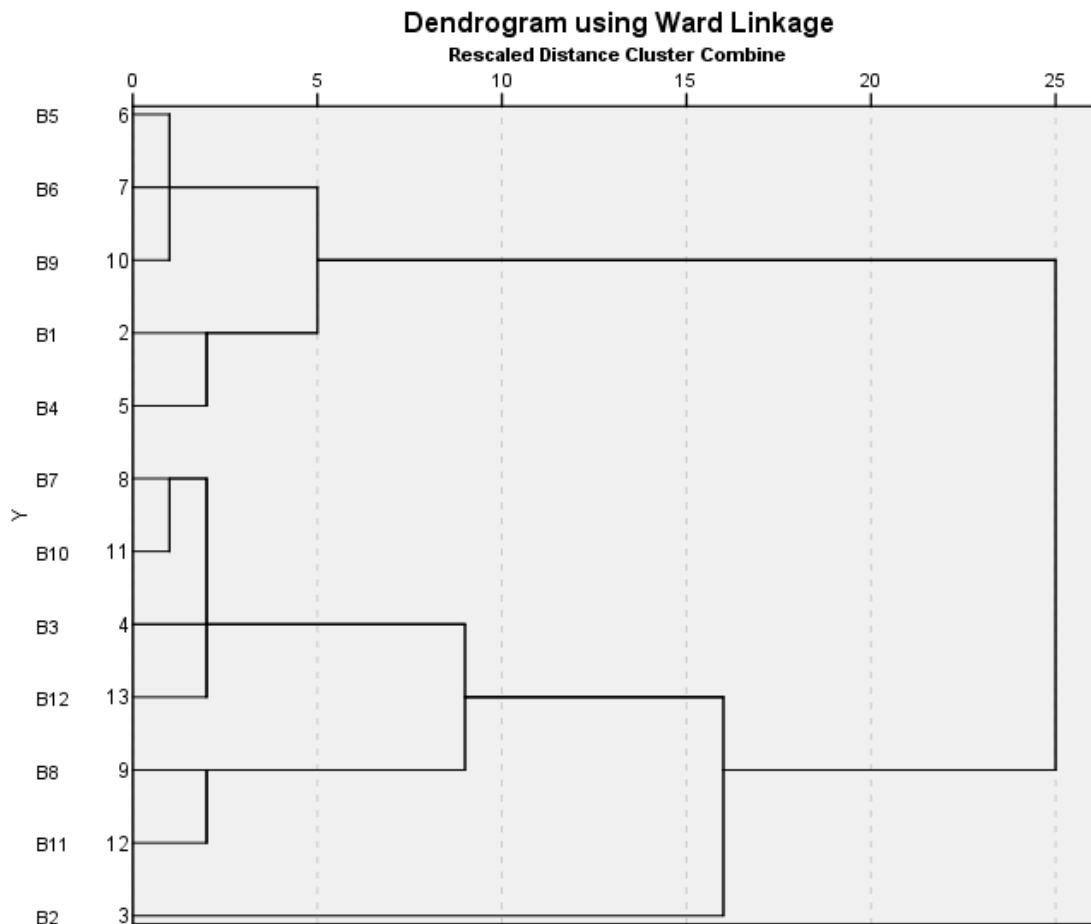


Figure 1 Cluster of 12 newly evolved cotton genotype

4. CONCLUSIONS

The mean square of genotypes, was differed significantly ($P < 0.05$) for all studied traits, representing that the genetic diversity exists in these cotton germplasms can be used for further utilization. Considering the agronomical performance, the genotype B-2 was on top in average values for the Plant Height (174.40 cm), Bolls Plant-1 (42.067), Seed Cotton Yield Plant-1 (139.34 g), GOT% (37.800%), and Staple Length (28.00 mm), hence indicates its valuable breeding resources for future cotton breeding. A greater, Genetic Distance of 92.683 was found between B-5 and B-2 genotypes, and revealing that this pair may be used in hybridization programs for the vigorous hybrid production and better selection in subsequent generations. The Variance Percentages for the first, second, and third principle components were 42.70, 23.10, and 17.20, respectively; the first three components contributed 83.00 percent of the variation for genotypes, which is high enough for cotton crop improvements. Clustering, based on phenotypic data, assigned the cotton genotypes into three major groups, the different groups obtained, might be proved useful for deriving the cotton genotypes with diverse features, and diversifying the Gene Pool of Cotton.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

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