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Assessment of Breeding Potential of *Gossypium Hirsutum* for Fiber Quality by using Multivariate Analyses

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Abstract

Cotton (Gossypium hirsutum L.) is a valuable crop due to its high-quality fiber, which is widely used in the textile industry. Cotton is also called "the white gold" and the "king of fiber," ranking first among all the available natural fibers in the world. In this research, 26 different cotton genotypes were planted in the field to study different quality parameters fiber strength, fiber elongation, fiber fineness, uniformity index, maturity index, fiber length, spinning consistency index and various morphological parameters including plant height, number of sympodial and monopodial branches, number of bolls per plant, number nodes per plant, number of seeds per boll, seed weight and the first fruiting node. A randomized complete block design (RCBD) was used in conducting a field experiment using three replications/blocks. Analysis of variance was also applied to the recorded data for statistical analysis and to check the significant differences among the genotypes. A mean graph was used to check the highest genotype of cotton and this graph showed that MNH-888 was best for plant height and the number of nodes per plant, MG-6 best for the number of monopodial branches and fiber lengths, S-3 best for the number of sympodial branches and the number of bolls per plant, NS-121 best for 1st fruiting node, CRS-2007 best for seed weight, CIM-602 best for number of seeds per boll and fiber elongation, NS-131 best for fiber fineness and maturity index, VH-329 best for fiber strength, KZ-189 best for fiber uniformity index and spinning consistency index. The cluster analysis and principal component analysis were used to explore the characteristics of cotton fib to find out which cotton genotype is better for fiber quality. It is concluded from the research that according to the principal component analysis for the fiber quality traits a genotype KZ-189 was the best for fiber quality whereases genotypes like CRS-2007, MNH-888 and CIM-602 were also better for most of the fiber characteristics but FH-114 is a better genotype for yielding traits and according to the cluster analysis, the genotype KZ-18 is the only one genotype belongs to cluster 7 is the best genotypes for most of the fiber and morphological traits.

KEYWORDS Fiber traits, Multivariate analyses, Cotton genotypes.

1 | INTRODUCTION

Cotton (*Gossypium hirsutum*) is a prominent member of family Malvaceae family and the genus *Gossypium*. Cotton is also called "white gold" and the "king of fiber." It is a vital agricultural product that provides about 90% of the world's textile fiber (Khokhar et al. 2018). Cotton is used as an important material of industry as raw fiber in textiles and the main crop of fiber and the foundation of Pakistan's economy. Pakistan's cotton and cotton products account for nearly 60% of its overseas earnings (Ashraf et al. 2018). The quality of cotton is determined by the fiber and seed qualities but the most linked attributes for the cotton quality are fiber attributes. Due to the increase in the use of fiber in many aspects like yarn manufacture and due to the

development of technology, the competition for the production and quality of fiber has increased at the global level (Hussain et al. 2022). In the long history of the textile industry *G. hirsutum* is used as a plant fiber crop due to its luxury and high-quality fiber. Other than the textile industry, cellulosic fiber is mostly used for the preparation of medical products like dressings, stitches and bandages and medical products which are being produced by its fiber are used at the global level.

Traditionally the focus of fiber quality is on the longest and strongest fibers for the system of yarn production and the major focus of the breeders is also on the improvement of the Length and strength of the fiber. Under suitable moisture when the temperature increased then the length of fiber decreased but fiber micronaire values increased (Abbas & Ahmad, 2018). But as the temperature decreased during the period of 7 weeks from the opening of flower to opening of bolls, the length of fiber and micronaire value of fiber decreased (Guo et al. 2023), even a single seed have a variety of fiber due to environmental fluctuation (Bauer & Bradow, 1996). Due to this, the physiological and genetic variation in size, shape and maturity of fiber cell is also affected. During the first week of flowering fiber and outer integument need a great amount of photosynthate, but after 1st week this distribution is equal in between the seed and fiber. It is because the elongation of fiber starts after 2 days of anthesis and it continues then 3 to 4 weeks and after 15 days the deposition of the secondary wall starts (Stewart, 1986). This deposition of the secondary wall determines the maturity of fibers and this maturity is associated with the micronaire and fineness of fiber. So, fiber cells of this wall determine the value of fiber micronaire (Bradow & Davidonis, 2000; Smith & Cothren, 1999). So optimal environmental conditions required for a better quality and quantity of fiber yield (Bradow & Davidonis, 2010).

At the crop level variability in the properties of fiber is also used to determine the genetic potential of cotton plants. If seed cotton samples are arranged according to weight categories then it would be revealed that the fiber length and fiber maturity increased by increasing the seed weight but the percentage of short fiber is decreased (Davidonis & Hinojosa, 1994). But if compare the cotton fiber by uptake of dye according to the category of seed weight then it was found that the nondyeing or colorless fiber have low seed-cotton weight than the colored fiber (Thomasson & Taylor, 1995). Even this variation in the properties of fiber quality is also associated with the position of seed in boll such as apical, medial and basal position of seed (Iyengar, 1941; Powell, 1969).

Cotton is one of the most important cash crops worldwide, but it faces a number of challenges, including insect and disease pressures, climate change and increasing competition from synthetic fibers (Gu et al. 2020). In order to maintain a sustainable and profitable cotton industry, it is important to develop effective breeding goals and strategies. The breeding goals in cotton may include yield, fiber quality, resistance to pests and diseases and tolerance to environmental stress. Conventional breeding, molecular breeding, and biotechnological approaches are some of the breeding strategies developed for cotton (Li et al. 2018). Many studies have been conducted to explore the genetic basis of fiber quality traits and identify markers associated with these traits, as well as to examine the use of biotechnological approaches such as gene editing to introduce desirable traits into cotton plants (Sun et al. 2012; Zhang et al. 2021).

The major objectives of any crop improvement program are aiming for yield improvement which is complex character and polygenically controlled. The information about the variability in genes, combining ability and other advances at the genetic level is helpful for planning and execution of the breeding program and selection of desirable parents to achieve heterotic combinations and to generate segregating populations with objectives of isolating superior genotypes (Rajamani et al. 2015). Therefore, the major objectives of this study are also to evaluate the genetic diversity of cotton germplasm for fiber quality and to identify the potential genotype to use as a parent in a breeding program. This research will be very helpful for the farmers and breeders with the help of this research, the variety of cotton can be easily selected according to their needs such as fiber quality and yield-related attributes.

2 MATERIALS AND METHODS

The study was performed in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The experimental material comprised the follow-up of 26 genotypes of hirsutum cotton (Gossypium L.) with three blocks/replications that were planted in the field. In this study the genotypes CIM-599, VH-333, MNH-886, FH-114, MG-6, MNH-888, VH-339, KZ-189, CRS-2007, KZ-191, FH-113, SB-149, AA-802, VH-329, NS-131, CIM-598, VH-324, FH-172, NS-121, VH-283, S-3, CIM-602, VH-259, VH-295, IR-901 and AA-703 were used.

The method of sowing cotton followed was bed sowing. During the preparation of land, the distance put between bed to bed was 0.762m, line to line 0.762m and plant to plant 0.3048m. The bolls were picked when they opened and dried. There were 6-7 plants in each replication and the seed cotton was collected from 30 bolls randomly from each plant of each replication. Seed cotton was collected for the identification of the fiber quality of every genotype. The morphological data of each genotype with three replications were collected to check the growth rate of the genotype and check the effect on fiber quality. After picking 30 bolls from each replication fiber was separated from the seed by the roller ginning machine which is available in the ginnery of department of Plant Breeding and Genetics, University of Agriculture Faisalabad. Data for fiber traits were measured by the machine High Volume Instrument (HVI) available in Ayyub Agriculture Research Institute (AARI) Faisalabad and values were recorded by using digitally computerized system.

The data of plant height (cm), monopodial branches, sympodial branches number of bolls number of nodes, 1st fruiting node, seed weight (g), number of seeds per boll and fiber characters such as fiber fineness (μ g/in), fiber length (mm), fiber strength (g/tex), maturity index, fiber uniformity index (%), fiber elongation (%) and spinning consistency index were collected in this study.

Statistical Analysis

Analysis of variance (ANOVA) was used to check the level of significance with the help of software statistics 8.1 following the method of Steel and Torrie (1985). Data that collected from the field and by experiment were analyzed through the principal component analysis (PCA) and cluster analysis as all genotypes were exploited by the partition of the total variance into its components. It also provided the best and most suitable genotypes to utilize in crop improvement for specific characteristics of plants (Pecetti & Damania, 1996; Sneath & Sokal, 1973).

3 RESULTS

There was different analysis like analysis of variance, mean comparison, principal component analysis (PCA) and cluster analysis performed on the data of twenty-six genotypes for fifteen traits to check which genotype show the better response for fiber quality and also have better physiological characteristics.

Plant Height

Analysis of variance ($\alpha = 5\%$) for the height of plant showed that the result for different genotypes of cotton was highly significant. The value of the coefficient of variation was 7.32 that showed its reliability. A mean bar graph for mean values of plant height for all genotypes clearly showed that the genotype MNH-888 best performed for the plant height with a value of 179.9cm and the lowest performance for plant height was recorded by genotype VH-295 (139.6cm) (Fig. 1).

Number of Monopodial Branches

ANOVA (α = 5%) for number of monopodial branches showed that the result for different genotypes of cotton was highly significant and the value of the coefficient of variation was 15.36 that show its reliability.

A bar graph for mean values of the number of monopodial branches for all genotypes showed that the genotype MG-6 best performed for the number of monopodial branches with a value of 7.0 and the lowest the number of monopodial branches was recorded for genotype FH-113 (1.5) (Fig. 2).

Number of Sympodial Branches

ANOVA ($\alpha = 5\%$) for number of sympodial branches showed that the result for different genotypes of cotton was highly significant and the value of the coefficient of variation was 8.77 that show its reliability. A bar graph for average values of the number of sympodial branches for all genotypes showed that the genotype S-3 best performed for the number of sympodial branches with a value of 36.5 and the lowest performance for the number of sympodial branches was recorded for genotype VH-324 (24.3) (Fig. 3).

Number of Bolls per plant

ANOVA ($\alpha = 5\%$) for number of bolls per plant showed that the result for different genotypes of cotton was highly significant and the value of the coefficient of variation was 13.90 that show its reliability. A mean bar graph of the number of bolls per plant for all genotypes showed that the genotype S-3 best performed for the number of bolls per plant with a value of 89.0 and the lowest performance for the number of bolls per plant was recorded by genotype VH-329 (29.0) (Fig. 4).

Number of Nodes per plant

ANOVA ($\alpha = 5\%$) for number of nodes per plant showed that the result for different genotypes of cotton was highly significant and the value of the coefficient of variation was 6.84 that show its reliability. A bar graph for mean values of the number of nodes per plant for all genotypes were formed that clearly showed the genotype MNH-888 best performed for the number of nodes per plant with a value of 54.8 and the lowest performance for the number of nodes per plant was recorded by genotype VH-339 (42.0) (Fig. 5).

1st Fruiting Node

ANOVA ($\alpha = 5\%$) for first fruiting nodes showed that the result for different genotypes of cotton was highly significant and the value of the coefficient of variation was 11.03 that show its reliability. A bar graph for mean values of the 1st fruiting node for all genotypes showed that the genotype NS-121 (11.5) best performed for the 1st fruiting node and the lowest performance for the1st fruiting node was recorded by genotype AA-802 (2.7) (Fig. 6).





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Genotypes

Fig. 2: Mean Graph for number of Monopodial Branches



Fig. 3: Mean Graph for number of Sympodial Branches

60.0 40.0 20.0 0.0

Seed Weight

ANOVA ($\alpha = 5\%$) for seed weight showed that the result for different genotypes of cotton was highly significant (p < 0.01) and the value of the coefficient of variation was 9.28 that show its reliability. A bar graph for mean values of the seed weight for all genotypes showed that the genotype CRS-2007 best performed for the seed weight with a value of 0.0763 and the lowest performance for the seed weight was recorded by genotype VH-283 (0.0509) (Fig. 7).

Number of Seeds per Boll

ANOVA ($\alpha = 5\%$) for the number of seeds per boll showed that the result for different genotypes of cotton was highly significant and the value of the coefficient of variation was 1.59 that show its reliability. A bar graph for mean values of the number of seeds per boll for all genotypes showed that the genotype CIM-602 best performed for the number of seeds per boll with a value of 29.9 and the lowest performance for the number of seeds per boll was recorded by genotype MNH-886 (22.0) (Fig. 8).

Fiber Fineness (Micronaire)

ANOVA ($\alpha = 5\%$) for fiber fineness showed that the result for different genotypes of cotton was highly significant (p < 0.01) and the value of the coefficient of variation was 6.83 that show its reliability. A bar graph for mean values of the fiber fineness for all genotypes showed that the genotype NS-131 best performed for fiber fineness with a value of 5.6 µg/in and the lowest performance for fiber fineness was recorded by genotype CIM-602 (4.1 µg/in) (Fig. 9).

Fiber Length

ANOVA ($\alpha = 5\%$) for fiber length showed that the result for different genotypes of cotton was highly significant (p < 0.01) and the value of the coefficient of variation was 4.99 that show its reliability. A bar graph for mean values of the fiber length for all genotypes showed that the genotype MG-6 best performed for fiber length with a value of 28.8 mm and the lowest performance for fiber length was recorded by genotype FH-113 (23.3 mm) (Fig. 10).

Fiber Strength

ANOVA ($\alpha = 5\%$) for fiber strength showed that the result for different genotypes of cotton was significant (p < 0.05) and the value of the coefficient of variation was 7.91 that show its reliability. A bar graph for mean values of the fiber strength for all genotypes showed that the

genotype VH-329 best performed for fiber strength with a value of 31.8 g/tex and the lowest performance for fiber strength was recorded by genotype FH-113 and by genotype CIM-602(25.6 g/tex) (Fig. 11).

Maturity Index

ANOVA (α = 5%) for fiber maturity index showed that the result for different genotypes of cotton was highly significant (p < 0.01) and The value of the coefficient of variation was 1.2 that show its reliability and results are same as discussed by Pinnamaneni et al. (2021). A bar graph for mean values of the maturity index for all genotypes showed that the genotype NS-131 best performed for maturity index with a value of 0.910 MI and the lowest performance for the maturity index was recorded by genotype CIM-602 (0.853 MI) (Fig. 12).

Uniformity Index

ANOVA ($\alpha = 5\%$) for fiber uniformity index showed that the result for different genotypes of cotton was highly significant (p < 0.01) and the value of the coefficient of variation was 2.22 that show its reliability. A bar graph for mean values of the uniformity index for all genotypes showed that the genotype KZ-189 best performed for uniformity index with a value of 85.7 % and the lowest performance for the uniformity index was recorded by genotype VH-295 (75.7 %) (Fig. 13).

Spinning Consistency Index

ANOVA (α = 5%) for fiber spinning consistency index showed that the result for different genotypes of cotton was highly significant (p < 0.01) and the value of the coefficient of variation was 10.92 that show its reliability. A bar graph for mean values of the spinning consistency index for all genotypes showed that the genotype KZ-189 best performed for the spinning consistency index with a value of 134.3 SCI and the lowest performance for the spinning consistency index was recorded by genotype FH-113 (87.7 SCI) (Fig. 14).

Fiber Elongation

ANOVA ($\alpha = 5\%$) for fiber elongation showed that the result for different genotypes of cotton was highly significant (p < 0.01) and the value of the coefficient of variation was 19.35 that show its reliability. A bar graph for mean values of the elongation for all genotypes showed that the genotype CIM-602 best performed for the elongation with a value of 6.4 % the lowest performance for fiber elongation was recorded by genotype VH-339 (3.2 %) (Fig. 15)



Fig. 5: Mean Graph for number of Nodes per Plant

Fig. 6: Mean Graph for 1st Fruiting Node

Summary Statistics

Table 1 has been below clearly demonstrated the summary statistics for all 26 genotypes and fifteen parameters. These statistics consisted of minimum values, maximum values, mean and standard deviation of all traits which were under study for all genotypes. A correlation presents between the traits shown in the table.





Fig. 7: Mean Graph for Seed Weight

Fig. 8: Mean Graph for number of Seeds per Boll

Fig. 9: Mean Graph for Fiber Fineness

Principal Component Analysis

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The variance is divided to preserve and take advantage of genetic diversity into different comparts and for that division principal component analysis (PCA) is the best technique to investigate the genotypes for effective breeding strategies (Akter et al. 2009; Nazir et al. 2020). Principal components 1,2,3,4,5 and 6 showed in Table 3 shown significant eigenvalues (3.9673, 2.4819, 2.2086, 1.7892, 1.5682 and 1.0828% respectively) as all these eigenvalues were greater than 1



M^{NH}886 Math 858

CR5-2001 58-149

AA-103

vH-259

Genotypes

FHATA

1R-901

VH295 CIM-602

s?

NS-131

Fig. 10: Mean Graph for Fiber Length

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Fig. 11: Mean Graph for Fiber Strength

Fig. 12: Mean Graph for Maturity Index



30.0

25.0

20.0

10.0

5.0

0.0

CIM-599 FH-11A JH-339 CIM-598 NSILI

AA802

R:191

¥1:189 FH-113

VH329 VH-32A VH283

MG-6

VH333

Fiber Length (mm) 15.0 27.3



Uniformity Index

Fig. 13: Mean Graph for

Fig. 14: Mean Graph for Spinning Consistency Index



Fig. 15: Mean Graph for Fiber Elongation



that's why all these principal components were considered significant and these 6 principal components contributed about 77.05% of total variability. Eigenvalues are the unique sets of scalar values connected to linear equations, which are most likely found in matrix equations. The characteristic roots are another name for the eigenvectors. It is a non-zero vector that, after applying linear transformations, can only be altered by its scalar factor. In PCA the number of factors depends upon the variability which present among them, that's why the maximum numbers of factors are equal to the number of traits but the minimum number of factors in PCA depends upon the variation present among them. All these values demonstrated that PC1 contributed more toward the variability and then followed by PC2, PC3, PC4, PC5 and PC6.

Eigenvectors of principal components 1, 2, 3, 4, 5 and 6 have been shown in Table 2. According to the values of Table 2, all parameters performed positively to PC1 except sympodial branches, number of bolls per plant, 1st fruiting node, fiber fineness, moisture, maturity index and surface fineness. In principal component 2 all parameters showed positive responses except monopodial branches, number of bolls per plant, seed weight, number of seeds per boll, surface fineness and fiber elongation. In PC3 all parameters showed negative responses except plant height, sympodial branches, and number of nodes per plant, seed weight, and number of seeds per boll, surface fineness and fiber elongation. All parameters except 1st fruiting node, number of seeds per boll, fiber length, fiber strength, moisture, spinning consistency index and surface fineness showed positive contributions in PC4. In PC5 all parameter showed negative contribution except plant height, number of nodes, 1st fruiting node, and uniformity index and fiber elongation. In PC6 all parameters showed negative contribution except sympodial branches, seed weight, number of seed per boll, fiber fineness, fiber strength, maturity index, uniformity index and fiber elongation.



Scree Plot

In each principal component analysis, the variability and cumulative variability percentage are shown by a graph for explanation and that graph which is used for this explanation called as scree plot. In this plot, all the factors of PC lied on the x-axis and eigenvalues are shown on the y-axis. According to the scree plot, PC1 can be attributed for the maximum variation. It means that those genotypes which were showed higher values in PC1 are beneficial for selection (Fig. 16).

Biplot

According to principal component 1, the better performance shown by CIM-602 because it showed the maximum positive values for most of the parameters. On the other hand, in negative values best performance shown by FH-113 because it showed the maximum negative values but it not better for most of the parameters. It meant that both these genotypes are negatively correlated to each other. Under the PC2, the genotypes FH-114 and MNH-888 showed the best performance for some parameters specially for number of sympodial branches, number of nodes, plant height, fiber fineness and moisture. On the other side, VH-324 showed the best performance for number of bolls per plant but lowest performance for sympodial branches, and number of nodes because these are strongly negatively correlated to each other. According to Fig. 17, genotypes which lied in quadrant 1 showed better performance for most of the fiber character such as fiber strength, fiber length, uniformity index and spinning consistency index then followed by quadrant 2 for most of the fiber characters like fiber fineness, maturity index and moisture. But the genotypes of guadrant 3 of PCA showed better performance for only fiber elongation and genotypes of quadrant 4 showed better performance only for fiber surface fineness.

> **Fig. 16:** Scree Plot in between principal component and variability, eigenvalues and cumulative variability

 Table 1: Summary statistics of Cotton genotypes for all parameters

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Variable	Minimum	Maximum	Mean	Std. deviation
PH	139.594	179.917	155.034	10.402
MB	1.500	7.000	3.974	1.381
SB	24.333	36.500	31.923	2.824
NOB	29.000	89.000	49.442	15.276
NON	42.000	54.833	46.756	2.864
1st FN	2.667	11.500	7.769	2.316
SW	0.051	0.076	0.064	0.006
NOSPB	22.011	29.911	25.515	1.889
FF	4.083	5.607	4.918	0.364
FL	23.290	28.820	26.146	1.392
FS	25.567	31.800	27.883	1.771
MI	0.853	0.910	0.890	0.012
UI	75.700	85.733	81.671	1.725
SCI	87.667	134.333	109.962	11.612
FE	3.167	6.433	4.155	0.767

PH= Plant Height, MB= Monopodial Branches, SB= Sympodial Branches, NOB= Number of Bolls, NON = Number of Nodes, 1st FN= 1st Fruiting Node, SW= Seed Weight, NOSPB= Number of Seed Per Boll, FF= Fiber Fineness, FL= Fiber Length, FS= Fiber Strength, MI= Maturity Index, UI= Uniformity Index, SCI= Spinning Consistency Index, FE= Fiber Elongation

In conclusion, KZ-189, CRS-2007, MNH-888 and CIM-602 was the best genotypes for most of the traits. But the genotypes NS-121 and FH-113 showed strongly negative response to each other for fiber traits. It showed the fiber fineness and fiber maturity index had strongly negative correlation with fiber strength, fiber length, fiber elongation, uniformity index and spinning consistency index.

Cluster Analysis

The name of genotypes belonged to which cluster were shown in Table 4. All of these clusters not only

based on the fiber characters but also, mainly on the morphological characters. The arrangement of cluster was independent and randomly and these clusters clearly showed the genetic diversity of cotton genotypes on the base of fiber and morphological characters. Cluster 2 was the largest cluster among all the clusters that consisted of 7 genotypes as shown in Table 4. Then the 2nd largest cluster was cluster 6 which comprised of 5 genotypes then followed by cluster 1, 3 and 4 had 3 genotypes in each, then followed by cluster 5 and cluster 8 in which 2 genotypes were belonged and at the last the smallest cluster was cluster 7 that had only 1 genotype.

 Table 2: Eigenvector values for the first 3 Principal

 Component for different Cotton genotypes

Component for amerent Cotten genetypee										
Variable	F1	F2	F3	F4	F5	F6				
PH	0.1093	0.3799	0.0656	0.3935	0.0043	-0.2831				
MB	0.1930	-0.2852	-0.1581	0.2908	-0.3039	-0.2566				
SB	-0.0386	0.4069	0.3943	0.1241	-0.0674	0.0738				
NOB	-0.0369	-0.3855	-0.0405	0.2906	-0.1666	-0.1296				
NON	0.1031	0.4221	0.3152	0.0559	0.1356	-0.2606				
1st FN	-0.0764	0.0649	-0.2425	-0.2622	0.5655	-0.1040				
SW	0.3510	-0.0215	0.1122	0.2661	-0.0037	0.3759				
NOSPB	0.1363	-0.0090	0.2544	-0.1167	-0.2603	0.5554				
FF	-0.3068	0.1905	-0.2885	0.2306	-0.0805	0.1773				
FL	0.3777	0.0395	-0.1034	-0.2436	-0.1652	-0.2948				
FS	0.2449	0.2335	-0.2829	-0.2538	-0.0978	0.2892				
MI	-0.3479	0.2219	-0.3466	0.1151	-0.1488	0.1613				
UI	0.1626	0.0982	-0.2444	0.4768	0.2013	0.1073				
SCI	0.4171	0.1193	-0.2732	-0.1732	-0.0311	-0.0276				
FE	0.3021	-0.1812	0.1887	0.0931	0.2344	0.0247				

PH= Plant Height, MB= Monopodial Branches, SB= Sympodial Branches, NOB= Number of Bolls, NON = Number of Nodes, 1st FN= 1st Fruiting Node, SW= Seed Weight, NOSPB= Number of Seed Per Boll, FF= Fiber Fineness, FL= Fiber Length, FS= Fiber Strength, MI= Maturity Index, UI= Uniformity Index, SCI= Spinning Consistency Index, FE= Fiber Elongation.



Fig. 17: Biplot of axes F1 and F2 showed variability 39.94%.

Table 3: Eigenvalues, variability and cumulative variability

	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12	F13	F14	F15	F16	F17
Eigenvalue	3.97	2.48	2.21	1.79	1.57	1.08	0.92	0.72	0.59	0.48	0.41	0.31	0.29	0.12	0.05	0.01	0.00
Variability (%)	23.34	14.60	12.99	10.52	9.22	6.37	5.43	4.21	3.48	2.84	2.43	1.82	1.69	0.68	0.28	0.07	0.03
Cumulative %	23.34	37.94	50.93	61.45	70.68	77.05	82.47	86.68	90.16	93.00	95.43	97.25	98.94	99.61	99.90	99.97	100.00

Table 4: Cotton varieties related to different clusters on the bases of various morphological and fiber traits

Cluster No.	No. of genotypes	Name of Genotypes
1	3	CIM-599, S-3, CIM-602
2	7	FH-114, VH-339, NS-121, FH-113, VH-283, MNH-886, IR-901
3	3	KZ-191, MNH-888, SB-149
4	3	AA-802, VH-333, FH-172
5	2	CIM-598, NS-131
6	5	MG-6, VH-329, AA-703, CRS-2007, VH-295
7	1	KZ-189
8	2	VH-324. VH-259

Table 5: D₂ statistics among the eight clusters

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8
Cluster1	0.0000	19.3717	28.7623	18.3174	24.6675	19.8643	29.8342	30.8508
Cluster2		0.0000	23.4169	28.1496	21.5482	20.9020	39.1212	46.4267
Cluster3			0.0000	37.0673	21.4088	25.0526	29.5745	55.7573
Cluster4				0.0000	21.4860	37.2567	41.1448	23.5761
Cluster5					0.0000	34.4772	39.0154	43.6712
Cluster6						0.0000	26.8397	48.5864
Cluster7							0.0000	47.1929
Cluster8								0.0000



Fig. 18: Dendrogram showing spatial position of Cotton Varieties

The pairwise Mahalanobis distances (D₂ statistics) among eight clusters for all 26 genotypes demonstrated in the Table 5. This table showed the distance among all the clusters to each other. According to the Table 5, the highest distance was recorded in between the cluster 3 and cluster 8 (55.7573). In the 2nd number highest distance was present in between the cluster 6 and cluster 8 (48.5864), then followed by cluster 7 and cluster 8 (47.1929), then cluster 2 and cluster 8 (46.4267), then cluster 5 and cluster 8 (43.6712), then cluster 4 and cluster 7 (41.1448). The lowest inter cluster distance were observed in the between the cluster 1 and cluster 4 (18.3174).

In order to get the best hybrid or recombinant, the cross between the genotypes lied cluster 7 with the genotypes lied cluster 5 then followed by genotypes of cluster 7 with genotypes of cluster 6 for getting the best fiber character and a greater number of sympodial branches, number of seed per boll. The result might be found useful and effective for the further research on the selection genotypes and it will be saved the sufficient time of breeders for further future breeding strategies. In Fig. 18 the dendrogram clearly indicated the grouping of 26 cotton genotypes into cluster based on the distance present between them. The diversity was witnessed in between the genotypes and clusters in figure 18 which

was obtained as the result of cluster analysis.

4 | DISCUSSION

To check the significance of plant height followed the rule which was discussed by Montgomery (2001). The results that were showed is totally agreed with Dhamayanathi et al. (2010) who described the highest heritability for height of plant. The heritability assessment along with genetic gain over mean can be beneficial in predicting the outcome of choosing the finest individual. Numerous investigators also described comparable consequences for all these traits (Igbal et al. 2013; Tang & Xiao, 2013). The variations among cotton genotypes for these traits effected by genetic as well as environmental factors (Khodarahmpour et al. 2011). Khan et al. (2018) also reported the same results. These findings recommended that among the assortment of required traits, tallness of plant can effectively be done in the generations of good crosses (Aziz et al. 2014). The finding of the plant height followed the results that were shown by Murtaza et al. (2006). Monopodial branches those make the bushy shape of cotton and produce difficulties in machinery picking. The results exposed that monopodial branches in every plant were chiefly controlled by genetic variances and there may be a chance in the said genotypes for more decline in vegetative branches as monopodial per plant were negatively associated with seed cotton production. Ahmad et al. (2008) obtained similar results and specified variability for the number of monopodial branches in each plant. The results also shown that mostly the cultivars had low no. of monopodial branches per plant and hence had higher seed cotton yield. therefore, in breeding for higher production preference should be given to less vegetative branches per plant. The results were also in agreement with Batool et al. (2010). On the other hand sympodial branches those are also called fruiting branches, number of sympodial branches revealed the production of cotton. Khan et al. (2007) and Khan et al. (2009) got the similar results and indicated variability amid G. hirsutum cultivars for this specific attribute. The number sympodial branches per plant have directly impact on the yield of cotton seeds and utmost of the preceding investigators observed optimistic association of maturing branches with production of seed cotton. The results were also in accordance with Batool et al. (2010). These number of sympodial branches make a relationship between the nodes and yield of a plant because the nodes not a yielding character but number of sympodial branches is a main yielding character. Significant variability in number of bolls in the genotypes of upland cotton had also been reported by Alkuddsi et al. (2013). Similar findings were also been described by Kale et al. (2007), Neelima and Reddy (2008) and Sakthi et al. (2007). A physiological term in cotton is nodes that are the points on the main stem and add height of plant. The data was collected as same collected by Munir et al. (2018). Directly number of nodes seems to be not related to yield but it had an indirect relation with number of sympodial branches, number of bolls, height to node ratio, seed index. The lowest node is better because the quality of the fiber of the lowest node is better than the upper node. (Bauer et al. 2000) due to this data for first fruiting node was collected. The data was collected as same collected by Sultan et al. (2018). Due to increase in non-additive gene action this trait will be used for hybrid breeding to improve cotton yield. first fruiting node had negative correlation with plant height and number of fruiting branches. With the increase in number of first fruiting node plant move towards the late maturity and ultimately yield effects. The weight of boll, seed and some biochemical like chlorophyll had high heritability values in both circumstances which demonstrated that all these characters were controlled by gene action. By the help of gene the weight of seed can be controlled and fiber quality is directed with the weight of seed (Manan et al. 2022). In genetic variation another important factor is seed per boll that also determined the productivity of cotton for getting cottonseed oil. The results agreed with Kumar and Katageri (2017). Results showed that seeds per boll mostly controlled by genetic variance due to its greater values and in presence of high heritability. Significant results were also described by Jarwar et al. (2018), Igbal et al. (2011) and Gibely (2021).

Fiber fineness is micronaire values of cotton that were measured by ratio of unit of mass per unit of length (µg/in). Fineness is inversely proportional to the length of fiber and strength of fiber (Bauer et al. 1998). The result of the fiber fineness is same which already discussed and significantly described by Darawsheh et al. (2022). The data of the strength of fiber showed the significant variability that was already described by Manan et al. (2022). This fiber strength is the main fiber character that depend upon the spinning strength with high speed. This strength was effected by different factors like nitrogen utilization have effect on the strength of fiber (Mukhametshina et al. 2021) and this strength is a main fiber character. Fiber strength is the maximum tension that a fiber can tolerate. Ghosh et al. (2016) obtained similar results of fiber uniformity index and indicated variability among G. hirsutum cultivars for this specific attribute. The data for spinning consistency index was collected is significant and followed the rule of Ghosh et al. (2016) and Ghosh et al. (2012) whose also worked on spinning consistency index. Van der Sluijs et al. (2015) obtained similar results for the fiber elongation and indicated variability amid G. hirsutum cultivars for this specific attribute. The outcomes for the fiber elongation were also in accordance with Li et al. (2016).

On the basis of various plant traits had most contributions of the first few PCs in the total variability already had been reported in the literature (Ali et al. 2011). For the execution of variables on a plot called vectors a graph used, named as biplot. Its name biplot is due to its character because it is the combination of two plots. In the biplot, part of the variation is indicated by specific parameters or characters. The biplot used to identify groups of observations that are similar to each other and different from other groups and it also used to identify variables that are strongly associated with each principal component, which can help to understand the underlying structure of the data. It indicated the cotton genotypes on the basis of different characters (Yan & Frégeau-Reid, 2008). In this experiment, principal component analysis briefly explained all the genetic diversity of cotton genotypes that can be used for the future breeding strategies and for the selection of better parents for the fiber characters. A biplot indicated its mathematical properties and illustrated for small and large metrics as well as for variance-covariance configurations and multivariate means of several samples (Gabriel, 1980).

Cluster analysis divide the large group of observation into smaller group of observations called clusters on the basis of similarity of observations. Genetic divergence among the 26 genotypes of cotton for fiber characters was determined using the morphological characters. All of these 26 accessions were divided into 8 clusters on the base of morphological and fiber traits. The grouping of Cotton genotypes in a specific cluster was on the basis of similarities in morphological characters and fiber traits, thus the representative genotypes of cluster could be selected for the future breeding programmed to get the better performance of cotton crop. It was revealed that the grouping pattern of genotypes suggested no parallelism in between the genetic diversity and geographical distribution of genotypes (Ghafoor et al. 2003; Nikolić et al. 2010).

Conclusion

This study demonstrated that cotton is a major fiber crop but there are many environmental problems occurred those can change the quality of fiber. There are also many diseases and attack of different pest and insects have a great effect on the quality of fiber. So, we need to make that varieties of cotton that are very tolerant and resistant. In this study with the help of multivariate analyses i.e., principal component analysis and cluster analysis we also concluded that out of 26 genotypes the four genotypes KZ-189, CRS-2007, CIM-602 and MNH-888 showed the best performance for most of the fiber traits and morphological traits. Out of four, KZ-189 is the best genotypes for most of the fiber characters. By selecting these four cotton genotypes and exploiting in breeding program valuable information for promising varieties can be generated that can be cultivated in diverse agro-climatic conditions. This can contribute to reducing the environmental impact of cotton cultivation while ensuring higher yields and better-quality fibers.

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