Original Article

J Genet Appl Biotechnol, 2026: *e2026018*
DOI: https://doi.org/10.66432/5dqevh08
Received: 24 Sep 2025; Revised: 26 Oct 2025; Accepted: 28 Oct 2025; Published online: 25 Feb 2026

Evaluation of diversity and estimation of association among various yield related and fiber quality traits in *Gossypium hirsutum* L.

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Abstract

Cotton is majorly grown for fiber in various regions of world. It has major role in Pakistan's economy. Cotton is affected by various biotic and abiotic factors that result in low yield and reduced quality of cotton fibers. Various yield and fiber quality traits are associated with each other and can be improved simultaneously. This research was performed under RCB design with three replications. 17 genotypes of upland cotton were utilized to estimate correlation coefficient between quantitative characters of *G. hirsutum*. 13 plant parameters including both morphological and fiber quality traits were observed for each accession. Analysis of variance exhibited significant variations among varieties for all the observed attributes at 5% level of significance. Mean value of genotypes demonstrated monopodial branches ranges from 1 to 3.33, sympodial branches from 13 to 28, plant height from 114.25 to 168.67cm, bolls per plant from 13 to 45, boll weight from 1.83 to 3.69g, number of seeds per boll from 16 to 24.67, seed cotton yield from 31.55 to 154.02g, ginning out turn from 21.61 to 50.91%, seed index from 4.44 to 7.25g, lint index from 1.45 to 5.45g, fiber length from 25.51 to 28.67mm, fiber strength from 38.42 to 17.89g/tex and fiber fineness from 2.5 to5.13µg/inch. However, among all observed genotypes KZ-191 showed maximum performance in terms of plant yield and AA-802 showed maximum performance in terms of fiber quality traits. Results of correlation analysis demonstrated that sympodial branches, height of plants, number of bolls, average seeds per boll, 100 seed weight and fiber length had linear relation with each other. Positive correlation also existed among GOT and lint index, fiber strength and fineness. Meanwhile, number of monopodia and boll weight had negative relation with fruiting branches, average number of bolls, plant height, count of seeds per boll, 100 seed weight and fiber length. Cluster analysis revealed four clusters of genotypes with cluster III was the smallest one. Cluster I, II, III and IV comprise of 6, 4, 1, 6 genotypes, respectively. The objective of the research was to determine correlation among yield and fiber traits and identify diversity among genotypes. This will lead to improve selection efficiency by focusing on positively correlated traits and may give rise to improved traits in hybrid development.

Keywords: Correlation Analysis, Hierarchical clustering, Multivariate, Morphological traits

How to cite this article: Fatima A, Perveen S and Zia A. Evaluation of diversity and estimation of association among various yield related and fiber quality traits in *Gossypium hirsutum* L. *J. Genet. Appl. Biotechnol.* 2026: e2026018. https://doi.org/10.66432/5dqevh08

Introduction

Cotton is a major cash crop, grown in various regions of world. It belongs to family Malvecaea and genus Gossypium, comprised of more than 50 species containing both diploid and tetraploid genomes with basic chromosome number 13. However, only two diploid (*G. arboreum* and *G. herbaceum*,) and two tetraploid (*G. barbadense* and *G. hirsutum*) species are cultivated worldwide also known as old world and new world cotton species, respectively (1). Cotton is considered as one of the economically important crops as it constitutes 35% of the total fiber being utilized worldwide (2). Fiber obtained from cotton plant is known as 'queen of fibers' serves as the cornerstone for textile industry due to its unique properties of breathability, softness and absorbency. It is commonly used to manufacture cloth, yarn and lint. Cotton weaving industry contributes approximately 600 billion US dollars in the economy of cotton producing countries annually all around the world (3). Cotton is considered as the 2nd largest cash crop in Pakistan after wheat. Pakistan 's economy is highly reliable on agriculture sector as it contributes 22.9% in GDP out of which cotton contributes 0.7% in GDP and 2.9% in overall agriculture production (4).

Despite the significant damage due to floods during previous years, cotton production has increased from 4.91 million bales to 10.22 million bales with an overall increase of 108.2% for the year 2023-24 (5). It is predominantly grown in the province of Punjab and Sindh. Nearly 1.5 million people of Pakistan earned their livelihood from cotton cultivation (6).

Cotton is highly susceptible to various biotic and abiotic stresses, which leads to severe yield reduction. Biotic factors include occurrence of various insect pests and pathogens (fungal bacterial and viral) and abiotic factors such as drought, heat, and salinity effects plant at different growth stages (7). Other major concerns to cotton production includes loss of genetic diversity among cultivars due to adaptation of high yielding genetically modified varieties (8). Moreover, demand for high quality and contamination free cotton fiber has increased as most of the textile industries obtain their raw materials from cotton.

Yield and fiber quality are quantitative traits that are controlled by various genes and highly influenced by environment (9) Moreover, various yield related and fiber traits are associated with each other. Such plant traits that are interrelated with each other can be improved simultaneously to improve overall yield of plant (10). However, selection solely based upon yield is not efficient while the knowledge of genetic basis of such traits is also crucial for plant breeders to develop genotypes with desired traits (11). The extent of association among yield related and fiber traits must be known to identify the important traits upon which selection can be made.

Correlation coefficient analysis explained by Pearson is used to identify the magnitude of association among various yield related traits and the component trait upon which selection can be made to improve yield and quality. Hence, the association between such traits is crucial for the formulation of various breeding programs to achieve the desired combination of yield and fiber quality components. Correlation coefficient analysis also depicted direction of relationship among traits along with the extent of association. It provides knowledge about how various character improves simultaneously when selection pressure is applied. Studies reported that there is significant association among yield and yield related traits including monopodial branches, boll weight, plant height, GOT, lint index, plant height and fruiting branches per plant (12). (13) also examined that sympodial per plant, plant height, staple length had strong direct relation with overall yield. (14) also noticed that plant production had significant positive association with average amount of bolls, boll weight and 100 seed weight.

Another major concern regarding cotton production is the loss of genetic diversity due to systematic selection for comparable traits among various cotton cultivars that leads to reduced yields and low fiber quality during last decades (8). Diversity among genotypes is crucial for effective selection of desired traits and helpful in the conservation of germplasm. Cotton genotypes provide different yield potential and fiber quality due to the difference in various quantitative and qualitative traits (15). Thus, such traits are considered as a powerful tool for effective selection of diverse genotypes. Genetic variations provide the baseline for improvement of desired attributes. Variations present among the present germplasm of cotton should be used to develop diverse and enhanced quality genotypes. Various univariate and multivariate analysis are used to estimate diversity among various genotypes. However, multivariate analysis such as cluster analysis are considered as more powerful tool to assess diversity among genotypes as it focusses on multiple variables at the same time (16). Cluster analysis is used to classify genotypes on the basis of observed traits into different groups and keeping alike genotypes in same group (17). Various researchers used hierarchical clustering to classify genotypes of *G. hirsutum* on the basis of yield and fiber traits (18).

Materials and Methods

The research was performed in field area of cotton of Department of Plant Breeding and Genetics at University of Agriculture, Faisalabad located at latitude 31°25′N and altitude 184.4m from sea level. Seeds from 17 varieties of *G. hirsutum* namely, AA-703, AA-802, FH-113, FH-169, FH-172, FH-154, FH-142, FH-170, IR-3701, KZ-181, KZ-189, KZ-191, MNH-886, MNH-888, NS-131, SB-149 and VH-282 were collected from Department of PBG at University of Agriculture, Faisalabad and planted during kharif season under RCB design with three replications. Bed sowing method was followed with 75cm bed to bed distance. Spacing among rows was kept 75cm and plant to plant spacing was kept 30 cm. Thinning was performed at the time of two leaf stage to keep single seedling per pot. All the management practices such as fertilizer application, weeding, hoeing and irrigation practices were accomplished as per growth requirement of crop. Morphological data was collected from five healthy and undamaged plants from each replication at the time of maturity. Bolls were picked after 130 to 150 days of sowing from each replication and seed cotton was obtained to identify quality of fiber. Seeds were detached from the lint by using a ginning machine at ginning department of University of Agriculture, Faisalabad. Fiber traits were calculated with the help of High-Volume Instrument machine (Model USTER@ HVI-900 SA) in the Department of Fiber Technology, University of Agriculture, Faisalabad. Plant traits namely, monopodial branches per plant, sympodia per plant, plant height (cm), number of bolls, number of seeds per boll, boll weight(g), GOT(%), seed index(g), lint index(g), fiber length(mm), fiber strength(g/tex) and fiber fineness(µg/inch) were observed.

Statistical Analysis

The observed data was checked for normality and homogeneity and further examined though Analysis of Variance (ANOVA) at 5% level of significance according to (19) to estimate the differences among genotypes for selected attributes. Correlation analysis was performed according to Pearson in Statistix 8.0 (20). Diversity among genotypes was estimated by using Ward's method of hierarchical clustering (21).

Results

The results of different analysis such as analysis of variance, correlation analysis and cluster analysis for all the observed plant traits are as follows.

Number of monopodial branches

ANOVA for monopodial branches at 5% level of significance showed highly significant differences among observed genotypes. Mean values of genotype for monopodial branches are shown in bar graph (Figure 1). Thus, it was shown that average number of monopodial branches per plant ranges from 1 to 3.33. The genotypes AA-802 (3.67) showed maximum monopodial branches per plant followed by FH-113 (3.33) and FH-169 (3.33). Minimum number of monopodial branches per plant were observed for the genotype FH-170 as it showed only one monopodial branch per plant.

Number of sympodial branches

ANOVA for fruiting branches at 5% level of significance showed highly significant differences among observed genotypes. Mean values of genotype for fruiting branches are shown in bar graph (Figure 1). Thus, it showed that average number of sympodial branches ranged from 13 to 28. Maximum sympodial branches were exhibited by the genotype FH-170 (18.33) followed by IR-3701 (27), FH-154 (26.33). However, the genotype AA-802 (13) followed by AA-703 (13.51) and VH-282 (13.33) showed minimum number of sympodial branches per plant among all other genotypes.

Plant height

ANOVA for height of plant at 5% level of significance showed highly significant differences among observed genotypes. Mean values of genotype for plant height are shown in bar graph (Figure 1). Thus, showed that average plant height ranged from 114.25cm to 168.67cm. Maximum plant height was observed for the genotype FH-170 (168.67) followed by IR-3701 (163.67), KZ-181 (160.83), VH-282 (158.67) and FH-169 (158.22). However, the genotype AA-802 (11.25) showed smallest plant among all other genotypes. Moderate heighted plants were observed for the genotypes MNH-886, NS-131 and FH-113.

Number of bolls per plant

ANOVA for bolls per plant at 5% level of significance showed highly significant differences among observed genotypes. Mean values of genotype for average bolls are shown in bar graph (Figure 1). Thus, it showed that average bolls per plant ranged from 13 to 45. Maximum bolls per plant were examined for the genotype FH-170 (45) followed by KZ-191 (42), KZ-181 (35), IR-3701 (35). However, the genotype FH-172 (13) followed by MNH-888 (19) showed minimum bolls per plant among other entries.

Boll weight

ANOVA for boll weight at 5% level of significance showed highly significant differences among observed genotypes. Mean values of genotype for boll weight are shown in bar graph (Figure 1). Thus, showed that average boll weight ranged from 1.83g to 3.69g. Maximum boll weight was observed for the genotype KZ-191 (3.69) followed by AA-802 (3.48) and FH-113 (3.31). However, the genotype FH-170 (1.83) followed by VH-282 (1.95) showed minimum boll weight among all other genotypes.

Number of seeds per boll

ANOVA for average seeds per boll at 5% level of significance showed highly significant differences among observed genotypes. Mean values of genotype for average seeds are shown in bar graph (Figure 1). Thus, showed that average seeds ranged from 16 to 24.67. Maximum number of seeds per boll were observed for the genotype IR-3701 (24.67) followed by FH-170 (23.33) and MNH-886 (22.67). However, the genotype MNH-888 (16) followed by AA-802 (17.67) and KZ-191 (18) showed minimum count of seeds in a boll among other entries.

Seed cotton yield

ANOVA for seed cotton yield at 5% level of significance showed significant differences among observed genotypes. Mean values of genotype for seed cotton yield are shown in bar graph (Figure 1). Thus, showed that average seed cotton yield per plant ranged from 31.55g to 154.02g. Maximum seed cotton yield was examined for genotype KZ-191 (154.02) followed by KZ-181 (91.35) and FH-170 (82.96). However, the genotype FH-172 (31.55) followed by MNH-886 (46.15) and FH-172 (50.07) showed minimum seed cotton yield among all other genotypes.

Ginning out turn

ANOVA for GOT at 5% level of significance showed favorable differences among observed genotypes. Mean values of genotype for GOT are shown in bar graph (Figure 1). Thus, it showed that average GOT ranged from 21.61% to 50.91%. Maximum GOT was observed for the genotype SB-149 (50.91) followed by FH-154 (49.17) and AA-802 (47). However, the genotype FH-170 (21.61) followed by FH-113 (22.82) and MNH-888 (23.66) showed minimum GOT among all other genotypes.

Seed index

ANOVA for seed index at 5% level of significance showed highly significant differences among observed genotypes. Mean values of genotype are shown in bar graph (Figure 1). Thus, it showed that average seed index ranged from 4.44g to 7.25g. Maximum seed index was observed for the genotype FH-170 (7.25) followed by KZ-181 (6.96) and IR-3701 (6.53). However, the genotype FH-154 (4.44) followed by AA-802 (4.58) and MNH-888 (4.67) showed minimum seed index among all other genotypes.

Lint index

ANOVA for lint index at 5% level of significance showed significant differences among observed genotypes. Mean values of genotype for lint index are shown in bar graph (Figure 1). Thus, showed that average lint index ranged from 1.45g to 5.45g. Maximum lint index was observed for the genotype IR-3701 (5.45) followed by SB-149 (5.06) and KZ-191 (4.74). However, the genotype MNH-888 (1.45) followed by FH-113 (1.46) and FH-172 (1.90) showed minimum lint index among all other genotypes.

Fiber length

Analysis of variance for fiber length at 5% level of significance showed significant differences among observed genotypes. Mean values of genotype for fiber length are shown in bar graph (Figure 1).

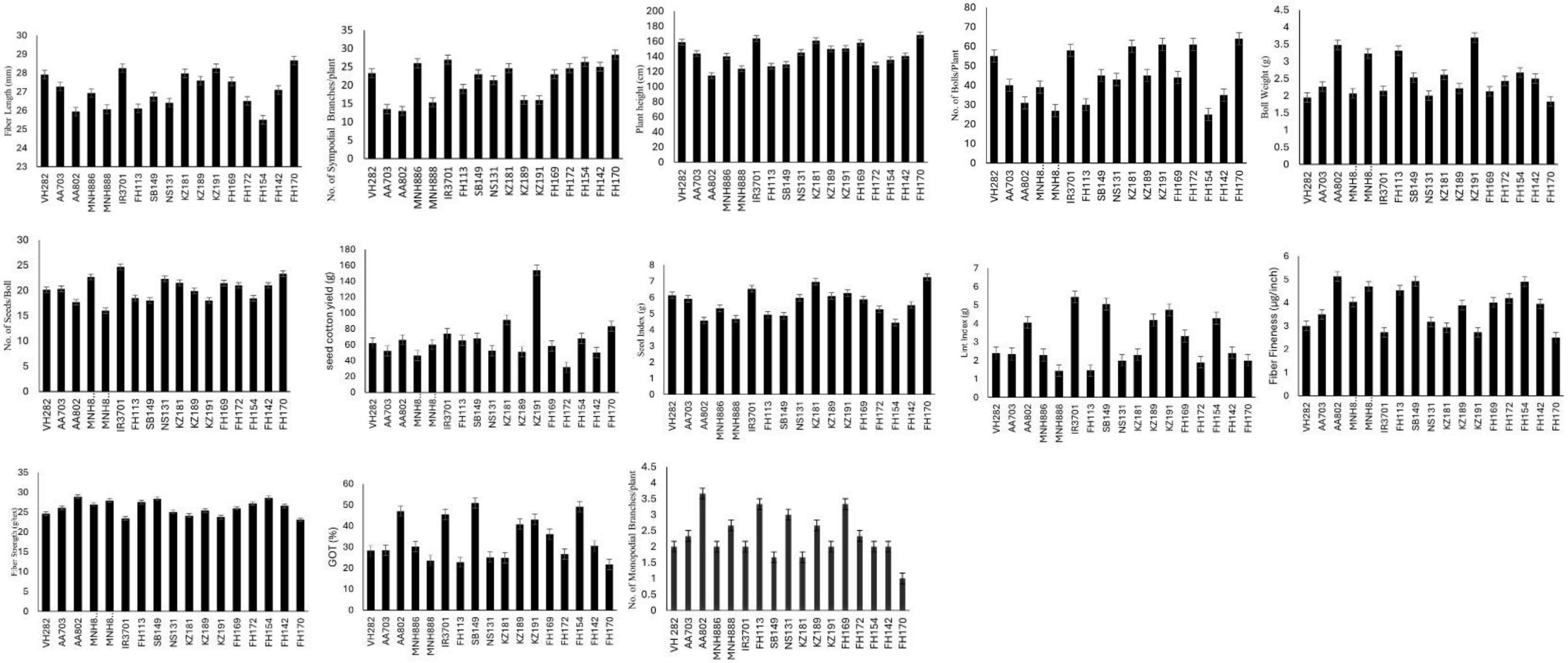

Figure 1: Performance of agronomic and fiber-quality traits among upland cotton genotypes. Values represent means of evaluated genotypes; error bars indicate standard error.

Table 1. Correlation analysis of various yield related and fiber quality traits of genotypes of upland cotton.

	MP	**SP**	**PH**	**NB**	**BW**	**NS**	**SCY**	**GOT**	**SI**	**LI**	**FL**	**FS**	**FF**
MP	1												
SP	-0.659**	1											
PH	-0.42 ^{NS}	0.648**	1										
NB	-0.598**	0.520**	0.787**	1									
BW	0.190^{NS}	-0.559*	-0.602**	0.178 ^{NS}	1								
NS	-0.191^{NS}	0.696*	0.700*	0.354^{NS}	-0.767*	1							
SCY	-0.495*	0.593**	0.914**	0.800**	-0.552*	0.710*	1						
GOT	-0.382^{NS}	-0.554*	-0.922*	0.801 ^{NS}	-0.416^{NS}	-0.541*	-0.853^{NS}	1					
SI	-0.434^{NS}	0.523*	0.913**	0.761**	-0.480*	0.680^{NS}	0.965	0.895**	1				
LI	-0.329^{NS}	-0.583*	-0.860**	0.753^{NS}	0.403 ^{NS}	-0.515*	-0.790^{NS}	0.965**	-0.811**	1			
FL	-0.489*	0.500*	0.879**	0.781**	-0.390^{NS}	0.561**	0.922**	0.873 ^{NS}	0.918**	0.807 ^{NS}	1		
FS	0.363^{NS}	-0.505^{NS}	-0.909**	-0.790**	0.406^{NS}	-0.644**	-0.941**	0.904*	-0.962**	0.839**	-0.903**	1	
FF	0.379^{NS}	-0.507^{NS}	-0.873**	-0.764**	0.414^{NS}	-0.653**	-0.914**	-0.865^{NS}	-0.941**	-0.782^{NS}	-0.863**	0.980**	1

**=P<0.01, Highly Significant; *=P<0.05, Significant; NS=P>0.05, Non-significant

MP; Monopodial branches, SP; Sympodial branches, PH; Plant height, NB; Number of bolls per plant, BW; Boll weight, NS; Number of seeds per boll, SCY; Seed cotton yield, GOT; Ginning out turn, SI; Seed index, LI; Lint index, FL; Fiber length, FS; Fiber strength, FF; Fiber fineness.

Table 2. Name of genotypes of upland cotton falling in each cluster through cluster analysis.

Clusters	No. of Genotypes	Name of Genotypes
I	6	VH-282, IR-3701, KZ-181, KZ-189, KZ-191, FH-169
II	4	AA-703, MNH-886, NS-131, FH-142.
III	1	FH-170
IV	6	AA-802, MNH-888, FH-113, SB-149, FH-172, FH-154

Thus, showed that average fiber length was ranged from 25.51mm to 28.67mm. Maximum fiber length was observed for the genotype FH-170 (28.67) followed by KZ-191 (28.46) and IR-3701 (28.25). However, the genotype FH-154 (23.12) followed by AA-802 (24.18) and MNH-888 (24.66) showed minimum fiber length among all other genotypes.

Fiber strength

Analysis of variance for fiber strength at 5% level of significance showed significant differences among observed genotypes. Mean values of genotype for fiber strength are shown in bar graph (Figure 1). Thus, it showed that average fiber strength ranged from 38.42g/tex to 17.89g/tex. Maximum fiber strength was observed for the genotype AA-802 (38.42) followed by FH-154 (37.29) and SB-149 (36.93). However, the genotype FH-170 (17.89) followed by IR-3701 (23.95) and KZ-191 (24.96) showed minimum fiber strength among all other genotypes.

Fiber fineness

Analysis of variance for fiber fineness at 5% level of significance showed significant differences among observed genotypes. Mean values of genotype for fiber fineness are shown in bar graph (Figure 1). Thus, showed that average fiber fineness was ranged from 2.5µg/inch to5.13µg/inch. Maximum fiber fineness was observed for the genotype AA-802 (5.13) followed by SB-149 (4.93) and FH-154 (4.90). However, the genotype FH-170 (2.5) followed by IR-3701 (2.73) and KZ-191 (2.73) showed minimum fiber fineness among all other genotypes.

Correlation analysis

Results of correlation analysis showed in Table 1 and Figure 2. Results elucidated that monopodia per plant had positive but negligible relation with fiber fineness boll weight, fiber strength while monopodial branches and boll weight showed strong negative relationship with fruiting branches, number of bolls, yield and staple length. Average fruiting branches manifested strong direct interrelation with average amount of bolls, plant height, total seeds per boll, cotton yield, 100 seed weight, and length of fine fibers. Sympodia branches were negatively linked with monopodia branches, boll weight, GOT, lint index. Plant height manifested significant direct effect on fruiting branches, total bolls per plant, seeds per boll, plant yield, seed index, fiber length, inversely interrelated with monopodial branches, weight of weight, lint index and GOT.

Total bolls of a plant showed strong direct relation with fruiting branches, plant height, cotton yield, seed index and fiber length meanwhile, inversely related with fiber strength and fineness. However, boll weight demonstrated strong inverse linkage with sympodial branches, plant height, total seeds in a boll, cotton yield and 100 seed weight. Total seeds in a boll had strong direct association with fruiting branches, plant height, cotton yield, seed index and fiber length while had inverse relation with boll weight, GOT, lint index, fiber strength and fiber fineness. Seed cotton yield was directly influenced by sympodial branches, plant height, total bolls, total seeds in a boll, seed index and length of fine fibers while it showed unfavorable linkage with monopodial branches, boll weight, fiber strength and fineness. GOT and lint index directly influenced fiber strength while these traits showed negative correlation with fruiting branches, plant height, total seeds per boll, plant yield and seed index.

100 seed weight was in direct correlation with total fruiting branches, plant height, total bolls of a plant, plant yield and fiber length meanwhile had negative linkage with plant boll weight, strength and fineness of fiber. Fiber length was directly influenced by fruiting branches, plant height, total bolls of a plant, total seeds of a boll, plant yield, seed index while had linkage with fiber strength and fiber fineness. Fiber strength was highly correlated with lint index, GOT and fiber fineness. However, strength and fineness were inversely influenced by total bolls of plant, plant height, total seeds of a boll, seed index, plant yield and length of fine fibers.

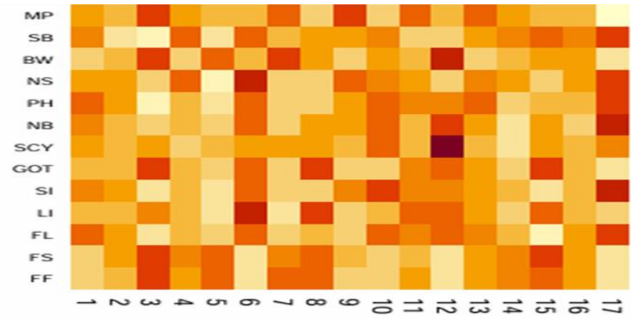

Figure 2: Heat map of correlation analysis among yield related and fiber quality traits of 17 upland cotton genotypes.

Cluster Analysis

Cluster analysis according to Ward's method of hierarchical clustering showed significant variation among observed genotypes. Dendogram demonstrated that 17 genotypes of cotton were grouped into four clusters with almost 70% similarity index (Figure 3). Cluster I, II, III and IV comprised of 6, 4, 1 and 6 genotypes, respectively (Table. 2). Cluster III was the smallest one, with only one genotype namely, FH-170. Cluster I comprised of six genotypes namely, VH-282, IR-3701, KZ-181, KZ-189, KZ-191 and FH-169. Cluster II consisted of four genotypes namely, AA-703, MNH-886, NS-131 and FH-142. While, AA-802, MNH-888, FH-113, SB-149, FH-172 and FH-154 fall in cluster IV.

Discussion

Results showed that most of plants showed less monopodial branches thus have increased plant yield. It exposed that monopodial branches have inverse relation with yield. (22) and (23) also reported similar results of negative correlation among monopodial branches and plant yield indicating that increase in monopodial branches lead to substantial decrease in seed cotton yield. However, the plants having more number of sympodial branches result in increased seed cotton yield thus, indicating that fruiting branches are a reliable yield trait upon which selection can be made. Similar results were presented by (24) and (25). Increase in number of sympodial branches also directly impact on other yield attributes such as total bolls per plant, seed cotton yield, seed index and fiber length. These findings were in accordance with the findings of (26).

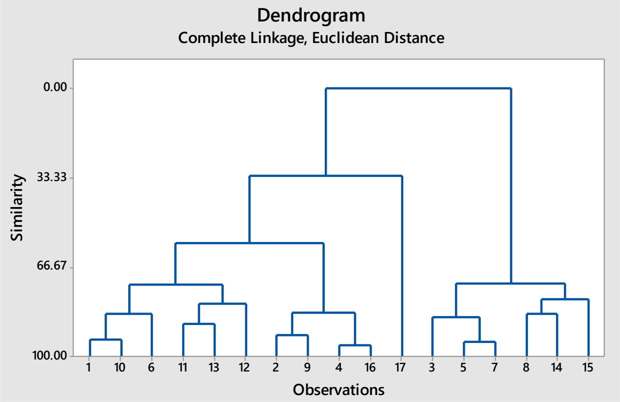

Figure 3: Dendrogram showing result of cluster analysis among 17 genotypes of upland cotton.

Plant height had direct relation with cotton seed production but inversely related with GOT, thus elucidating that taller plants tend to have increase yield with decreased lint production. Negative correlation of plant height with GOT was also reported by (24). On the other hand, increased number of bolls per plant resulted in increased cotton production which was in accordance with the results observed by (27). Increased number of bolls also lead to substantial decrease in boll weight which shows in agreement of the results observed by (28). Similarly, boll weight was also in inverse relation with number of seeds per boll which is a yield attributing parameter. Thus, boll weight can't be considered as a reliable parameter for cotton yield. However, other parameters that contribute to lint yield of cotton are GOT and lint index which showed direct dependence on each other. (29) got the Similar positive association among GOT and lint index. (30) also observed corresponding results of negative correlation between GOT and seed index.

Among fiber parameters, fiber strength and fineness are the most reliable fiber parameter upon which quality of fiber could rely. However, both showed inverse relation with fiber length. Negative correlation of fiber length with other fiber traits such as strength and fineness were also observed by (31). Negative correlation of fiber strength and fiber fineness with other yield traits were in correspondence with the findings of (32). Results depicted high correspondence with correlation analysis observed by (30) and (33). The contrasting performance of different genotypes highlights the opportunity to exploit their complementary traits through strategic hybridization thereby creating novel breeding lines that balance productivity with superior fiber characteristics.

Cluster analysis divided 17 accessions of upland cotton into four major clusters on the basis of similarities and differences in morphological traits and fiber quality traits. (34) and (35) also proved that hierarchical clustering is one of the effective methods of multivariate analysis that helps to compare various genotypes and assess diversity among them on the basis of various observed traits. (18) reported two major clusters with two sub-clusters each whereas, (36) observed four clusters of genotypes on the basis of variability among yield related and fiber quality traits. Similarly, seven major clusters were reported by (37) and four main clusters were noticed by (38).

Conclusion

The study was performed to identify interrelation between various yield related and fiber quality attributes and to investigate variability and diversity among cotton genotypes. Results exhibited that the genotype KZ-191 showed maximum performance in terms of plant yield and the genotype AA-802 showed maximum performance in terms of fiber quality traits. Moreover, yield had direct relation with fruiting branches, plant height, total bolls of a plant, total seeds of a boll, seed index and length of fine fibers while cotton yield demonstrated inverse association with boll weight, GOT, lint index, fiber strength and staple fineness. Sympodia per plant and plant height exhibited strong inverse relationship with monopodia per plant, boll weight, GOT, lint index. GOT and fiber strength were significantly correlated with lint index and fiber fineness, respectively. Fiber strength and fiber fineness were inversely correlated with fiber length. Thus, focusing on such breeding strategies incorporated with marker assisted selection and genomic improvements may result in balance improvements in various yield and fiber quality traits.

Cluster analysis showed four discrete clusters, comprised of 6, 4, 1 and 6 genotypes, respectively. Cluster III was the smallest one with a single genotype followed by cluster II and comprised of four genotypes followed by cluster I and IV comprised of six genotypes each. Cluster analysis could help in improving heterosis and adaptability by crossing genotypes from different clusters.

Disclaimer: None.

Conflicts of Interest: The authors declare no conflict of interest.

Source of Funding: None

Ethics approval statement: Not Applicable

Authors' Contribution Statements: AIA: Execution of experiment, Statistical analysis, data collection: MT, AS: Execution of experiment, data collection, HMR: Proofread the manuscript, SHK: Final revision and editing, and IAR supervised the experiment and provided the resources.

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