Principal Component Analysis of Yield and Fibre-Related Traits in Cotton Genotypes

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Abstract

Studies on principal component analysis of cotton genotypes for hereditary diversity by yield and related characters, including fibre quality attributes, were conducted at the Research Farm of the Plant Breeding and Genetics Department, Faculty of Agriculture, Gomal University, D I K, during the cotton crop season 2023. The trial was conducted to examine the impact of genetic variability in cotton accessions, using Principal Component Analysis (PCA), and to estimate heritability and genetic gain for fibre quality, yield, and associated factors in cotton germplasm. Sixty-four cotton germplasms were assessed in an RCB design with three replications. Statistics were documented for various yield and related attributes along with fibre quality attributes like plant height, monopodia, sympodia, and No. of bolls, weight, population, seed cotton produce, GOT, fibre length, strength, micronaire value, and uniformity index. Results revealed that estimations of genotypic and phenotypic quantity of difference were observed to be maximum and commonly similar to each other, whereas environmental quantity of variance was low, indicating that all evaluated traits were organized heritarily with a minute environmental impact. Heritability estimates were highest for all the studied attributes, depicting very little influence of the environment on these genotypes. Similarly, genetic advance was also maximum for all the evaluated attributes. Among the 14 principal components, 5 had eigenvalues greater than 1 and an aggregate variation of 78% for entirely evaluated traits. PC I and PC II contribute approximately 50 % of the aggregate variances. Sixty-four germplasms were organized into three clusters (1, 2, and 3) with an average similarity level of 79.83% among clusters. Baghdadi, CIM 622, Sitara 008, CEMB 66, Leader 5, Cyto 178, FH Lalazar, CRIS 600, AA 703, and Sitara 009 were assessed as heritably maximum varied genotypes which can be successfully used in the cotton development program in the future.

Keywords: Genetic, diversity, heritability, cluster, component, analysis

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Introduction

Cotton is a natural fibre commonly known as “Queen of the fibre plants” and “White Gold”. It is grown in more than sixty tropical and sub-tropical countries of the world (Vineela *et al*., 2013). In Pakistan, cotton is widely grown as a cash crop to support the country's economy by earning foreign exchange (Haidar *et al*., 2012). Cotton adds 0.8 % to GDP and 4.1 % of value added in the agricultural sector. During 2019-20, it rose to 2,527 thousand ha, which is greater by 6.5 % over the previous year’s area of 2,373 thousand ha. Cotton production is expected at about 9,178 thousand bales, which is less by 6.9 % over the previous year’s production of 9,861 thousand bales. Cotton yield is estimated at around 618 Kgs/Hectares, which is lower by -12.6 % over the previous year’s yield of 707 Kgs/Hectares. Even though the total area improved over the previous year, the total performance stayed lower on account of unfavourable climate conditions and poor accessibility to water during major phases of growth and development, as well as insect pest attacks. This might be due to various production constraints like biotic stresses (insect pests and diseases), abiotic (elevated temperature, rainfall, scarcity of water, etc.) and selection of cultivars (Farooq *et al*., 2011).

In cotton breeding, conservation of genetic material, i.e., varieties, lines, and wild types are greatest consideration (Latif *et al*., 2014). Elementary principal is incessant enhancement in the heredities of accessible plant germplasms for the establishment of new variability with the aim of potential yield per unit area with satisfactory fibre attributes by different agro-ecological circumstances (Ali & Khan, 2007). Genetic variances regarding various agronomical and morphology-associated traits, as well as their interface with the different biotic and abiotic impacts, have been previously elaborated for improving the cotton breeding schemes (Liaqat *et al*., 2015). Variability in a population may be heritable (genotypic) variance or non-heritable (environmental) variance, which leads to an efficient selection process in future breeding programs (Dhivya *et al*., 2014).

To advance an operative breeding program for future improvement, information regarding the mode of inheritance in quantitative attributes is very important. Broad sense heritability and genetic advance allow breeders in phenotypic selection in early generation (Vineela *et al*., 2013), and support that the traits are determined by the additive nature of genes. The heritability & expected genetic advance favour the early generation selection process (Reddy & Reddy, 2016). Yield and fibre superiority hinge on sympodial and monopodial branches, bolls, boll weight, seed and lint index & GOT along with its correlation with seed cotton yield (Latif *et al*., 2014). Principal component analysis is utilised by breeders to investigate relationships and diversity in various germplasms (Saeed *et al*., 2014a, b; Rehman *et al*., 2015).

Keeping in view cotton as the most significant crop and genetic variation as the key and basic requirements of any breeding program, the present experiment was carried out having below mentioned aims.

1. To examine the level of genetic diversity amongst cotton germplasm, using Principal Component Analysis (PCA).
2. To estimate heritability and hereditary gain for fibre quality, production, and related factors in cotton germplasm.

Materials & Methods

Field trial site

A field trial was conducted for assessment of genetic divergence, genotype and phenotype variation, genotypic and phenotypic variances, heritability estimates, and hereditary gain among sixty-four upland cotton germplasms. The germplasm was collected from the Cotton Research Station (CRS), D.I. Khan. These germplasms were planted at the research site of the PBG Department, Faculty of Agriculture, Gomal University, D.I. Khan, during the cotton crop season 2023.

Field layout, research design, and sowing of cotton germplasm.

Seedbed was prepared and applied with phosphoric fertiliser (P_2O_5) in the form of single super phosphate (18%) @ 60 kg ha^{-1}. The ridges were made with a space of 0.75m between ridges. The seeds of all germplasms were delinted through sulphuric acid treatment. The delinted seeds of all germplasms were planted according to a triplicate Randomised Complete Block design. Plot size was 3 × 3 m^2 with a space of 0.30m within hills, and the seeds were sown at a rate of 5 seeds/hill. The field was directly watered after sowing, and 50 kg per hectare of N in the form of urea fertilizer was applied. After three weeks, thinning was performed, and one plant was left to ensure the recommended plant population. The rest of the nitrogenous fertilizer was applied in split doses at the rate of 50 kg ha^{-1} N in urea form at the flower formation and boll formation stages. All cultural operations were performed as per the recommendations.

The matured open bolls were picked, comprising 2 pickings, in October and November. The picked seed cotton was kept separate in ba~~gs and stored under~~ fumigated conditions.

Data Recording

Data was recorded for various yield and connected characteristics, as well as fibre quality attributes, as below:

Agronomic Traits

1. Plant height (cm)

The height of 5 mature plants was measured with a measuring tape from the base to the main stem tip.

2. Monopodia plant^{-1}

In the early growing periods of the cotton plant, the main stem emerges the vegetative branches from its base, which were counted in five selected plants, and their average was calculated.

3. Sympodia plant^{-1}

During cotton plant growth, the fruit-bearing branches that emerged from the main stem and monopodia were counted in five plants at maturity, and their mean was computed.

4. Bolls Plant^{-1}

Mature bolls from five selected plants were totalled and their average was calculated.

5. Ball weight (g)

From each genotype, about a hundred bolls were randomly picked at maturity and weighed on an electric balance in grams (g), then their average boll weight was estimated.

6. Plant Population

The number of plants was counted from each genotype, and the plant population was estimated using the following formula:

$$\text{Plant Population ha}^{-1} = \frac{\text{Number of Plants plot}^{-1} \text{ x Size of ha}}{\text{Size of plot}}$$

7. Seed cotton yield (Kg ha-1)

A total of all picks from each genotype at regular intervals was taken and weighed through an electric balance in kilograms (kg), and then seed cotton yield per hectare was determined by formulation:

$$\text{Seed cotton yield (Kg Hec}^{-1}\text{)} = \frac{\text{Yield plot}^{-1} \text{ x Size of hectare}}{\text{Size of plot}}$$

8. Lint% % (GOT)

Cottonseed samples of each genotype were balanced and then ginned using the electronic ginning machine. Lint attained from every genotype was weighed, and % (GOT) was calculated:

$$\text{Lint \% (GOT)} = \frac{\text{Weight of lint in a sample}}{\text{Weight of the seed cotton sample}} \times 100$$

Fibre Quality Traits

All fibre quality attributes, viz., staple length, uniformity, fibre fineness, and staple strength, were measured through (HVI-900 SA) in Fibre Tech. Section, CCRI Multan, Pakistan.

Staple Length (mm)

It is the length of fibres expressed in millimetres.

Fibre strength (g tex^{-1})

It is the tensile strength of fibre expressed in g tex.

Micronaire value (µg inch^{-1})

Micronaire value is the fineness of fibres measured in µg inch.

Statistical Analysis

The documented replicated data were subjected to the ANOVA method, and Estimates of broad-sense heritability were investigated as suggested by Steel et al. (1997. The Ward's Linkage Cluster Analysis (WLCA) and Dendrogram were constructed to calculate Euclidean distances and relationships among various germplasms according to Ward (1963). Principal component analysis (PCA) was done on the mean data by using XLSTAT software (Khodadadi et al., 2011).

Results & Discussion

Hereditary attributes

Average SS, genotypic variance (GV), environment variance (EV) and phenotype (PV) variance, genotype coefficient of variance (GCV), environment coefficient of variance (ECV) and phenotype coefficient of variance (PCV), broad sense heritability (h^2) and hereditary advance (GA) were calculated for produce, related characteristics and fiber parameters. Estimates of mean sum of squares and F values of yield and correlated characteristics are given in Tables 1 and 2. Data portrayed extremely significant variances (P≤0.01) among genotypes for entirely assessed characteristics, i.e., plant height, monopodia, sympodia, bolls, boll weight, population, and seed cotton yield. Similarly, the variances were also significant for the fibre quality attributes like GOT, fibre length, strength, micronaire value, and uniformity index.

Table 1 Analysis of variance of seed cotton yield and related attributes in cotton genotypes.

Attributes	**Mean sum of squares**			**F value**	**CV %**
	Replications	**Genotypes**	**Error**		
Plant height (cm)	1198	1352	53	25.45**	5.68
Monopodia plant^{-1}	1.63	1.93	0.15	12.95**	18.33
Sympodia plant^{-1}	8.5	34.3	0.23	147.42**	2.50
Number of bolls plant^{-1}	9.58	40.9	0.13	311.13**	1.59
Boll weight (g)	0.02	0.47	0.00	167.55**	1.78
Plant population (ha^{-1})	5310833	60480000	311487	194.18**	1.74
Seed cotton yield (kg ha^{-1})	121983	747585	776	963.59**	1.29

** Significant at P≤0.01

Table 2: Mean sum of squares, F value, and coefficient of variation of fibre quality attributes in cotton genotypes.

Attributes	**Mean sum of squares**			**F value**	**CV %**
	Replications	**Genotypes**	**Error**		
Ginning out turn (%)	16.2	4.8	0.1	59.41**	0.73
Fibre length (mm)	6.03	3.66	0.07	54.80**	0.93
Fiber strength	12.9	7.7	0.1	61.37**	1.26
Micronaire	0.98	0.56	0.01	105.18**	1.68
Uniformity index (%)	18.6	7.0	0.1	63.96**	0.41

** Significant at P≤0.01

Estimates of genotypic variance for the yield and related attributes are presented in Table 3 while estimates of the fiber quality attributes are given in Table 4. these estimates ranged from maximum value examined in plant population (20056171), seed cotton yield (248936.33), plant height (432.96) and bolls plant^{-1} (13.62) to minimum value observed in boll weight (0.15). The estimates of phenotypic variance ranged from the maximum value observed in the plant population (20367658), seed cotton yield (249712.33), plant height (486.08), and bolls per plant (13.75) to the minimum value examined in boll weight (0.16). The estimates of environmental variance ranged from the maximum value examined in the plant population (311487), seed cotton yield (776), and plant height (53.12) to the minimum value observed in boll weight (0.01).

Table 3 Estimation of various genetic attributes for seed cotton yield and related characters in cotton genotypes.

	Plant height (cm)	Monopodia plant^{-1}	Sympodia plant^{-1}	Number of bolls plant^{-1}	Boll weight (g)	Plant population (ha^{-1})	Seed cotton yield (kg ha^{-1})
Genotypic variance	432.96	0.59	11.35	13.62	0.15	20056171	248936.33
Environmental variance	53.12	0.15	0.23	0.13	0.01	311487	776
Phenotypic variance	486.08	0.74	11.58	13.75	0.16	20367658	249712.33
Genotypic coefficient of variance	16.20	36.57	17.47	16.21	13.23	13.93	23.02
Environmental coefficient of variance	5.67	18.33	2.50	1.59	1.77	1.74	1.28
Phenotypic coefficient of variance	17.17	40.91	17.64	16.28	13.34	14.03	23.06
Heritability %	89.07	79.93	97.99	99.04	98.23	98.47	99.69
Genetic advance	40.45	1.42	333.49	7.56	0.80	9154.71	1026.21
Genetic advance %	31.5	67.4	35.6	33.2	35.6	28.5	47.3

Table 4: Estimation of various genetic components for fibre quality traits in cotton genotypes.

	Ginning out turn (%)	Fiber length	Fiber strength	Micronaire	Uniformity index %
Genotypic variance	1.58	1.19	2.52	0.18	2.31
Environmental variance	0.08	0.07	0.12	0.01	0.11
Phenotypic variance	1.66	1.26	2.65	0.19	2.42
Genotypic coefficient of variance	3.20	3.92	5.66	9.92	1.87
Environmental coefficient of variance	0.73	0.92	1.26	1.68	0.41
Phenotypic coefficient of variance	3.29	4.03	5.80	10.06	1.91
Heritability %	95.11	94.72	95.27	97.20	95.45
Genetic advance	2.52	2.19	3.19	0.87	3.06
Genetic advance %	6.4	7.9	11.4	20.1	3.80

Estimation of GCV for the yield and related attributes is presented in Table 3, while estimates of the fibre quality attributes are given in Table 4. These coefficients of variance ranged from the maximum value observed in monopodia plant^{-1} (36.57), seed cotton yield (23.02), sympodia (17.47), and number of bolls (16.21) to the minimum value examined in uniformity index (1.87). The estimates of phenotypic coefficient of variation ranged from the maximum value examined in monopodia plant^{-1} (40.91), seed cotton yield (23.06), sympodia plant^{-1} (17.64), and plant height (17.17) to the minimum value examined in uniformity index (1.91). The estimates of environmental coefficient of variation ranged from the maximum value observed in monopodia plant^{-1} (18.33), plant height (5.67), to the minimum value examined in uniformity index (0.41). Analogous results were also previously described by Sadettin (2022 and Yahia et al. (2022 who found maximum variability and genetic variation for various yield-associated characters in cotton genotypes. Similarly, the previous consequences of Ravansiddaya et al. (2024, Mehran et al. (2023 and Farooq et al. (2023 also supported these results.

The estimates of heritability and genetic advance calculated for the yield and associated traits and fibre quality traits are offered in Tables 3 and 4. Heritability estimations ranged from the maximum value examined in seed cotton yield (99.69), bolls per plant^{-1} (99.04), plant population (98.47), and boll weight (98.23) to the minimum value observed in monopodia (79.93). Estimates of genetic advance fluctuated from the maximum value observed in plant population (9154.71), seed cotton yield (1026.21), monopodia plant^{-1} (333.49), and plant height (40.45) to the minimum value examined in boll weight (0.80). Estimations of genetic advance ranged from a maximum value examined in monopodia plant^{-1} 67.35), seed cotton yield (47.35), sympodia (35.62), and bolls (33.23) to a minimum value observed in uniformity index (3.76). The overall variance estimates reproduced a handy equilibrium with one another for all assessed characteristics. Parallel results were also previously described by Sadettin (2022 and Yahia et al. (2022 who found maximum heritability estimates and genetic advance for various yield-related characters in cotton genotypes. Similarly, previous consequences of Ravansiddaya et al. (2024, Mehran et al. (2023, and Farooq et al. (2023 also supported these results.

Principal component analysis (PCA)

To discover significant variances in 64 genotypes, principal component analysis was utilized on recorded average observations of all attributes simultaneously (Tables 5 and 6). Among 14 principal components (PC's), 5 principal components exposed Eigenvalue > 1 and 78.409% of aggregate variances for characteristics examined. PC I portrayed 4.314 eigenvalue and 37.19% variance. Genotypes in PC I demonstrated positive impacts for seed cotton yield (0.479), bolls (0.371), and sympodia (0.345), whereas negative impacts for monopodia (-0.193) and micronaire value (-0.145). PC II exposed 1.825 eigenvalue and 13.47% of variance. Genotypes in PC II presented positive scores for population (0.471), strength of fibre (0.493), height (0.451), and uniformity (0.392), whereas negative scores for boll weight (-0.342), sympodia (0.131), and bolls (-0.126). PC III portrayed 1.525 eigenvalues and 11.231% of variance. Genotypes in PC III offered positive consequences for population (0.475), height (0.217), and lint% % (0.208), whereas staple length (-0.457), strength (-0.370), and monopodia (-0.368). PC IV exposed 1.332 eigenvalues and 9.510 % of variance. Consequently of genotypes in PC IV revealed positive impacts for lint% % (0.510) and staple length (0.252), whereas negative impacts for micronaire value (-0.634) and plant height (-0.328). PC V portrayed 1.012 eigenvalue and 7.012 % of variance. Genotypes in PC V offered positive scores for boll weight (0.546), Micronaire value (0.284), and lint% % (0.262) while negative scores for sympodia (-0.434) and bolls (-0.433). In PCA, the most commonly utilised standard to obtain principal components is the eigenvalue-one criterion, also termed as the criterion suggested by Kaleri *et al.* (2015. Using this technique of PCA, any component can be maintained and analysed having a value more than 1. Among the 14 PCS, five depicted more than 1 eigenvalue, and they depicted 78.409% of the variability cumulatively. Furthermore, among these, PC-1 and 2 contributed 50.656% of the variability cumulatively, which were the two major PCS of the present study. Various relevant characteristics that significantly contributed to these two PCS were seed cotton yield, sympodia, and No. Of bolls and population, which articulated a pronounced influence on the variability cumulatively. Thus, it is suggested that, based on this major contribution by these characteristics, they must be given special emphasis in any breeding scheme for cotton development in the future. Similar findings were also previously presented by Saeed *et al.* (2014b, Kaleri *et al.* (2015 and Latif *et al.* (2015 regarding the significant contribution of these and other like traits in cotton development.

Table 5: Estimates of principal component analysis for seed cotton yield and related traits in cotton genotypes.

Numerical variable	**PC I**	**PC II**	**PC III**	**PC IV**	**PC V**
Eigenvalue	4.314	1.825	1.525	1.332	1.012
Variability (%)	37.186	13.470	11.231	9.510	7.012
Cumulative (%)	37.186	50.656	61.878	71.397	78.409
Traits	**PC I**	**PC II**	**PC III**	**PC IV**	**PC V**
Plant height	-0.0173	0.4510	0.2169	-0.3284	-0.0591
Monopodia plant^{-1}	-0.1928	-0.0535	-0.3680	-0.0948	-0.1256
Sympodia palnt^{-1}	0.3450	-0.1312	-0.1309	-0.2005	-0.4345
No. of bolls plant^{-1}	0.3711	-0.1264	-0.1126	-0.1555	-0.4333
Boll weight (g)	0.3211	-0.3421	-0.1213	-0.1779	0.5465
Plant population (ha^{-1})	0.0643	0.4710	0.4747	0.1035	-0.1006
Seed cotton yield (kg ha^{-1})	0.4790	0.0061	0.1310	-0.1056	-0.0059

Table 6: Estimates of principal component analysis for fibre quality traits in cotton genotypes.

Statistical variable	**PC I**	**PC II**	**PC III**	**PC IV**	**PC V**
Eigenvalue	4.314	1.825	1.525	1.332	1.012
Variability (%)	37.186	13.470	11.231	9.510	7.012
Cumulative (%)	37.186	50.656	61.878	71.397	78.409
Traits	**PC I**	**PC II**	**PC III**	**PC IV**	**PC V**
Ginning out turn (%)	0.1854	-0.0672	0.2078	0.5096	0.2617
Fibre length (mm)	0.2190	0.2176	-0.4571	0.2524	0.1123
Fiber strength	0.1635	0.4930	-0.3698	0.0165	0.0321
Micronaire	-0.1448	-0.0061	0.1201	-0.6336	0.2844
Uniformity index (%)	0.1875	0.3920	-0.2394	-0.1693	0.3414

Score plot

Score plot analysis classified these 64 germplasms based on their genetic structure (Fig. 1). The germplasms that were found at the vertex of the score plot or polygon and considered as the most diverse genotypes were AA 703, BH 184, Sitara 008, CEMB 66, Baghdadi, CIM 622, SLH 8, FH Lalazar, CRIS 600 and Sitara 009. The remaining germplasm was found near the origin of the score plot, which was reported to be genetically at par and have very low genetic diversity on account of their narrow genetic base. Among the 64 germplasms, the most closely related germplasms were BH 185, CRIS 508, IR 3701, SLH 12, CEMB 55, IUB 63, NIBGE 4, RH 647, TH 21/09, and NIAB 874 B. These germplasms depicted very little diversity, a narrow genetic base, and less opportunity for cotton improvement in future breeding programs. These results are in complete analogy with the previous findings of Ravansiddaya et al. (2024 and Mehran et al.

(2023, who also reported a similar trend of diversity and genetic variation in cotton germplasm. These results are also in line with Farooq et al. (2023 who also observed divergence in cotton germplasm during their investigations.

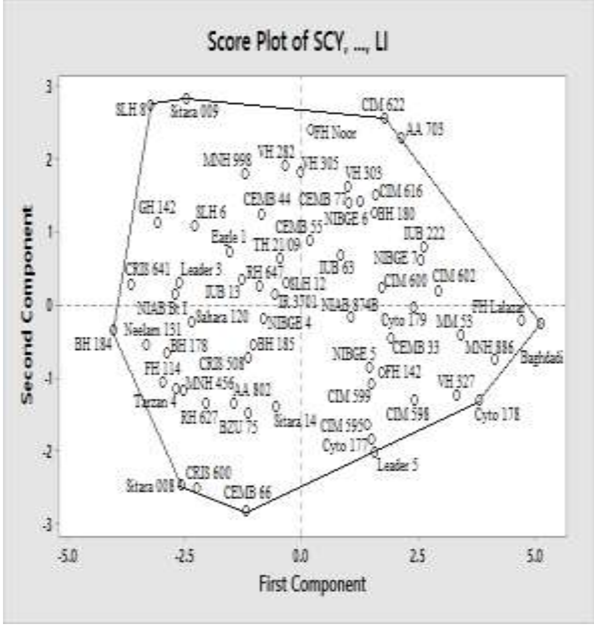


Figure 1: Score plot using the mean data of sixty-four cotton germplasms.

Biplot Graph

In a biplot graph of principal component analysis, the base of a biplot graph joining marked point of various attributes is designated as 'traits vector' and the cosine angle between attributes explained correlation among all the examined attributes (Fig. 2). When the cosine angle between attributes having < 90° depicted positive correlation, angle having > 90° exhibited negative correlation and when angle is of right angle (90°) represented independent behaviour between attributes. Biplot graph depicted that seed cotton yield showed positive correlation effects with number of bolls per plant^{-1}, number of sympodia plant^{-1}, average boll weight, plant population, ginning out turn, fibre length, uniformity index, and fibre strength. The graph represented a negative correlation of seed cotton yield with plant height at maturity, number of monopodia per plant^{-1} and micronaire value. The previous findings of Farooq et al. (2023 and Mehran et al 2023 were also supported by the present results, which further supported these findings of genetic diversity in cotton germplasm.

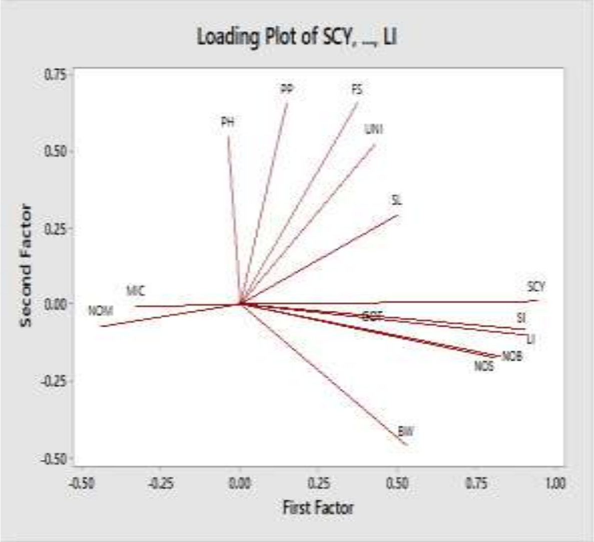
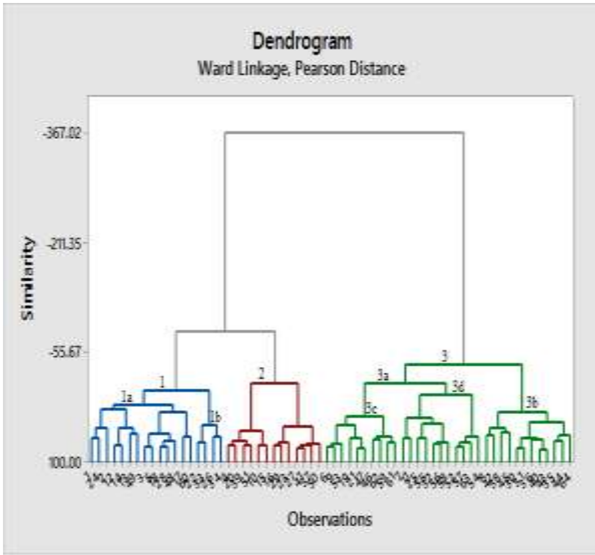


Figure 2: Biplot graph using the mean data of sixty-four cotton germplasms.

Ward's linkage cluster analysis

Sixty-four genotypes were organized into three clusters (1, 2 and 3) by using the Ward's linkage cluster analysis (Fig. 3). In Ward's linkage cluster analysis, a cluster of genotypes Sitara 008 and MNH 456 was found in sub cluster 3b of cluster 3, exhibited similarity level (79.83%) and distance level (1.93) from centroid (Fig. 3). A cluster of genotypes CIM 599 and Cyto 177 was found in cluster 2 with similarity level (79.49%) and distance level (1.967) from centroid. A cluster of genotypes, RH 647 and CEMB 55, found in sub-cluster 3c of cluster 3 exhibited a similarity level (79.42%) and distance level from the centroid (1.97). A cluster of genotypes FH 142 and VH 305 constituted in Ward's cluster analysis with the highest negative similarity level of -367.023% and distance level (44.78) from the centroid. Genotype CIM 599 made maximum clusters with positive similarity level, i.e., Cyto 177 (79.49%), CIM 598 (74.60%), NIBGE 5

(71.64%), and IUB 222 (48.84%). FH 114 constructed maximum clusters with positive similarity level, i.e., BH 178 (78.42%), BH 184 (63.82%), CRIS 600 (41.91%), and CRIS 641 (27.16%).



cotton germplasMs.

Conclusion

The instant results concluded that the estimates of genotypic and phenotypic variances, genotypic and phenotypic coefficient of variation, heritability estimates and genetic advance were highest for all the studied traits while the environmental variances and environmental coefficient of variation was low and negligible showing that traits were genetically controlled and are not under the influence of environment. Out of 14 principal components, 5 components depicted eigenvalues greater than 1 and an aggregate variability of about 78% for the assessed characteristics. The PCI and PCII contributed about 50% of the variability. CIM-622, BH-184, Cemb-66, Leader, sitara-006, SLH-8, cyto-178, and FH Lalazar were found to be genetically maximum deviating germplasm, and these could be exploited in the upcoming breeding package for cotton yield and fibre quality improvement.

Authors Contribution

Nasr Ullah Khan, Muhammad Mohibullah, and Muzammil Mahboob Ur Rehman conceived the idea, designed the study, and drafted the manuscript. Muhammad Mudasir, Irfan Ahmad Khan, Rima Bibi, and Riffat Mustansir conducted the experiments, collected and analysed the data. All authors read the drafted manuscript.

References

Ali, M. A. and I. A. Khan. 2007. Assessment of genetic variation and inheritance mode in some metric traits of cotton (Gossypium hirsutum L.). J. Agric. Social Sci. 4(3):112-116.

Dhivya, R., P. Amalabalu, R. Pushpa & D. Kavithamani. 2014. Variability, heritability and genetic advance in upland cotton (Gossypium hirsutum L.). Afr. J. Plant Sci., 8(1): 1-5.

Farooq, A., Shakeel, A., Saeed, A., Farooq, J., Rizwan, M., Chattha, W. S., ... & Ramzan, Y. (2023). Genetic variability predicting breeding potential of upland cotton (Gossypium hirsutum L.) for high temperature tolerance. Journal of Cotton Research, 6(1), 1-17.

Haidar, S., M. Aslam, M.U. Hassan, H.M. Hassan & A. Ditta. 2012. Genetic diversity among upland cotton genotypes for different economic traits and response to cotton leaf curl virus (CLCV) disease. Pak J. Bot., 44(5): 1779–1784.

Kaleri, A.A., S.Y. Rajput, G.A. Kaleri and J.A. Marri. 2015. Analysis of Genetic diversity in genetically modified and non-modified cotton (Gossypium hirsutum L.) genotypes. J. Agric. Vet. Sci. 8(12): 70-76.

Khodadadi, M., Fotokian, M. H., & Miransari, M. (2011). Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. Australian Journal of Crop Science, 5(1), 17-24.

Latif A., T. Ahmad, S. Hayat, G. Sarwar, M.Z. Ehsan, M. Raza, M. Sarwer and I.A. Khan. 2014. Genetics of yield and some yield contributing traits in upland cotton (Gossypium hirsutum L.). J. Plant Breed. Crop Sci., 6(5): 57-63.

Liaqat, S., R.I. Ahmed, S. Ahmad, M. Bilal, A. Karim, A. Qayyum, R.T. Ahmed & M. Rafiq. 2015. Evaluation of diverse germplasms of cotton (Gossypium hirsutum L.) for yield and fibre attributes by multivariate analysis approach. J. Agric. Sci. & Review, 4(5): 146-150.

Mehran, M., M. Ashraf, S.M. Shahzad, M.S. Shakir, M.T. Azhar, F. Ahmad, and A. Alvi. 2023. Growth, yield, and fibre quality characteristics of Bt and non-Bt cotton cultivars in response to boron nutrition. Journal of Cotton Research, 6 (1): 1.

Reddy, K.B. & V.C. Reddy. 2016. Genetic variability and heritability in upland cotton (Gossypium hirsutum L.). Int. J. Agri. Sc. & Vet. Med., 4(3): 17-21.

Rehman, S., M.A. Abid, M. Bilal, J. Asharaf, S. Liaqat, R.I. Ahmad & G. Qambar. 2015. Genotype by trait analysis and estimates of heritability of wheat (Triticum aestivum L.) under drought and control conditions. Basic Res. J. of Agric. Sci. & Review 4(4): 127–134.

Revanasiddaya, J.M. Nidagundi, B. Fakrudin, P. Kuchanur, L.N. Yogeesh, S. Hanchinal, T.C. Suma, G. Sunkad, B. Muralidhara, D. Maheshkumar, C.P. Sudha, S. Rashmi, V.C. Raghavendra. 2024. Genetic diversity among colored cotton genotypes about their fibre colour and ploidy level using SSR markers. Czech journal of plant breeding. 60(1): 12-24.

Sadettin, C. 2022. Genetic diversity analysis of some upland cotton (Gossypium hirsutum L.) genotypes using SSR markers. Turkish journal of nature and science. 11(1): 80-89.

Saeed, F., J. Farooq, A. Mahmood, T. Hussain, M. Riaz and S. Ahmad. 2014a. Genetic diversity in upland cotton for cotton leaf curl virus disease, earliness, and fibre quality. Pak. J. Agric. Res., 27(3): 226-236.

Steel, R.G.D., J.H. Torrie and D.A. Dickey. 1997. Principles and procedures of statistics: A biometrical approach. 3rd ed. McGraw-Hill, New York.

Vineela, N., J.S.V.S. Murthy, P.V. Ramakumar & S.R. Kumari. 2013. Variability studies for physio-morphological and yield components traits in American cotton (Gossypium hirsutum L.). J. Agri. & Vet. Sci., 4(3): 07-10.

Ward, J.H. 1963. Hierarchical Grouping to Optimise an Objective Function. J. Amer. Stat. Association, 58: 236-244.

Yehia, W., & El-Hashash, E. F. (2022). Estimates of genetic parameters for cotton yield, its components, and fibre quality traits based on line x tester mating design and principal component analysis. Egyptian Journal of Agricultural Research, 100(3), 302-315.