www.als-journal.com/ ISSN 2310-5380/ July 2022

Full Length Research Article
Advancements in Life Sciences – International Quarterly Journal of Biological Sciences

ARTICLE INFO

Date Received:
23/10/2021;
Date Revised:
18/04/2022;
Date Published Online:
31/07/2022;

Authors' Affiliation:
1. Department of Microbiology and Molecular Genetics, The Women University, Multan - Pakistan
2. Department of Biochemistry and Biotechnology, The Women University, Multan - Pakistan
3. Department of Botany, The Women University, Multan - Pakistan
4. Institute of Botany, University of the Punjab, Lahore - Pakistan

***Corresponding Author:**
Iqra Arooj
Email:
iqra.6051@wum.edu.pk

How to Cite:
Jabbar N, Waheed R, Arooj I, Janiad S, Yasmeen H, et al., (2022). Estimation of Genetic Divergence in 40 Elite Cotton Germplasm. Adv. Life Sci. 9(2): 182-187.

Keywords:
Gossypium hirsutum; Morphological agronomic traits; Statistical analysis

Open Access

Estimation of Genetic Divergence in 40 Elite Cotton Germplasm

Nadia Jabbar[1], Raheela Waheed[2], Iqra Arooj[1*], Sara Janiad[1], Humaira Yasmeen[1], Uzma Irfan[3], Naima Zaheer[4], Ambreen Ahmed[4], Atia Iqbal[1]

Abstract

Background: Identification and development of superior cotton genotypes and their further improvement has been one of the primitive aims of plant breeding programmers. Therefore, necessity of analyzing the agro-morphological and yield attributes of advanced lines of cotton is doubtless.

Methods: Mean performance and correlation between ten different morphological, yield and fiber related attributes of forty cotton genotypes from all over the Pakistan under National Coordinated Varietal Trial were studied at Central Cotton Research Institute of Multan. Selected traits included several sympodial and monopodial branches, plant height, number of bolls per plant, staple length, seed cotton yield, boll weight, fiber strength, percentage ginning out turn and micronaire value.

Results: Statistical analysis of variance disclosed highly significant ($p<0.01$) differences among all cotton genotypes for majority of the characteristics. Basic descriptive statistical analysis of selected agronomic traits revealed the presence of substantial genetic variation among 40 genotypes of cotton for 10 selected traits. The correlation coefficient was determined both at $p<0.05$ and $p<0.01$ levels and the observations demonstrated that some of the characteristics exhibited positive correlation, while others displayed negative correlation with each other. Micronaire showed highly significant positive association with percentage ginning out turn (0.3412) and boll weight (0.2421 g) as well as highly significant negative association with fiber strength (-0.5973).

Conclusion: Convincingly, mean performances and correlation of different traits with one another can be utilized in cotton breeding programs in future to improve the yield of cotton seed and to select fiber related attributes with desired characteristics.

Introduction

Being a pivotal cash crop, cotton (*Gossypium hirsutum* L.) constitutes a lot of space in the fiber industry as well as economical equilibrium of many countries all over the world and has successively gained the attention of more than eighty countries owing to its excellent fiber and good adaptability characteristics [1]. By the reason of its multifaceted possessions in terms of fruitful yield and profitable earnings, it is designated as "white gold" [2]. In course of producing cotton (*Gossypium hirsutum* L.) fiber yield, Pakistan holds fourth position worldwide and the economy of Pakistan vigorously depends on cotton and its subordinates [3, 4, 5].

The limiting abiotic and biotic factors restricting cotton generation in Pakistan are heat stress, cotton leaf curl virus infection (CLCuV), high cost of sources (pesticide, fertilizer, insecticide, seeds etc.), less availability of water, almost high severity of pests, deficiency of best quality seed, seed contamination, retailing issues of cotton and the yield product coverage [6]. Genetically modified and diversified cotton genotypes have much potential to combat with aforementioned limitations and to achieve superior quality genotypes harvesting impressive qualitative as well as quantitative results [7].

For the identification and development of enviable genotypes in accessible germplasm, exploitation of genetic divergence is obligatory for upgrading cotton yield [5]. Cotton genotypes with less divergence and low genetic differences are the major routes leading to declining yield quality [8]. Accordingly, data on the genetic diversity and connections among plant varieties is vital to perceive the unpredictability of the quality pool, to recognize gaps in genotype accumulations and to create viable conservation and administration techniques [9].

Breeding programs can be improved through better selection of parents for the generation of segregating populations. This is also used for the study of genetic lines, their population structure and heterotypic groups [10]. Yield is an immensely complicated character which is influenced directly by the various morpho-yield traits including plant height (cm), number of monopodia, yield (kg hec-1), fiber length (mm), fiber fines or micronaire(µg inch-1), ginning out turn (G.O.T %), fiber strength (G Tex-1), number of sympodia, number of bolls and boll weight.

Genetic diversity analysis and studies are made by using pedigree and morphological data [11], as production of cotton either by lint or seed cotton yield relies upon phenotypic characters including plant height, boll weight, number of bolls per plant, non-fruiting branches (monopodia), fruiting branches (sympodia), ginning out turn (G.O.T %), fiber strength, fiber length, micronaire as well as seed index [12].

Information of genetic diversity amongst commercial cotton genotypes will possibly help cotton-breeding systems and encourage the use of promising germplasm. Keeping this in view, the present study was carried out to statistically analyze the genetic diversity, mean performances and correlation of ten selected morphological yield and fiber-related attributes of forty genotypes of cotton (*Gossypium hirsutum* L.). The prime aim of the present investigation was to evaluate the genetic diversity among selected cotton genotypes from all over Pakistan under NCVT (National Coordinated Varietal Trial) for different agronomic traits.

Methods

Place of study and breeding material

This study was conducted at breeding section of experimental farm of Central Cotton Research Institute (CCRI), Multan, Pakistan and Department of Microbiology and Molecular Genetics (MMG), The Women University, Multan, Pakistan during cotton crop growing season 2017-2018. Breeding material included forty different BT-tolerant genotypes (B-1:CEMB-3; B-2: B-2; B-3: GH-Deebal; B-4: FH-152; B-5: Eagle-2; B-6: Cyto-313; B-7: Crystal-313; B-8: Crystal-12; B-9: CRIS-600; B-10: FH-142 (Std); B-11:CIM-534; B-12:CIM-496; B-13:CIM-707; B-14:CIM-554; B-15:CIM-573; B-16:CIM-608; B-17:CIM-602; B-18:CYTO-178; B-19:CIM-608; B-20:CYTO-124; C-1:Ghauri-1; C-2:CEMB Kiean Cotton-2; C-3:CEMB-100; C-4:BS-80; C-5:BS-18; C-6:BH-221; C-7:Bahar-2017; C-8:Badar-1; C-9:FH-142 (Std-2); C-10:Auriga-216; C-11:AA-933; C-12:Weal ag-216; C-13:VH-gulzar; C-14:Tipu-1; C-15:Thakkar-808; C-16:Tarzan-5; C-17:CIM-602 (Std-1); C-18:Shaheen-1; C-19:RH-662; C-20:RH-668) of private sector in National Coordinated Varietal Trial – NCVT (Set-B and Set-C) at CCRI, Multan having cotton seed, fiber yield and fiber quality characters including fiber strength, fiber fineness and fiber length.

Experimental design and field procedures

The research work covered up the study of the genetic variability of genotypes, genetic gain and correlation between seed cotton yield and seed characters as well as fiber in G. hirsutum which was carried out in the 2017-2018 season under prevailing environment of CCRI. CCRI lies between 71.4697° East longitude and 30.1978° North latitude. Breeding material encompassed forty different cotton genotypes which were hand sown on April 28, 2017 in a randomized complete block (RCB) design including three replicates. Every sub-plot of a cultivar had four rows, the plot size being 30′×10′. Recommended agronomic and cultural practices were used and for each entry, data was noted for ten consecutively undamaged as well as representative plants. Picking was done on November 24, 2017 on the basis of single plant and ginning was made with ten saw-gins.

Measurement of traits

The included measured traits were plant height, boll weight, number of bolls per plant, ginning out turn, number of sympodial branches per plant, number of monopodial branches per plant, micronaire, fiber strength, fiber length and cotton yield. Measurement of plant height was done from the ground level at the base of plant to the tip of tallest branch after maturity. The height was recorded in centimeters. Number of sympodia (fruiting branches), monopodia (non-fruiting branches), and total number of bolls present on each plant for tagged plants were counted manually for each genotype in all three replicated fields as it corresponds with the yield of the plant. Using USTER® HVI-1000, fiber quality traits such as fiber fineness, fiber strength and fiber length were calculated for each plant. For calculating boll weight, 25 bolls from the four rows were collected and weighed. The total weight of bolls was divided by 25 and the resulting weight was of one boll. Ginning was made with ten saw-gins machine and the following formula was used to calculate ginning outturn (G.O.T):

Lint % (G.O.T.) = Wt. of lint in a sample / Wt. of seed cotton sample × 100

Statistical Analysis

The average or mean of the agronomic traits was subjected to analysis of the variance (ANOVA) by employing the software, Statistix 8.1. Statistical analysis was performed for the data collected from varieties for aforementioned phenotypic characters and quality traits using this software.

Results

The mean performances of selected cotton genotypes for yield and yield components are described in Table 1. Maximum plant height was observed in genotype C-1 (124.27 cm) and minimum in C-11 (82.00 cm). Likewise, maximum number of monopodia was observed in B-14 (3.40-1) and minimum in B-16 (0.20-1). Sympodial branches are distal fruiting branches, and each sympodial branch ends in a boll generating flower. Genotype B-15 harvested with maximum number of sympodia (66.87-1) while minimum was observed in C-7 (36.800-1). Number of bolls per plant determines the quantity of seed cotton which subsequently defines the cotton yield per unit area. Maximum number of bolls was observed in B-17 (48.13-1) and minimum in B-20 (17.06-1). On the other hand, maximum boll weight (g) was observed in C-3 (4.0 g) and minimum in B-10 (2.1 g). Maximum yield was observed in C-5 (3581.3 kg hec-1) and minimum in B-18 (1789.0 kg hec-1). The ginning turn-out is given prime importance while measuring quality of a cotton variety. Maximum ginning out turn was observed in C-13 (40.700 %) and minimum in C-18 (35.133 %). Maximum fiber length was observed in B-10 (29.533 mm) and minimum in C-13 (24.400 mm). Maximum micronaire was observed in B-1 (5.667 µg inch-1) and minimum in B-17 (4.36 µg inch-1). Maximum fiber strength was observed in B-4 (30.3 G Tex-1) and minimum in C-5 (23.53 G Tex-1) among all forty cotton genotypes (Table 1).

Statistical analysis of variance (ANOVA) exposed highly significant genetic differences ($p<0.01$) among all cotton genotypes for plant height (cm), no. of monopodia-1, yield (kg hec-1), fiber length (mm), ginning out turn (G.O.T %), fiber strength (G Tex-1), and fiber fines or micronaire (µg inch-1), whereas no. of sympodia-1, no. of bolls-1 and boll weight (g) showed non-significant difference as demonstrated by $P>0.05$ (Table 2). The results relevant to descriptive statistics of different selected traits confirmed the presence of considerable genetic variation in 40 genotypes of cotton for 10 studied characters. The minimum and maximum range of means for different traits has been described in Table 3.

Correlation coefficient of ten quantitative traits of upland cotton accessions was calculated at $p<0.05$ as well as $p<0.01$ levels. Micronaire (µg inch-1) showed highly significant positive association with G.O.T (0.3412) and boll weight (0.2421) but highly significant negative association with fiber strength (-0.5973). Yield also showed highly significant positive association with boll weight (0.3197) and plant height (0.2790) as in addition to significant positive correlation with ginning out turn (0.2129). Fiber length indicated highly positive significant association with fiber strength with a correlation value of 0.8556along with highly negative significant correlation with micronaire at a value of (-0.6077). These observations manifested that some of the characteristics depicted positive correlation whereas others presented negative correlation with each other (Table 4).

Discussion

This study of field evaluation of 40 cotton breeding lines aimed to find out best genetic divergent lines. The first parameter studied for 40 genotypes was height and among all genotypes there was a significant height difference which is obviously because of genetic diversity and the environmental influences. As medium height cotton varieties are preferred by cotton breeders

Genotypes	Plant height (cm)	No. of monopodia^{-1}	No. of sympodia^{-1}	No. of bolls^{-1}	Boll weight (g)	Yield (kg hec^{-1})	Ginning out turn (G.O.T %)	Fiber length (mm)	Micronaire (µg inch^{-1})	Fiber strength (G Tex^{-1})
B-1	116.670	1.067	50.400	20.533	3.200	2158.300	38.367	25.900	5.667	26.433
B-2	94.000	1.600	39.333	21.086	2.933	2627.700	37.233	28.067	4.700	28.467
B-3	104.530	0.800	44.933	33.000	3.200	2586.000	38.700	28.433	4.733	28.433
B-4	111.000	1.667	39.467	23.000	3.567	2425.000	36.000	29.133	4.733	30.300
B-5	122.600	1.067	43.867	29.867	3.333	2794.700	37.933	26.900	5.167	27.667
B-6	111.200	2.400	50.400	28.200	3.100	3078.300	37.900	27.833	4.700	29.067
B-7	111.600	1.800	51.733	24.333	3.233	2742.300	37.633	28.733	4.733	28.333
B-8	105.930	1.267	50.667	23.600	2.933	2243.700	35.867	26.400	4.667	26.533
B-9	102.870	0.733	41.600	24.933	3.100	2291.300	39.500	27.200	5.367	27.333
B-10	114.600	0.400	37.800	25.333	2.100	3088.700	39.033	29.533	4.667	29.333
B-11	103.530	1.670	64.270	19.470	3.230	2232.000	39.530	25.900	5.400	26.230
B-12	96.670	1.200	52.870	21.330	2.770	2331.000	38.000	27.300	5.300	26.830
B-13	103.200	1.530	49.730	23.930	3.130	2330.330	35.930	27.000	5.160	26.670
B-14	90.130	3.400	60.400	21.530	2.900	2185.000	38.870	25.300	5.460	24.500
B-15	108.330	2.000	66.870	26.130	3.130	2765.670	37.930	28.900	4.760	30.070
B-16	82.470	0.200	39.400	19.130	2.470	1853.330	36.670	27.300	5.260	23.730
B-17	111.330	1.130	47.400	48.130	2.630	2459.670	37.270	28.300	4.360	28.670
B-18	97.670	0.400	40.330	23.070	3.400	1789.000	36.930	27.400	4.930	28.300
B-19	106.200	1.470	55.000	30.530	2.630	3100.330	36.970	27.800	4.700	28.630
B-20	85.600	2.600	61.600	17.060	3.230	2881.000	38.870	27.900	4.900	28.930
C-1	124.270	1.800	55.467	34.067	3.000	2544.000	37.167	24.633	5.433	23.967
C-2	121.930	0.867	42.767	33.333	2.630	2264.300	38.567	24.833	5.267	24.800
C-3	92.670	1.333	48.367	24.400	4.000	2746.000	38.067	26.400	5.467	25.200
C-4	94.400	0.660	39.000	33.467	2.700	2286.000	36.867	25.500	4.967	25.000
C-5	115.930	1.133	49.000	37.200	3.460	3581.300	40.467	24.733	5.667	23.530
C-6	97.800	1.867	55.400	25.200	3.200	2825.300	38.967	25.433	5.133	25.230
C-7	107.730	0.533	36.800	27.467	3.160	2604.000	37.500	24.967	5.300	24.200
C-8	118.600	1.060	44.860	33.400	3.430	3116.000	38.400	25.500	5.100	25.160
C-9	107.470	1.800	58.200	29.400	3.300	3102.700	38.867	25.460	5.060	24.830
C-10	113.870	1.730	56.533	28.733	3.200	2768.300	36.900	25.633	5.400	25.267
C-11	82.000	0.667	43.900	21.400	2.200	1821.300	37.933	25.600	5.167	25.767
C-12	106.870	1.000	49.460	24.867	3.130	2660.700	39.233	25.533	5.067	24.333
C-13	96.930	0.800	50.700	18.933	3.300	2485.300	40.700	24.400	5.400	23.833
C-14	107.800	0.600	41.500	21.333	3.200	2636.000	38.767	25.533	5.433	25.333
C-15	108.270	1.867	64.000	25.467	3.030	2759.300	38.667	24.567	5.200	24.233
C-16	108.130	0.800	40.100	24.933	3.230	3077.300	36.900	26.600	5.500	26.767
C-17	102.600	1.333	57.100	27.000	2.560	2196.700	36.067	26.967	4.467	25.967
C-18	105.000	0.667	47.600	23.933	3.030	3077.300	35.133	25.700	4.933	25.167
C-19	107.670	1.533	55.800	22.067	3.530	3478.300	37.633	27.567	4.800	27.533
C-20	106.100	0.600	43.600	36.200	2.460	2276.700	35.300	26.700	5.133	27.167

Table 1: Mean performances of selected cotton genotypes for yield and yield components.

Character	Mean Squares			
	Replications df=2	Genotypes Df=39	Error df=78	C.V. %
PH (cm)	156.948	313.816**	166.082	12.26
MN	0.05633	1.29975**	0.39616	49.24
SYM	1386.38	195.66	109.06	21.22
NB	433.423	112.400	86.197	35.11
BW (g)	0.02508	0.43738	0.01782	4.37
YIELD (kg hec^{-1})	70828	535243**	30596	6.71
G.O.T (%)	0.2520	5.14983**	0.29918	1.45
SL (mm)	0.49808	5.852**	0.419	2.43
MIC (µg inch^{-1})	0.0123	0.329**	0.02310	2.99
FS (g/tex)	0.0563	10.94**	0.3227	2.15

* = Significant at $p<0.05$, **= Highly Significant (Significant at $p<0.01$)

Table 2: Analysis of variance (ANOVA) for selected traits of forty cotton genotypes.

Characters	Range	Mean	SEM	SD
Plant height (cm)	32.8-133.0	105.16	1.3365	14.64
No. of monopodia^{-1}	0.200-4.00	1.2767	0.0756	0.8286
No. of sympodia^{-1}	25.60-83.20	49.203	1.1507	12.606
No. of bolls^{-1}	7.20-91.80	26.445	0.9157	10.031
Boll weight (g)	2.00-4.10	3.0542	0.0360	0.3943
Yield (kg hec^{-1})	2606.8-3699	2606.8	40.483	443.46
Ginning out turn (G.O.T %)	34.50-41.20	37.833	0.1254	1.3741
Fiber length (mm)	24.00-29.70	26.597	0.1354	1.4836
Fiber fines/Micronaire (µg inch^{-1})	4.300-5.800	5.0867	0.0320	0.3510
Fiber strength (G Tex^{-1})	23.10-30.60	26.445	0.1780	1.9494

SEM= Standard error of the mean; SD= Standard deviation

Table 3: Descriptive statistics for various agronomic traits of selected cotton genotypes.

Characters	**Boll weight (g)**	**Fiber strength (G Tex^{-1})**	**Ginning out turn (G.O.T %)**	**Micronaire (µg inch^{-1})**	**No. of monopodia^{-1}**	**No. of bolls^{-1}**	**Plant height (cm)**
Fiber strength (G Tex^{-1})	-0.0455	-	-	-	-	-	-
Ginning out turn (G.O.T %)	0.1934	-0.2134*	-	-	-	-	-
Micronaire (µg Inch^{-1})	0.2421 **	-0.5973**	0.3412**	-	-	-	-
No. of monopodia^{-1}	0.1700	0.1214	0.0677	-0.0790	-	-	-
No. of bolls^{-1}	-0.0901	-0.0110	-0.1054	-0.1271	-0.0122	-	-
Plant height (cm)	0.1238	0.0318	-0.0006	-0.0051	-0.0805	0.4403**	-
Fiber length (mm)	-0.1163	0.8556 **	-0.2372	-0.6077**	0.0262	-0.0017	-0.0464
No. of sympodia-^{1}	0.1312	-0.0178	0.1345	0.0012	0.5600**	-0.1048	0.0419
Yield (kg.hec^{-1})	0.3197 **	0.0762	0.2129*	-0.0637	0.1605	0.1468	0.2790**

*Significant at $p<0.05$, ** Significant at $p<0.01$

Table 4: Correlation among different parameters of selected genotypes of upland cotton.

and farmers [13] so the best genotypes regarding height among these 40 genotypes are those having medium height like B-3, B-8, B-9, B-11, B-13, B-15 and B-19.

To determine cotton yield, number of monopodia can be considered as one of the most important factors as the development of sympodia which ends in a boll generating flower is directly dependent on this character [14]. Cotton plants flower periodically throughout its growing season. When flowers are successful, they develop into cotton yield which is referred to as cotton bolls [15]. Number of bolls per plant determines the quantity of seed cotton which subsequently defines the cotton yield per unit area. In our study, B-14 (3.40-1) stood 1st with highest monopodial and sympodial branches which leads to good ginning out turn (G.O.T) of 38.87%. Although number of sympodial branches and bolls are directly proportional to each other, and it was expected that the genotypes having greater number of sympodial branches will be having maximum bolls, but the results are different as besides genetic influences, there are certain environmental factors that affect the development of bolls. Water and nutrient availability, sunlight intensity, temperature and internal hormonal balance are some of the factors that can influence boll development and retention. Cotton is considered as an important crop because of its fiber. The ginning out-turn is given prime importance while measuring quality of a cotton variety. Similarly, micronaire value serves as an indicator of fiber fitness, fiber quality and fiber maturity. It is the most rapid and the least expensive indicator of fiber strength and maturity. Genotype, C-13 showed maximum ginning out turn (40.700 %) and good fiber micronaire value of 5.4 µg inch-1 (Table 1).

Statistical analysis of variance (ANOVA) exposed highly significant genetic differences ($p<0.01$) among all cotton genotypes for plant height (cm), no. of monopodia-1, yield (kg hec-1), fiber length (mm), ginning out turn (G.O.T %), fiber strength (G Tex-1), and fiber fines or micronaire (µg inch-1), whereas no. of sympodia-1, no. of bolls-1 and boll weight (g) showed non-significant yield (kg hec-1), fiber length (mm), ginning out turn (G.O.T %), fiber strength (G Tex-1), and fiber fines or micronaire (µg inch-1), whereas no. of sympodia-1, no. of bolls-1 and boll weight (g) showed non-significant difference as demonstrated by $P>0.05$ (Table 2). Similar significant genotypic differences were observed previously in an experiment conducted on five varieties.

Same traits that were selected for present research work to evaluate genetic variation for yield and fiber-related of *Gossypium hirsutum* L. namely F-281, SLH-41, 69-j.70, H-88-8-J, LA-85-52-1 and COKER-3113, for the traits [16]. Genetic variation in upland cotton was studied by Batool et al in 2010 and they reported manifestation of highly significant differences concerning seed cotton yield plant-1, monopodia and sympodia plant-1 as well as plant height by the cultivars [17]. Another report in the same year also observed significant differences between yield of cotton, length of fiber and other fiber-related characteristics in an advanced cotton breeding program that was conducted for two years [15]. The results relevant to descriptive statistics of different selected traits confirmed the presence of considerable genetic variation in 40 genotypes of cotton for 10 studied characters (Table 3). In 2017, Khan et al used descriptive stats, principal component analysis and correlation analysis to evaluate genetic variation among exotic lines of G. arboreum for traits like boll weight, bolls per plant, sympodial branches, seed cotton yield, lint percentage and micronaire [16].

In our study, the correlation coefficient of ten quantitative traits of upland cotton accessions revealed highly significant positive association with plant height (0.2790) (Table 4). In line with this observation, Khan et al reported in 2009 that the trait yield is directly influenced by plant height because of positive correlation between these two parameters [17]. Based on present findings, it is concluded that success in the area of cotton breeding is principally reliant upon the selection as well as utilization of capable genotypes having increased genetic divergence levels to achieve higher seed cotton yield. The knowledge about genetic variation, genotype potential and correlation between desired traits provides dependable foundation for the improvement of crop and attainment of superior cotton yield. B-1 (micronaire), B-4 (fiber strength), B-10 (fiber length), B-14 (number of monopodia), B-15 (number of sympodia), B-17 (number of bolls), C-1 (plant height), C-3 (boll weight), C-5 (yield), C-13 (ginning out turn) are considered best cotton varieties among 40 genotypes. Being a pivotal cash crop, cotton (*Gossypium hirsutum* L.) constitutes a lot of space in the fiber industry as well as economical equilibrium of many countries all over the world and has successively gained the attention of more than eighty countries owing to its excellent fiber and good adaptability characteristics [18]. By the reason of its multifaceted possessions in terms of fruitful yield and profitable earnings, it is designated as "white gold" [19].

Competing Interests

The author declares that there is no conflict of interest regarding the publication of this paper.

Acknowledgements

We acknowledge the contribution of Dr. Muhammad Idrees Khan for providing technical assistance during the whole study at Central Cotton Research Institute, Multan. We would also like to thank Amber Masood, Iqra Batool and Samia Tahir for providing data.

Author Contributions

All authors contributed equally to this study.

References

1. Bakhsh A, Rao A Q, Shahid A A, Husnain T, Riazuddin S. Insect resistance and risk assessment studies in advance lines of Bt cotton harboring Cry1Ac and Cry2A genes. American-Eurasian Journal of Agricultural and Environmental Sciences, (2009); 6(1): 1-11.
2. Sial K B, Kalhoro A D, Ahsan M Z, Mojidano M S, Soomro A W, Hashmi R Q, Keerio A. Performance of different upland cotton varieties under the climatic condition of central zone of Sindh. American-Eurasian Journal of Agriculture and Environmental Sciences, (2014); 14: 1447-1449.
3. Rizwan M, Jehanzeb F, Muhammad F, Aqeel S, Abid A, Farrukh I, Muhammad A, Ghulam S. Quantitative studies in upland cotton (*Gossypium hirsutum* L.) using multivariate techniques. Pakistan Journal of Agricultural Research, (2021); 34:1.
4. Malik TH, Ahsan MZ. Review of the cotton market in Pakistan and its future prospects. Oilseeds and fats, Crops and Lipids, (2016); 23(6): D606.
5. Bakhtavar M A, Afzal I, Basra S M, Ahmad A U, Noor M A. Physiological strategies to improve the performance of spring maize (*Zea mays* L.) planted under early and optimum sowing conditions. PloS one, (2015); 10(4): e0124441.
6. Rathinavel K. Exploration of genetic diversity for qualitative traits among the extant upland cotton (*Gossypium hirsutum* L.) varieties and parental lines. International Journal of Current Microbiology and Applied Sciences, (2017); 6(8): 2407-2421.
7. Tyagi P, Gore M A, Bowman D T, Campbell B T, Udall J A, Kuraparthy V. Genetic diversity and population structure in the US Upland cotton (*Gossypium hirsutum* L.). Theoretical and Applied Genetics, (2014); 127(2): 283-295.
8. Van Esbroeck G A, Bowman D T, May O L Calhoun D S. Genetic similarity indices for ancestral cotton cultivars and their impact on genetic diversity estimates of modern cultivars. Crop Science, (1999); 39(2): 323-328.
9. Salahuddin S, Abro S, Rehman A, Iqbal K. Correlation analysis of seed cotton yield with some quantitative traits in upland cotton (*Gossypium hirsutum* L.). Pakistan Journal of Botany, (2010); 42(6): 3799-3805.
10. Soomro A W. Estimation of genetic variability parameters in segregating F2 Generation of cotton. FUUAST Journal of Biology, (2020); 10(2): 83-87.
11. Sahito A, Baloch Z A, Mahar A, Otho S A, Kalhoro S A, Ali A, Kalhoro F A, Soomro R N, Ali F. Effect of water stress on the growth and yield of cotton crop (*Gossypium hirsutum* L.). American Journal of Plant Sciences, (2015); 6(07): p.1027.
12. Indest M O. Factors affecting within-plant variation of cotton fiber quality and yield. LSU Doctoral Dissertations. (2015).
13. Iqbal M, Naeem M, Rizwan M, Nazeer W, Shahid M Q, Aziz U, Ijaz, M. Studies of genetic variation for yield related traits in upland cotton. American-Eurasian Journal Agriculture and Environment Science, (2013); 13(5): 611-618.
14. Batool S, Khan N U, Makhdoom K, Bibi Z, Hassan G, Marwat K B, Khan I A. Heritability and genetic potential of upland cotton genotypes for morpho-yield traits. Pakistan Journal of Botany, (2010); 42(2): 1057-1064.
15. Karademir E, Karademir C, Ekininci R, Gencer O. Relationship between yield, fiber length and other fiber-related traits in advanced cotton strains. Notulae Botanicae Horti Agrobotanici Cluj-Napoca, (2010); 38(3):111.
16. Khan M I, Haq H A, Ullah K, Arshad M, Majid, A. Genetic diversity and correlation studies for Cotton Leaf Curl Disease (CLCuD), fiber and yield related attributes in exotic lines of *Gossypium arboreum* L. American Journal of Plant Sciences, (2017); 8(03): 615.
17. Khan N U, Hassan G, Marwat K B, Farhatullah, Kumbhar M B, Parveen A, Umm-E-Aiman, Khan M Z, Soomro Z A. Diallel analysis of some quantitative trait in *Gossypium hirsutum* L. Pakistan Journal of Botany, (2009); 4(6): 3009-3022.
18. Sarwar G, Nazir A, Rizwan M, Shahzadi E, Mahmood A. Genetic diversity among cotton genotypes for earliness, yield and fiber quality traits using correlation, principal component and cluster analyses. Sarhad Journal of Agriculture, (2021); 37(1): 307-314.
19. Saeed F, Farooq J, Mahmood A, Hussain T, Riaz M, Ahmad S. Genetic diversity in upland cotton for cotton leaf curl virus disease, earliness and fiber quality. Pakistan Journal of Agricultural Research, (2014); 27(3): 226-236.

This work is licensed under a Creative Commons Attribution-Non Commercial 4.0 International License. To read the copy of this license please visit: https://creativecommons.org/licenses/by-nc/4.0/