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DIVERSITY ESTIMATION OF FIBER RELATED TRAITS OF COTTON GERMPLASM THROUGH MULTIVARIATE ANALYSIS

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The dependence among traits, gene and environmental interaction affects the *Gossypium hirsutum* L. (Malvaceae) crop improvement. The data from 100 cotton genotypes were collected for yield and fiber traits for this purpose. The results revealed notable differences for studied traits. Maximum value for cotton yield was showed by FH-313 (113.50 g/plant). FH-182 showed highest GOT (40.40%) as compared to S-3 which showed lowest (24.23%). MNH-554 (55.40) showed maximum value of mean for number of bolls per plant and lowest for LA-17801. Four PCs with Eigen value more than one were screened through scree plot analysis which contributed 70.1% in total variation. Biplot analysis revealed that total variation exhibited by PC1 was about 28.9%, 17.7% by PC2, 12.9% by PC3, 10.6% by PC4. It was concluded that differences among genotypes for quality and yield traits, higher heritability (97.93%) and genetic advance (33.049) for strength of fiber and height of plant and lower for lint index (54.26%) and boll size (0.67), would be beneficial for cotton breeding programs. Significant correlations among NSB, NB/P, GOT (%), SCY, FS, FL and FF along with greater heritability, genetic advance suggested that choice would be beneficial for enhancement of cotton yield and fiber quality traits among cotton genotypes in Pakistan.

Keywords: Genotypes, heritability, correlation, fiber and yield traits.

INTRODUCTION

Cotton crop, *Gossypium hirsutum* (L) is special in industry and history aspects and attracts global attention. It is key crop of Pakistan. It supports our economy as it is source of foreign exchange and occupation in our country (Imran *et al.*, 2016). Pakistan ranks fifth in the production of cotton and the largest exporter of cotton yarn among the world (Maleia *et al.*, 2017). Cotton shares around ten percent to GDP and fifty five percent to the foreign exchange earnings (Ahmed *et al.*, 2018). World demand for cotton is increasing day by day, which surpass the world population growth rate (Li *et al.*, 2013). Environment plays its important role in performance of any crop (Khan *et al.*, 2017). If the value of heritability is higher it can assist the breeder in selection process. In addition, a good knowledge about the correlation of yield and agronomic traits is necessary for a breeder to solve yield and quality related problems (Nie *et al.*, 2016). The correlation study tells about; to how much extent traits affect each other (Shar *et al.*, 2017; Ahmed *et al.*, 2018). There are different values among cotton genotypes for morphological and yield traits (Lacape *et al.*, 2005; Batool *et al.*, 2010). Positive correlation among cotton genotypes for SCY, NB/P and GOT (%) was reported by various scientists who showed that this can be helpful in the breeding programs for the improvement of cotton in Pakistan (Iqbal *et al*., 2001). Principal component analysis had been used by the researchers in order to get similarity among the genotypes, so that it could be placed into different groups (Khan *et al.*, 2017). In view of the above, present research was executed to perform a multivariate tactics together with correlation and heritability approximations on the one hundred cotton cultivars, which will allow us to distinguish cotton genotypes on the foundation of fiber quality and yield characteristics. The knowledge attained will useful in cotton hybrid breeding programs.

MATERIALS AND METHODS

In this study one hundred (100) cotton genotypes were planted in two cropping seasons in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan between 2017-2019 to study broad sense heritability (H^2), Genetic advance, Genotypic and phenotypic variances, correlation, quality and yield related traits with the aid of PCA. All the genotypes were grown in completely randomized block design layout replicated twice. Seeds of each line were planted 30 cm from other seed in the same row and 75 cm distant from the other row. All recommended agronomic practices and plant protection measure were taken during sowing till harvesting.

Trait measurement and statistical analysis**:** The data for phenotypic variation of 100 *G. hirsutum* genotypes was recorded in field conditions. The data of following parameters for individual plant was recorded i.e., plant height (cm), number of monopodial branches, number of sympodial branches, number of bolls on individual plant basis and size of boll (g). Seed cotton yield (g) was calculated by weighing up all cotton harvested from separate single plant by the use of an electrical balance, lint index was calculated with the aid of given below formula, small saw gin machine was used to gin cotton seeds in order to calculate GOT percentage by using formula given below.

The methodology given by Steel *et al*. (1997) was used to compute variance from the data collected for the traits to determine the differences among various genotypes for variability. For every attribute the genetic variance, ecological variance and morphological variance, broad sense heritability (*H2*) and genetic advance were supplementary assessed from the Analysis of Variance (ANOVA) values conferring to (Savaliya *et al*., 2009) shown as under. The linear correlation coefficient (r) of seed cotton produce with additional return constituents was also determined conferring to (Kwon and Torrie, 1964). The average results was also examined through principal component analysis as described by (Ogunbayo *et al.,* 2005).

$$\mathrm{GCV}\ (\%) = \frac{\mathrm{GMS} - \mathrm{EMS}}{\text{Replication number (r)}} \times 100$$

Where GMS = Genotypes mean squares; EMS = Error mean squares

Environmental variance (Ve) = Error means squares (EMS)

Phenotypic variance (Vp) = Vg + Ve

Heritability (*H2*) broad sense:

$$\mathrm{PCV}\ (\%) = \frac{\mathrm{Vg}}{\mathrm{Vp}} \times 100$$

Genetic Advance:

$$\mathrm{GA} = \mathrm{K.h2}$$

Where: K- constant = 2.06 at 5% level of significance

$$\mathrm{GCV}\ (\%) = \frac{\sqrt{\mathrm{Vp}}.100}{\mathrm{X}} \times 100$$

$$\mathrm{PCV}\ (\%) = \frac{\sqrt{\mathrm{Vp}}.100}{\mathrm{X}} \times 100$$

Vg = genotypic variance, Vp = phenotypic variance, X = mean of sample

$$\text{Lint index} = \frac{\text{Seed Index x GOT\%}}{100 - \text{GOT \%}} \times 100$$

$$\text{GOT \%} = \frac{\text{Lint weight}}{\text{Total seed cotton weight}} \times 100$$

For the measurement of quality character of cotton genotypes greater-volume equipment (HVI-900 SA) was practiced. This computer assisted equipment makes available a complete summary of raw fiber. It computes the vital` properties of cotton fiber such as fiber fineness (µg/ inch), fiber strength (g/tex), and fiber length (mm) (Shakeel *et al.*, 2018).

RESULTS AND DISCUSSION

Conferring to ANOVA (Table 1), the average records of 100 cotton genotypes showed extremely noteworthy variations ($p \leq 0.05$) for traits i.e., seed cotton yield, number of monopodial branches, sympodial branches, plant height, lint index, bolls number, boll size, fiber fineness, fiber length and strength.

The mean performance of cotton genotypes showed that plant height had range of 148.60 cm to 94.50cm. FH-214 (Okra leaf) produced the tallest plants (148.60 cm) followed by Lalazar (147.16 cm). Lowest was recorded for Mubarak (94.50 cm) followed by NS-131 (95.25 cm). Highest number of monopodial branches were recorded for FH 87 (5.90) followed by FH-214 (okra leaf) (5.80) and BH-160 (5.65), while lowest for NIAB-820 (2.00) followed by CIM-282(2.20), NIAB-999 (2.20) and BH-36 (2.25). FH-113 had highest value (47.15) for number of sympodial branches followed by FH-172 (35.95) and MG-6 (35.70) as compared to Red Acala (10.65), Coker 304 (10.75) and Acala SJ (10.85) which had lowest values for the said trait. Highest number of bolls per plant was recorded for MNH-554 (55.40) followed by FH-313 (54.90) while lowest for AA-703 (16.85) followed by LA-17801 (18) and Carolina Queen (20.15), which showed that plant height was not playing vital role in number of bolls per plant. Plant height was also playing its indirect role in seed cotton yield. Lowest value (1.82) for boll size was recorded against BH-121, MNH 129 (1.85) and AGL-2 (1.98) while LA-17801 Showed highest value (2.35) followed by MNH-786 (2.30) and Lalazar (2.24). S-3 showed lowest value (1.87) followed by FH- 941 (2.35) followed by MS.DK (2.65) and CO-2-1 (2.41) while FH-182 (5.86) CRIS 121 (5.73) and CIM-496 (5.06) showed highest value for lint index. FH-313

Table 1. Mean values belonged to different sources of variation for various traits under study in upland cotton.

SOV	DF	PH (cm)	NMB	NSB	NB/P	SCY(g)	LI (g)	GOT %	BS (g)	FF (µg/ inch)	FS (g/tex)	FL (mm)
Replication	1	347.58	2.163	118.73	112.2	106.81	1.57	2.05	2.64	1.60	11.80	2.87
Treatment	99	603.84**	2.26**	75.10**	9.19*	544.81**	2.16*	25.74**	0.32**	0.477**	12.46**	7.72**
Error	199	32.15	0.93	2.94	12.2	21.40	1.28	3.80	0.068	0.023	0.26	0.19

** highly Significant at $p<0.05$ percent level of probability; PH (plant height); SOV (source of variation); DF (degree of freedom); PH (plant height); NMB (number of monopodial branches); NSB (number of sympodial branches); NB/P (Number of bolls per plant; SCY (seed cotton yield); LI (lint index); GOT % (Ginning Out turn; BS (boll size); FF (fiber fineness); FS (fiber strength); FL (fiber length).

Showed highest seed cotton yield per plant (113.50 g) followed by Arizona-6218 (113.15g). Similarly, lowest seed cotton yield was recorded for AA-703 (37.45 g) followed by LA-17801 (41.15 g). Ginning out turn was highest for FH-182 (40.40%) pursued by FH-113 (38.63%) while S3 showed lowest (24.23%) followed by CIM-600 (26.22%). Maximum value for fiber fineness was recorded for FH-1000 (6.30 µg/ inch) followed by FH-114 while S-3 and AA-703 showed lowest values 3.80 µg/ inch and 3.87 µg/ inch for fineness, respectively. FH-172 and FH-113 showed maximum values (3.40 g/tex); 30.81 g/tex) for fiber strength, respectively. While F-281 and Acala SJ had lowest values (22.13 µg/ inch; 22.32 µg/ inch) for this trait, respectively. Highest value for fiber length was recorded for FH-114 (31.69 mm) followed by FH-942 (31.64 mm) and FH-313 (31.40 mm). BH-121 showed minimum value (24.24 mm) followed by S-3 (24.42 mm) for this trait.

Analysis of heritability: Genotypic, phenotypic and environmental variances, heritability (h^2b), genetic advance of seed cotton yield and fiber quality traits of one hundred cotton accessions are presented in Table 2. The value of genotypic coefficient of variance (GCV) fluctuated from 10.16 to 35.99 for traits under study. The greatest value of GCV% (35.99) was found for number of sympodial branches followed by number of monopodial branches (35.92). Phenotypic coefficient of variance (PCV) had range from 31.68 to 231.60 for all traits under study. Plant height, seed cotton yield, NSB and GOT %, fiber strength had greater variation at the level of phenotype (PCV). Most traits showed highest broad sense heritability which ranged from 54.26% for lint index to 97.93% for fiber strength. Genetic advance value was highest for plant height (33.049) followed by seed cotton yield (31.72) and lowest for boll size (0.67) followed by fiber fineness (0.92).

Principal Component Analysis: The average data of 100 cotton genotypes on the foundation of 11 different traits was investigated by PCA (Ogunbayo *et al.*, 2005). The results matrix of 11 x 100 was organized in order to do analysis. In order to do analysis all the variables were made unit less for the purpose of doing PCA. Genotypic component scores were calculated with the aid of character loading. The major 2 constituents were used for a two dimensional consecrations of successions (Fig 1).

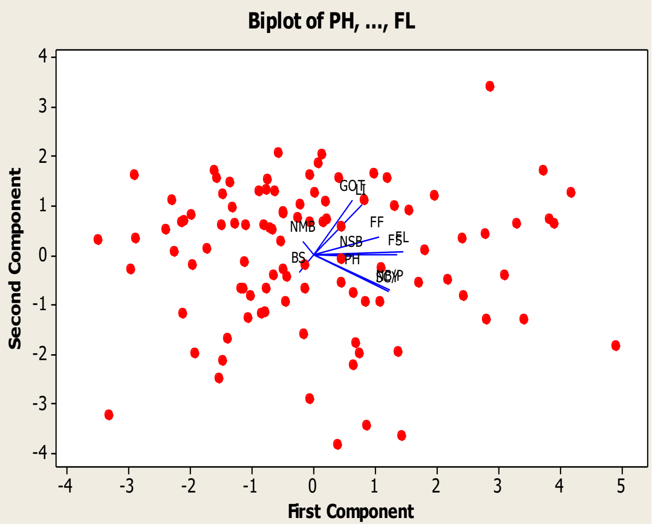

Figure 1. Principal Component's Biplot of 100 cotton germplasm lines for fiber and yield traits

From eleven, only four PCs displayed greater compared to 1 Eigen value, contributed 70.1% in total variation. Among them first four PCs indicated about 28.9% by PC1, 17.7% by PC2, 12.9% by PC3, 10.6% by PC4 and were used for further explanation (Table 3). The factor loading values are given in table 4. Among total variation contributed by PC1 more shared by fiber length (4.58) followed by fiber length (0.426) and bolls number (0.393). All fiber traits under study contributed variation in positive direction. Number of monopodial branches and lint index negatively affected the PC1 i.e., -0.051, -0.381, respectively. Seed cotton yield and NSB contributed less to total variation 0.069 and 0.200,

Table 2. Estimation of parameters of genetic variability and heritability for yield and fiber quality parameters in 100 genotypes of upland cotton.

Traits	GV	GCV %	PV	PCV%	EV	ECV%	H_2B	GA
PH	587.76	20.97	619.92	231.60	32.15	52.47	94.81	33.05
NMB	1.80	35.92	2.74	85.51	0.93	49.86	65.99	1.53
NSB	73.63	35.99	76.57	179.22	2.94	35.11	96.16	11.78
NBP	133.82	35.48	133.97	35.51	0.15	1.18	0.99	16.18
SCY	534.11	34.43	555.51	287.66	21.40	56.46	96.15	31.72
LI	1.52	31.94	2.80	85.16	1.28	57.58	54.26	1.27
GOT	23.84	14.32	27.64	90.05	3.80	33.39	86.25	6.34
BS	0.29	19.30	0.35	35.74	0.07	15.66	80.79	0.67
FF	0.45	14.14	0.48	31.68	0.02	6.70	95.42	0.92
FS	12.33	73.30	12.59	162.23	0.26	23.29	97.93	4.86
FL	7.62	10.16	7.82	53.64	0.19	8.30	97.56	3.81

respectively. PC2 carried 17.7% variation which was mainly due to number of monopodial branches (0.143), boll size (0.570), ginning out turn (0.526), bolls number (0.362) and fiber fineness (0.180) and influences this component positively while plant height, number of monopodial branches, lint index negatively influenced the PC2. Similarly, PC3 and PC4 contributed 12.9% and 10.6% to total variation, respectively. Plant height, number of sympodial branches influenced both the PCs in negative direction. While behavior of seed cotton yield, NMB, lint index, NB/P and fiber strength behaved differently to PC3 and PC4. GOT% and fiber fineness affected PC4 and PC5 positively (Table 3).

Loading plot: A principal component loading plot depicted the variables in the form of vectors. Length of the vectors explained the variation. Variables, i.e., ginning out turn, bolls number on the basis of individual plant, fineness, length and strength of fiber, yield of cotton and lint index, contributed more to total variation as shown by the relative length of their respective vectors. While monopodial branches, size of boll contributed less variation. These two were in opposite direction as compared to other traits, so these had contributed in total variation in negative direction (Fig. 2).

Score Plot: A Principle Component scatter plot/score plot well represented the 100 cotton genotypes in PC1 and PC2 which indicated the variation among cotton germplasm. Genotypes which were close together had less difference among them as compared to genotypes which were distant from one another. Genotypes: FH-182, MNH-129, FH-313, FH-113, Arizona 6218, Lalazar, BH-36, IUB-13, S-3, Acala SJ, Carolina Queen, Gumbo, FH-215, MNH-886 were different from remaining genotypes as these were far away from point of origin when rated on 11 variables. Genotypes: S-3, FH-313 were opposite to FH-182 and Acala SJ as one lies in positive region and other in negative region (Fig. 3).

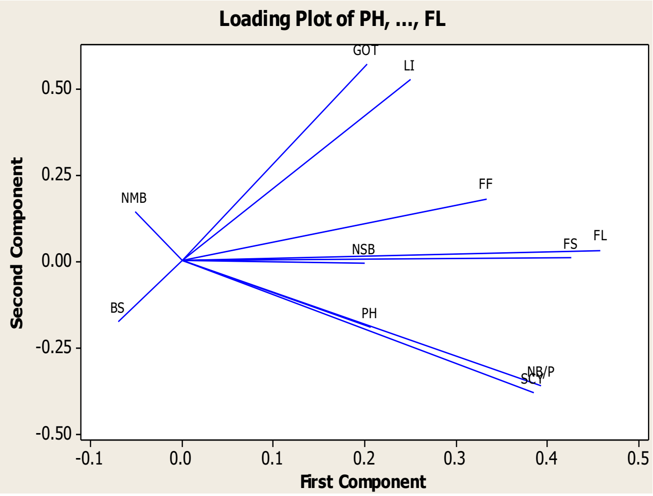

Figure 2. Principal Component's Loading plot of 100 cotton germplasm lines for fiber and yield traits.

Correlation coefficient (r): Table 4 showed correlations among seed cotton yield, its components and fiber traits; are very crucial for improvement of cotton genotypes. Simple correlation coefficient (r) between SCY and fiber related traits among hundred cotton genotypes indicated that PH had strong +ve correlations with NSB, NBP, GOT (%) and with SCY, while NSB was notably and positively related with NBP, GOT %, and SCY. The correlations among NBP, GOT (%), and SCY per plant were highly significant and positive correlated. There was a notable relationship in desirable

Table 3. Eigenvector for yield and fiber quality traits of 100 cotton genotypes.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Eigen value	3.1745	1.9455	1.4172	1.1667	0.9908	0.8396	0.6969	0.3517	0.2658	0.1475	0.0035
Proportion	28.9	17.7	12.9	10.6	9.0	7.6	6.3	3.2	2.4	1.3	0.0
Cumulative	28.9	46.6	59.5	70.1	79.1	86.7	93.0	96.2	98.6	99.9	99.9

Table 4. Factor loadings for yield and fiber quality traits of 100 cotton genotypes.

Variables	**Eigen Vectors**										
	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**	**PC11**
PH	0.206	-0.192	-0.411	-0.458	0.111	0.233	0.516	-0.387	-0.199	0.140	0.014
NMB	-0.051	0.143	-0.551	0.059	0.349	0.539	-0.432	0.230	0.116	0.067	-0.002
NSB	0.200	0.006	-0.156	-0.463	0.336	-0.627	-0.454	-0.079	-0.010	-0.055	-0.011
NBP	0.393	0.362	-0.216	0.360	-0.141	-0.104	-0.091	-0.004	-0.004	0.000	0.706
SCY	0.069	0.177	0.045	-0.550	-0.655	0.243	-0.332	0.201	-0.085	-0.050	0.104
LI	-0.385	-0.381	-0.228	0.285	-0.250	-0.057	-0.123	0.014	-0.044	-0.038	-0.699
GOT	0.250	0.526	0.183	0.007	-0.320	-0.197	0.085	0.157	0.089	0.668	-0.010
BS	0.202	0.570	-0.258	0.056	-0.238	-0.023	0.072	-0.104	-0.179	-0.677	0.028
FF	0.334	0.180	0.418	0.075	0.060	0.319	-0.395	-0.538	-0.300	0.186	-0.001
FS	0.426	0.008	0.268	-0.113	0.277	0.105	0.174	0.652	-0.434	-0.046	0.001
FL	0.458	0.032	0.236	-0.194	0.053	0.191	0.097	0.002	0.787	-0.166	-0.012

Table.5. Correlations of various characters

	PH	NMB	NSB	SCY	NB	LI	GOT	BS	FF	FL
NMB	0.0856									
NSB	0.2807*	0.0088								
SCY	0.2589*	-0.0848	0.1325*							
NB	0.2252*	-0.0775	0.1445*	0.9852*						
LI	-0.0161	0.0252	0.1503	0.0543	0.0568					
GOT	0.0074*	0.1763	0.0719*	0.0154*	-0.0162	0.8152				
BS	0.1578	-0.0576	0.0049	0.0657	-0.0865	-0.0854	-0.1128			
FF	-0.1310	-0.0627	0.0498	0.1509	0.1654	0.2330*	0.2482*	-0.0952		
FL	0.2820*	0.1589*	0.2363*	0.3463*	0.3553*	-0.3000*	0.2051	-0.0334	0.5681	
FS	0.1887*	-0.1719	0.2326	0.3069*	0.3352*	0.2015	0.1226*	-0.1678	0.4994	0.6818

** = Significant (P>0.05); * = Highly significant (P<0.01)

direction between GOT (%) and SCY per plant was also observed. The correlation between BS and FL was significant but negatively correlated with each other (Table.5).

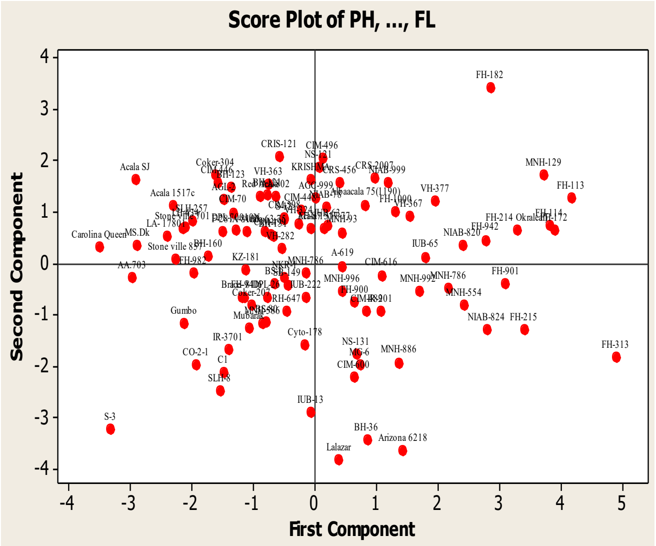

Figure 3. Principal Component's score plot of 100 cotton germplasm lines for fiber and yield traits.

DISCUSSION

Plants which have less height are desirable not only for high yield but also for manual or machine picking. In our study plant height ranged from medium to height which is good for plant breeder to use this variation in breeding programs. The significant positive correlation between NSB, NB/P and SCY supported that plant height is playing indirect role in seed cotton yield. High value of heritability (94.81) and genetic advance (33.049) and low value of environmental variance (32.15) indicated that genetic variances are playing their crucial role for the said trait and it can be used for further breeding programs Table 2. The Principal Components Analysis was used to find out role of eleven traits of cotton in the overall variation. The results showed that first four PCs contributed 70.1 % to total variation. First four PCs carried most of variation and Eigen value more than one. The partitioning of total variation into components makes it possible to use potential of genotypes in order to improve particular trait with the aid of breeding programs (Ashfaq *et al*., 2014). It is powerful method which practically provides good chance to get suitable parental genotypes which can be used in cotton betterment programs (Li *et al*., 2013). Vinodhana and Gunasekaran (2019) conducted a research on fifty cotton genotypes. In the current study out of eleven PCs only first four PCs carried 76% variation and having value greater than 1. The PC1 and PC2 shared 42% in total variation. Traits like SCY, NB/P, NSB, boll size, micronaire value and span length strongly influence loading factor.

Tabasum *et al.* (2012) conducted research to study stability based on difference among *G. hirsutum* cultivars for plant height and other yield components and reported important differences and positive correlation among plant height and other yield related traits (Rao *et al*., 2013; Yu *et al*., 2013; Islam *et al*., 2016; Farooq *et al*., 2018) studied divers *Gossypium hirsutum* genotypes for cotton yield and other vital economic parameters and reported considerable positive correlation among PH, NB/P, NSB, SCY, GOT (%) and fiber characters. It is concluded that variation among researchers might be due to the different environment and genetic makeup of *G. hirsutum* cultivars. Results showed that bolls number had positive relation with PH, NSB, GOT % and SCY. The heritability value for this trait was 0.99 and genetic advance 16.18 which indicated higher value of genotypic variance 133.82 as compared to environment variance 0.15, Table 2. It indicated that environmental role is little in the expression of above-mentioned trait. FH 313 had high value not only for NB/P but also for NSB and SCY which supported the hypothesis that with increase in bolls number, yields also increased. It indicated that yield may be increased by increasing NB/P, NSB and PH (Kaleri, 2016). Kaleri (2016) studied Bt and non Bt cotton genotypes and reported significant differences between cotton genotypes for PH, NBP, SCY, GOT, FF, FL and also found positive correlation among traits suggesting that these are playing their role in the quality and yield of cotton genotypes. The results similar to our findings were also described by (Liu *et al.*, 2001; Nazir *et al.*, 2013; Tulasi *et al.*, 2014; Rizwan *et al.*, 2021) who studied 33 cotton genotypes and reported that plant height, number of fruit carrying branches on single plant, NB/P, single boll weight and bundle strength, span length had association with SCY in positive direction.

It was noted that NSB was positively correlated with GOT, FL, FS and SCY while NMB were positively correlated with GOT and FL and had negative correlation with SCY, NB/P and fiber strength. This indicated that increases in monopodial branches might reduce cotton yield and affect quality traits. The genetic study for these traits showed moderate to high heritability value for number of monopodial branches, sympodial branches and seed cotton yield (Table 2). High value of environmental variance (56.46) for seed cotton yield showed that environment was playing a little more role than gene in the expression of this trait. Mugheri (2015) studied Bt cotton genotypes and found positive correlation between number of bolls, seed cotton yield, sympodial branches, GOT and negative with fiber fineness. He further studied genetic variances and found moderate to high heritability value for number of monopodial branches and sympodial branches respectively. He further added high heritability value (0.97) for seed cotton yield can be utilized in breeding programs. Different researchers studied upland cotton genotypes to analyze genetic behavior and relation among traits. It was reported that seed cotton yield had high heritability value (0.99) and had positive correlation with other yield and fiber quality traits and improvement in this trait may improve quality traits indirectly. GOT had positive correlation with NB/P, SCY, lint index, fiber fineness and FS but it had correlation in negative direction with boll size and fiber length (Aremu *et al.*, 2005; Hulse-Kemp *et al.*, 2015). The strong correlation in positive direction among agronomic and quality traits suggested that quality traits along with yield can be increased by improving agronomic traits (Wang *et al.*, 2010; Zhao *et al.*, 2011; Tabasum *et al.*, 2012; Saeed *et al.*, 2014). Similar results kindred to significant differences among cotton genotypes were also reported by (Handi & Katageri, 1980; Meredith, 2005; Asha *et al.*, 2013) studied 320 diverse cotton genotypes in 5 different environments and found SCY positive correlation with number of bolls, number of monopodia, plant height, ginning out turn and lint index at phenotypic and genotypic level. So improvement in these traits will help to improve seed cotton yield. It is desirable as it tells that improvement in one trait will help to improve another trait as the said traits depend on each other. The genotypic variance for GOT and lint index were 23.84 and 1.52, respectively table 2. The low value for heritability (54.26) for lint index told that material was not suitable for further breeding programs for said trait. Similar results were for ginning outturn, seed index, fiber strength, lint index and fiber fineness at phenotypic and genotypic level were also obtained by different researches (Sahito *et al.*, 2016; Javed *et al.*, 2017; Diouf *et al.*, 2018). High heritability value for fiber quality traits and low environmental variance (table 2) showed that genotypes under study had good potential for breeding programs. Fiber fineness, fiber length and fiber strength had negative correlation with plant height, boll size and number of monopodial branches respectively. Similar results for association among SCY and yield related traits were reported. Positive relation was found among traits which was in line with our study (May, 2002; Chee *et al.*, 2005; Qin *et al.*, 2009). This betoken that all the cotton varieties in the study have high genetic potential. This feature is required for heterosis breeding programme as the index of transmissibility to the next generation (heritability) is in dire need.

***Conclusion**:* The result of this study showed significant variation, notable relationship among traits under study, higher values for inheritance and genetic advance for sympodial branches, number of bolls, monopodial branches, plant height, GOT (%), seed cotton yield, and fiber strength, fiber length, fiber fineness among 100 cotton genotypes. It is concluded on the base of high heritability values that cotton genotypes under study have significant genetic variation. So, good hybrid of cotton may be produced by using these genotypes and significant genotypic correlation among traits may be helpful for breeders to select high yield and good quality traits of cotton genotypes.

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