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Research Article

EVALUATION OF VARIOUS COTTON GENOTYPES THROUGH GENETIC DIVERSITY ANALYSIS

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Abstract

Fifty-two varieties/strains of cotton were studied to explore the genetic divergence in the yield trials at Cotton Research Station, Faisalabad. The study aimed to identify strains with earliness, CLCuD tolerance, and superior yield with better fiber quality. Correlation analysis showed significant positive association of seed cotton yield (SCY) with boll number, boll weight(g), ginning out turn (GOT) and fiber length, while significant negative association with leaf curl disease and first flower appearance date was observed. Principal components analysis revealed that four out of 11 principal component showed Eigen value >1. The contribution of these PCs towards total variability was 76.8% with PC-1 with maximum (44.4%), followed by PC-2 (12.2%), PC-3 (10.9 %) and PC-4 (9.3%). Traits including yield, bolls number, boll weight and plant height exhibited noteworthy positive factor loading in PC-1, while cotton leaf curl virus, days to first boll opening and first flower had maximum negative loadings. The findings of cluster analysis indicated that the genotypes present in cluster V (FH-1131, FH-1133, FH-1214, FH-525, FH-453, FH-333, FH-1132, FH-1135, FH-416, FH-1134 and FH-938) have excellent combination of all desirable traits viz., earliness, fiber quality, seed cotton yield (SCY) and its contributing traits. As apparent from the results of cluster and principal components analyses, topmost genotypes based on genetic divergence data may also be tested in provincial and national yield trials because they have combination of better yield and quality parameters.

Keywords: *Correlation, Principal components, Cluster, Cotton, Quality*.
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1. INTRODUCTION

Cotton is considered to be the most important source of oil and natural fiber. According to Huang et al., (2021) cotton (Gossypium spp.) is a leading fiber crop grown all over the world and is also employed as a model system for plant polyploidization, cell wall biogenesis and cell elongation. The chief cotton producers are China, United States of America (USA), Pakistan, Turkey, Uzbekistan, Brazil, Egypt and Greece sharing nearly 85% of the world cotton production, Isong et al., 2022. About 98% of the demand for natural fiber comes from the tertraploid (4X) cotton G. barbadense and G. hirsutum (Isong et al.,2017). Cotton is mainly cultivated in tropical and sub-tropical climate with temperatures range between 40 and 45 °C (Zafaret al., 2021).

The climate changes including erratic rainfall, temperature fluctuations and high humidity induced severe damages to cotton crop during 2022–2023 seasons in Pakistan. Though in 2022–23, the cultivated area of cotton crop climbed from 1,937 thousand hectares to 2,144 thousand hectares represented an increase of 10.7 percent. But climatic fluctuations badly hit Punjab's major cotton-growing regions like Rajanpur, DG Khan, and Taunsa. In addition, severe pest pressure persisted throughout the season, including Pink bollworm, Whitefly, and Thrips which become another cause of declined cotton production (Anonymous, 2022).

The breeders always aim for higher and sustainable yield by selecting genotypes having traits that contribute to increased yield. Yehia and El-Hashash, 2019 explored genetic diversity in Egyptian varieties. Exploitation of principal component analysis, which demonstrates the patterns of variation that occur between hybrids, one can learn about genotypes that are genetically varied but have significant agronomic value. For the purpose of improving these qualities, morphological and fiber quality traits genetic differences within and between various cotton genotypes have been investigated by Sahar et al.,2021.

The key benefit of PCA is arrangement of each strain in one set only (Munir et al., 2020). In addition to understanding the correlations between yield, its components, and fiber quality parameters, Yehia and El-Hashash, 2021 employed the PCA analysis to evaluate the relationship and diversity between different cotton genotypes. In most cases, the character that contributes the most in variation is chosen. The benefit of PCA is that it can pinpoint the variable or characteristic that separates the population into clusters or groups. As reported by Javed et al., 2017, the PCA is being used extensively to investigate level of variation amongst different useful traits for the purpose of developing CLCuD tolerant genotypes.

According to Fonseca & Paterson, 1968 correlation coefficient analysis determines the component character that can be selected to improve seed cotton production by measuring the strength of association between various plant traits. With the exception of fiber quality, there is significant genetic variability across different cotton genotypes for seed cotton output and yield contributing variables (Khokhar et al., 2017).Seed cotton yield (SCY), boll weight (g), uniformity ratio, Sympodia number, boll numbers and plant height were principal components with the most variability (Isong et al., 2017).

To create more productive cotton genotypes for Pakistan's varied agro-ecological production regions, these studies will be helpful in development of genotypes suitable for changing environmental conditions. Likewise by knowing the strength of the association involving yield and its numerous components shall help plant breeders to choose plants with desirable traits keeping in view the needs of the farmers.

2. Strategy Adopted

2.1. Breeding materials used

The field area which was used for study was research farm of Cotton Research Station, Faisalabad, during cropping season 2022–2023, where fifty-two cotton elite lines, including a check variety, were assessed. On 5th of May, the breeding material was planted in order to identify strains with earliness, CLCuD tolerance, and superior yield with better fiber quality. The strains were sown in completely randomized block pattern (RCBD) in three (03) replications. Each entry's plot measured 6.09m × 3.04m, having four (04) rows, whereas plant and row spacing’s was 30cms and 60 cms, respectively. Required field related as well as plant protection related procedures were strictly adopted to maintain the health of the plants for better conduct of the experimental material.

2.2. Measurement of Characters

The measuring of characteristics was done using a random selection of 10 plants. By simply counting the days from seeding to the first flower's emergence and the first boll's opening, respectively, the information on days to first bloom and first boll opening was obtained. The primary stem's height (measured in cm) was measured from base to top. Simply counting the entire plant yielded bolls per plant. Each experimental plot's seed cotton output was measured and translated to kg ha-1. To determine the average weight of a boll, twenty five (25) bolls were selected from the top, middle, and base of every guarded plant. Single roller machine was used for ginning and ginning out turn (GOT) % was commuted as:

GOT (%) = Lint Weight / Seed cotton Weight× 100

The seed cotton for fiber quality features, such as fiber length, strength, and fineness, was carefully selected at the crop's peak maturity and allowed to dry out in the sun. Following that, samples from each genotype were taken in order to measure the fiber quality metrics. These samples were ginned using a small experimental ginning machine. To evaluate the fiber quality characteristics, the USTER®- HVI 1000 was utilized. The disease incidence (%) of CLCuD was calculated following the disease scale (Table-1) as mentioned by Saeed et al., 2014.

Disease incidence(%) = Sum of all disease rating/total no. of plants ×16.16

Table -1: Scale for Rating CLCuD disease symptom

Description of Symptom	CLCuD rating	CLCuD incidence (%)	CLCuD reaction
No CLCuD symptoms	0	0	Immune
Swollen secondary along-with tertiary veins	1	0.1- 10	Highly Tolerant
Swollen primary; secondary and tertiary veins	2	10 -30	Tolerant
Veins swelling, leaf curl or enation or both	3	30- 50	Susceptible
Veins swollen leaf curl/enation with Stunting alone	4	> 50	Highly susceptible

2.3. Statistical Analysis

For basic statistics the softwares Statistix 8.1 and Minitab- 17 were used. According to Sneath and Sokal, (1973) pearson's correlation, principal components analysis (PCA) and cluster analysis were carried out.

3. Results & Discussion:

3.1. The Correlation study

Basic statistical procedures depicted sufficient variance amongst the 52 cotton strains for parameters under study, (Table-2). Leaf curl disease was significantly and negatively associated with yield and fiber length (Table 3).Yield has significant positive alliance with boll numbers, boll weight, plant height, fiber length and ginning out-turn while significant negative alliance with Leaf curl disease, days to 1st boll opening and first flower (Table 3). The studies of Memon et al., (2016) reported positive correlation of days to first boll opening with the yield. Bolls per plant has significant positive association with boll weight (g), plant height, ginning out-turn and fiber length. Boll weight (g) has significant positive alliance with plant height, ginning out-turn, and fiber length along with negative association with days to 1st flower. Remarkable positive association of Plant height was noted with ginning out-turn and fiber length however it showed noteworthy negative alliance with days to first flower. Previously, Nikhil et al., (2018) reported positive alliance of sympodia plant-1 with plant height. Days to 1st flower showed considerable positive alliance with 1st boll opening while revealed considerable negative alliance with fiber length and ginning out-turn. First boll opening has significant negative association with GOT%, but GOT %has significant positive association with fiber length.

Cotton Leaf Curl Virus values ranged from 0.40-14.46, while yield values ranged between 2322-4369kg/ha, bolls per plant value ranged between 22-45, boll weight 2.64-4.20g,plant height 134-162cm, days to first flower values ranged between 49-60, days to first boll opening range was from 91-105, ginning out turn 34.90-41.20%, fiber length value ranges between 25.95-29.01mm, fiber fineness value ranges between 4.06-4.90µg/inch, and fiber strength value ranged between 28.20-37.6 g/tex (Table 2). These research findings are also depicted in the previous studies of Khan et al., (2017).

Table:2 Basic Statistic of 52 cotton Strains

Trait	Minimum	Maximum	Mean	S.E. Mean	Std. deviation
CLCuD (%)	0.40	14.46	3.48	0.41	2.97
YLD (kg/ha	2322	4369	3248.2	71.5	515.4
BPP	22	45	32.77	0.86	6.16
BW (g)	2.64	4.2	3.35	0.06	0.4
PH (cm)	134	162	146.48	1.07	7.68
DFF	49	60	54.71	0.41	2.92
DBO	91	105	97.39	0.5	3.61
GOT (%)	34.90	41.2	37.98	0.17	1.19
FL (mm)	25.95	29.01	27.73	0.13	0.91
FF (µg/inch)	4.06	4.9	4.53	0.03	0.21
FS (g/tex)	28.2	37.6	33.49	0.27	1.96

List of abbreviations used: Cotton leaf curl virus disease; YLD: Yield; BPP: Bolls per plant; BW: Boll weight; PH: Plant height; DFF: Days to first square; DBO: Days to first boll open; GOT: Ginning out turn; FL: Fiber length; FF: Fiber fineness; FS: Fiber strength

Table 3: Correlation analysis (Pearson)

Traits	CLCuD	YLD	BPP	BW	PH	DFF	DBO	GOT	FL	FF
YLD	-0.294*									
BPP	-0.220	0.955**								
BW	-0.111	0.896**	0.901**							
PH	-0.275	0.700**	0.731**	0.653**						
DFF	0.236	-0.538**	-0.543**	-0.510**	-0.516**					
DBO	0.274	-0.282	-0.170	-0.271	-0.165	0.545**				
GOT	-0.245	0.575**	0.488**	0.516**	0.369**	-0.402**	-0.422**			
FL	-0.497**	0.602**	0.511**	0.480**	0.498**	-0.483**	-0.262	0.381**		
FF	-0.032	-0.072	-0.091	-0.121	-0.014	-0.002	-0.107	0.054	-0.129	
FS	-0.136	0.005	-0.048	0.117	-0.021	0.212	0.005	0.158	-0.048	-0.071

: Cotton leaf curl virus disease; YLD: Yield; BPP: Bolls per plant; BW: Boll weight; PH: Plant height; DFF: Days to first square; DBO: Days to first boll open; GOT: Ginning out turn; FL: Fiber length; FF: Fiber fineness; FS: Fiber strength

Table 4: Principal component analysis of different traits of cotton genotypes

Variable	PC1	PC11	PC111	PC1V
Eigen value	4.88	1.345	1.2025	1.0202
% of total variation	44.4	12.2	10.9	9.3
Cummulative variance %	44.4	56.6	67.6	76.8
Factors loading by various characters				
Yield	0.423	0.177	-0.010	-0.083
BPP	0.407	0.275	-0.093	-0.092
BW	0.394	0.270	0.013	-0.218
PH	0.354	0.152	-0.082	0.017
FL	0.321	-0.100	0.082	0.450
GOT	0.298	-0.182	0.206	-0.322
FS	0.003	0.077	0.815	-0.294
FF	-0.030	-0.436	-0.190	-0.553
CLCuV	-0.185	0.389	-0.381	-0.470
DBO	-0.203	0.584	0.014	0.112
DFF	-0.325	0.256	0.299	-0.073

Table-5: Cluster examination for earliness, CLCuD, quality and yield related parameters of cotton strains

Trait	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6
CLCuD	3.03	5.10	2.73	4.78	2.36	2.67
YLD	3471.85	2487.13	2881.18	3149.33	4116.17	3828.20
BPP	34.77	24.50	28.27	31.67	43.33	40.00
BW	3.51	2.94	2.95	3.30	3.98	3.84
PH	148.15	139.88	140.18	148.44	154.50	153.40
DFF	54.23	56.13	56.64	55.11	52.33	51.60
DBO	96.54	97.13	99.09	99.44	95.00	95.40
GOT	38.35	37.10	37.25	37.97	38.87	39.00
FL	27.82	26.77	27.50	27.88	28.44	28.46
FF	4.59	4.64	4.48	4.45	4.54	4.39
FS	33.49	33.42	33.55	33.62	33.32	33.50

Table -6: Cluster membership (Cotton strains)

Clusters #	No. of Genotypes	Name of Genotypes
Cluster 1	13	FH-630, FH-613, FH-622, FH-618, FH-545, FH-537, FH-889, FH-614, FH-522, FH-530, FH-535, FH-632, FH-1150
Cluster 2	8	FH-615, FH-624, FH-631, FH-617, FH-627, FH-490, FH-6028, FH-6010
Cluster 3	11	FH-616, FH-611, FH-6041, FH-1148, FH-621, FH-612, FH-619, FH-628, FH-629, FH-1143, FH-6012
Cluster 4	9	FH-620, FH-623, FH-625, FH-6005, FH-626, FH-529, FH-1136, FH-551, FH-6007
Cluster 5	6	FH-1131, FH-1133, FH-1214, FH-525, FH-453, FH-333
Cluster 6	5	FH-1132, FH-1135, FH-416, FH-1134, FH-938

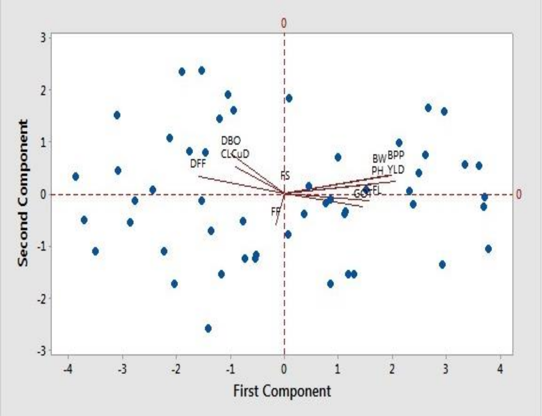

Figure 1: Biplot of Yield and Fiber Related Traits

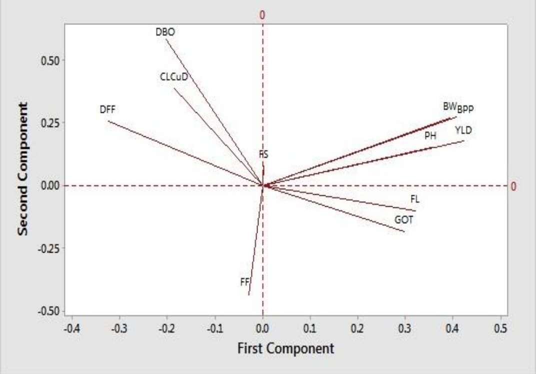

Figure 2: Loading Plot of Yield and Fiber Related Traits

3.2. Principal component and cluster analyses

For exploitation of genetic divergence, the variation is dissected into different components. Principal component analysis (PCA) is reported to be a useful method for exploration of genotypes in breeding strategy (Nazir et al., 2013). In current experimental work, four (04) beyond 11 principal component chosen showing eigen value greater than one (1) (Table_4; Figure_4). Above discussed PCs contributed 76.8% of total variability which depicts the presence of valuable information in these components. The contribution of PC-1 was utmost (44.4%), following PC-2 (12.2%), PC-3 (10.9 %) and PC-4(9.3%). Above findings are in agreement with citations of Latif et al., 2015, Kaleri et al., 2015, Shah et al., 2018 and Kumari and Gunasikaran , 2019. Seed cotton yield(SCY), boll weight(g), bolls number per plant, and plant height configured noteworthy positive factor loading for PC-1, while leaf curl virus , days to first boll opening and first flower had utmost negative loading. Previously, it

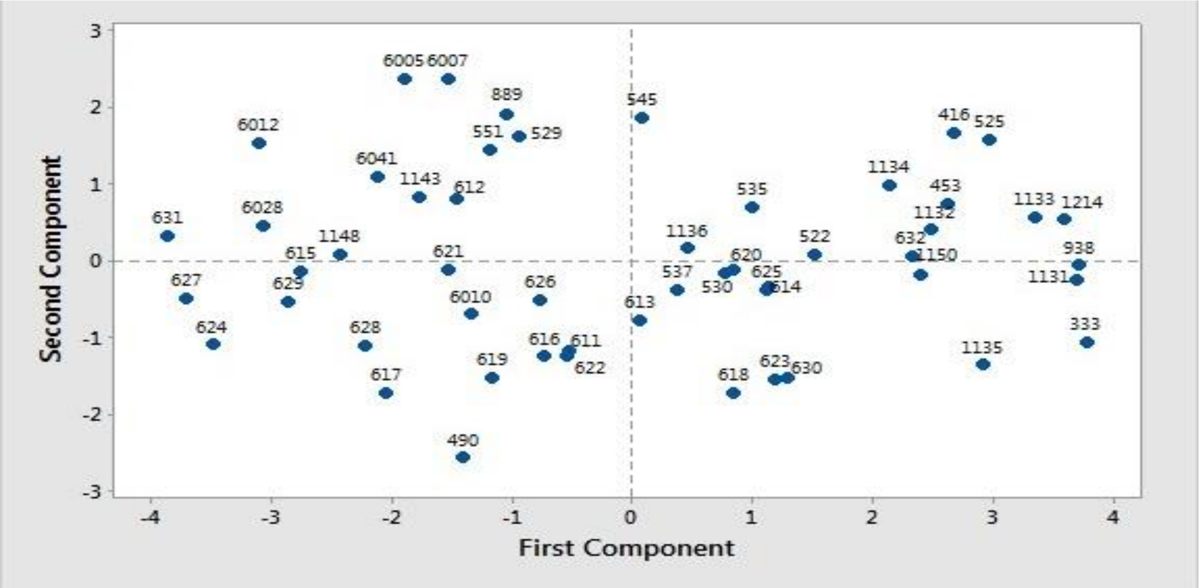

Figure 3: Score plot of Yield and Fiber Related Traits

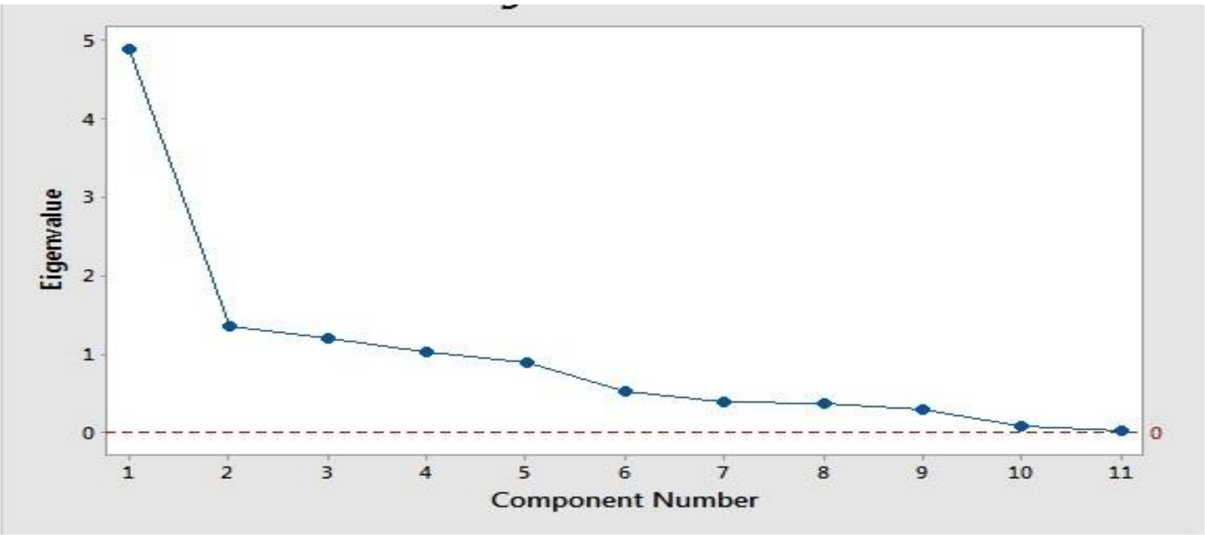

Figure 4: Scree Plot

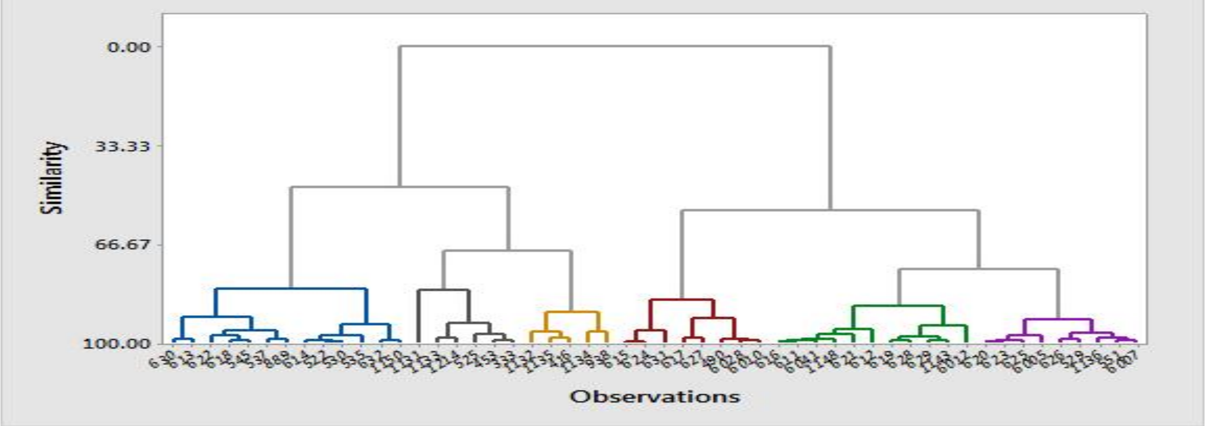

Figure 5: Dendogram of Studied Cotton Genotypes

was reported by Isong et al., 2017 and Jarwar et al., 2017 that yield and sympodia plant-1 has major contribution of in PC-1. While Shakeel et al., 2015 opposing these findings. Highest positive loading on PC-2 was depicted in days to 1st boll opening, CLCuD% and bolls number while, fiber fineness and GOT% exposed utmost negative factor loading. Nazir et al., 2013 and Farooq et al., 2017 confirmed above findings by reporting that GOT % and bolls per plant comprise highest positive loading in PC-2.

In PC-3, GOT% and fiber strength depicted highest positive factor loadings, whereas vice versa for CLCuD% and fiber fineness. Same was reported by Farooq et al., 2015 and Shakeel et al., 2018. In PC-4, it was observed that there was positive factor loadings for fiber length, days to first boll opening and plant height whereas vice versa for fiber fineness. Similar findings were mentioned by Latif et al., 2015 stating positive response among monopodia and GOT% whereas negative lodgings intended for CLCuD%. Magnitude of variation amongst the traits was articulated in PCA which may be used in future breeding strategies aimed for enhancement of yield related traits Nazir et al., 2013. While selecting parents for development of CLCuD% tolerant varieties in cotton, PCA is extensively adopted tool use to investigate level of variance between different parameters, (Javed et al., 2017).

Different strains and studied variables were plotted in PC biplot as vectors (Figure-2). The input of studied variables towards total variability was elaborated by distance of respective variable from PC-1 and PC-2. Previously, Saeed et al., 2014 reported involvement of initial two components in variability. Highest input towards yield was revealed by boll weight, plant height and fiber related traits in biplot and loading plot (Figure 1 & 2). Biplot also depicted the level of correlation between studied parameters. Boll number per plant and yield depicted positive relationship among each other whereas it was negative with CLCuD%. In Figures 1&3, score plot and biplot presented excellent prospective for yield, boll weight(g) and boll number per plant for studied genotypes FH-1131, FH-1214, FH-453, FH-938 FH-525 and FH-333. While considering GOT, the genotypes FH-530, FH-333, FH-614, FH-630, FH-522, FH-1150, FH-1131 and FH-1135 showed maximum potential. The genotypes FH-1135, FH-333, FH-537, FH-619, FH-938, FH-623, FH-616, FH-530, FH-630 and FH-1131 were good for earliness traits. While taking into account the fiber characters; good potential for fiber length was showed by FH-632, FH-1150, FH-938, FH-535, FH-1133, FH-1131, FH-1136, FH-620 and FH-1214 while the genotypes FH-1136, FH-416, FH-535, FH-1134 and FH-545 have good potential for fiber strength and fiber fineness. The genotypes identified for specific traits may be considered in future breeding strategies for incorporation of these traits in any germplasm.

In cluster analysis a group of different observations is splitted into sub groups depending upon the similarities. Fifty two (52) strains were grouped into six clusters. The cluster-1, comprises 13 strains after that cluster no.3; cluster no.4; cluster no.2; cluster no.5 and cluster no.7 comprising 11, 9, 8, 6 and 5 strains, respectively (Table-6). Cluster-5 presented highest values regarding earliness parameters, yield and its causative traits, while acceptable values for fiber characters (Table-5). After that was cluster VI which showed maximum potential for fiber traits while good potential for earliness and yield related characters.

Dendrogram depicted the clustering of studied strains into clusters and further sub clusters (Figure- 5). Derived from cluster study the strains of Cluster 5 & 6 possibly used to incorporate earliness, fiber and yield related traits. This information might be subjugated in breeding practices for developing cotton genotypes with high yield and desirable traits.

3.3. Conclusions and Recommendations

From correlation studies, it is concluded that for yield improvement, selection for characters like boll number, boll weight, ginning out turn and days to 1st boll opening may be considered. The results from principal component analysis are also in line with that of correlation. The findings of cluster analysis discovered that the strains present in cluster-5 and 6 (FH-1131, FH-1133, FH-1214, FH-525, FH-453, FH-333, FH-1132, FH-1135, FH-416, FH-1134 and FH-938) have excellent combination of all desirable traits viz., earliness, fiber quality, seed cotton yield(SCY) and its contributing traits. The genetic divergence in studied germplasm As evident from principle component and clusters analyses will be useful in obtaining better parents which can be used in future breeding strategies and will also be used for testing in yield trials at national and provincial level as they have combination of quality and yield traits.

3.4. Novelty Statement

As the clusters of strain were identified owing advantageous trait combination, therefore these superior strains will be novel for upcoming breeding strategies.

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