

## Genetic Evaluation of *Gossypium hirsutum* L. for Yield and Fiber Contributing Attributes in Segregating Population

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### ABSTRACT

Cotton (*Gossypium* spp.) belongs to the genus *Gossypium*, which is an agricultural commodity substantially involved in international trade for its fiber and fiber products. This research was conducted to study genetic variability in the M2 population of FH-Lalazar. For this purpose, cotton variety FH-Lalazar was bombarded with different doses of gamma radiation i.e., 20kr, 25 Kr, 30 Kr, 35 Kr, and the untreated seed were used as a control group to grow M1 generation. The seed obtained from M1 was used to grow M2 generation. This research was conducted in a randomized complete block design, with three replications. The data for M2 generation were collected at maturity with three pickings of bolls. The average data of all three replications was analyzed through analysis of variance, correlation analysis and principle component analysis. Analysis of variance was performed and found that all the treatments were significantly different for all the yield and fiber related character i.e., plant height, number of sympodial branches, first fruiting branch number, total number of nodes, height to node ratio, number of bolls per plant, seed cotton yield, boll weight, seed index, lint index, got%, seeds per boll, fiber fineness, fiber strength, fiber maturity, uniformity index, fiber length and short fibers index. While non-significant differences were observed for number of monopodial branches. Correlation analysis revealed that seed cotton yield showed positive association with number of sympodial branches, first fruiting branch number, height to node ratio, number of bolls per plant, boll weight and negatively correlated with GOT%, and fiber maturity. Out of six principal components, four components had extracted eigen value of >1. This contributed for 80.93% of the variation among treatments. Traits such as plant height, number of sympodial branches, number of bolls per plant and height to node ratio were well represented with high amount of variability as these traits were far from origin, while remaining traits showed the lowest variability. The range of variability in each trait of M2 population under study exhibited greater divergence which may be useful for an effective cotton breeding program.

**Keywords:** Cotton, Gamma radiation, Sympodial branches, Breeding program

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## INTRODUCTION

Cotton is a major cash crop grown all over the world. It is the backbone of Pakistan's economy and provides raw material for the textile industry (H. Ali, Ali, Faridi, & Ali, 2013; & Malik & Ahsan, 2016). It is mainly grown for its fiber, but its seed is crushed to yield edible oil of significant importance. In 2018-19 total area under cotton cultivation was recorded as 32 million hectares and world cotton production is projected as 121.9 million bales. According to production, Pakistan ranks at 5th number in the world after India, USA, China, and Brazil respectively (Ashraf, Sangi, Hassan, & Luqman, 2018; Bakhsh, Hassan, & Maqbool, 2005). Pakistan ranks third according to the export of raw cotton, fourth according to consumption, and 1st according to yarn consumption. Cotton and its products have a share of about 0.8% in GDP and about 4.5% in agriculture value addition. In the year 2018-19, the area under cotton cultivation remained 2.37 million hectares and production limited to 1.1 million bales Pakistan's agriculture production lags behind other agriculture countries and the same is the case with cotton (Ashraf et al., 2018). The development of high yielding varieties can increase the production of cotton (Jans, von Bloh, Schaphoff, & Müller, 2021).

For a successful breeding program, the first and foremost prerequisite is the presence of genetic variability. If genetic variability is present in a population, the effective selection is possible (C. P. S. Kumar, Raju, Rajan, Muraleedharan, & Suji, 2019). Otherwise, the breeder will carry junk with him and it will be a wastage of time and resources. Genetic variability in the plant is key for the selection of plants with desirable characteristics (N. Kumar & Katageri, 2017). More the genetic variability is present in a population more are the chances of effective selection. There are fewer genetic differences among the cultivated varieties of cotton. It is the need of the hour to broaden the genetic makeup of our cultivated varieties (Monisha, 2018). There are several ways to create genetic variability. Conventional techniques are failing or making

less improvement in a targeted trait. Conventional approaches are also time-consuming and laborious (Joshi & Patil, 2018). The mutation is one of the effective and widely used techniques to create genetic variability. The X-rays, gamma rays, fast neutrons can be bombarded on the seed of cotton to create genetic variability in the cotton (Hussain et al., 2018; Zafar, Hussain, Abbas, & Till, 2021). In addition to these physical mutagens, there also exist some biological mutagen e.g., insertion of T-DNA and tagging of transposons. There are several advances in the techniques to create mutations (Zhou et al., 2020).

The information about the relation of yield and its components possesses considerable importance for the selection of desirable plants (Jarwar et al., 2019). It is found that change in one character alters the behavior of another trait because the trait depends upon each other. In cotton, the yield is dependent upon several traits e.g., no. of bolls/plant, no. of sympodia and monopodia etc. (Rehman, Mustafa, DU, & Azhar, 2020). The analysis of correlation is a prerequisite for fruitful research in cotton. Yield is directly associated with some traits either positively or negatively. Without correlation analysis, we cannot conclude about our research that how the component traits are contributing to yield (Xia et al., 2020). Principal component analysis has been used by the researchers to uncover the similarities and differences among different genotypes and placed them into various components (ZHANG et al., 2018). Principal component analysis is the most appropriate statistical method to partition total variation that facilitates selection of elite parent lines. It also tells about the importance of main contributor to total variability. Moreover, genetic variability among existent genotypes can be assessed by principal component analysis which will help in calculating phenotypic variability (Jarwar et al., 2019). The knowledge of variability provided by PCA is helpful to select genetically and agronomically important genotypes (Malaquias et al., 2017).

So, the purpose of this research study was: 1) Creation of genetic variability. 2) To estimate the performance of the M2 population of FH-Lalazar for yield-related traits and fiber quality traits. 3) To estimate correlation co-efficient, PCA and cluster analysis for yield-related traits.

### MATERIALS AND METHODS

The research work under consideration was conducted in the research area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The present research was conducted to grow the M2 generation of FH-Lalazar. For M1 generation seed was previously collected from the Cotton Research Group, Department of Plant Breeding and Genetics, UAF, and bombarded with gamma radiation at the Nuclear Institute of Agriculture and Biology (NIAB) in 2017-18. The doses given to M1 seed were 20 Kr, 25 Kr, 30 Kr and 35 Kr. In 2018-19, the seed of M1 generation was sown to raise the M2 population in the research area of University of Agriculture, Faisalabad. Non-mutated seeds along with mutated seeds were sown in five lines for each treatment using a randomized complete block design (RCBD). Row to row distance and plant to plant distance was maintained at 75cm and 30cm respectively. At maturity, data was collected for the following traits: 1) Plant height (cm) 2) Number of monopodial branches 3) Number of sympodial branches 4) First fruiting branch number 5) Total number of nodes 6) Height to node ratio 7) Number of bolls per plant 8) Seed cotton yield (g) 9) Boll weight (g) 10) Seed index (g) 11) Lint Index (g) 12) GOT% 13) Seeds per boll 14) Fiber fineness ( $\mu\text{g}/\text{inch}$ ) 15) Fiber Strength (g/tex) 16) Fiber Maturity 17) Uniformity Index (%) 18) Fiber length (mm) 19) Short fibers index.

### Statistical analysis

The data were analyzed through analysis of variance by following the method described by (Steel, 1997) by STATISTIX 8.1. The correlation analysis was performed according to the method described by (Dewey & Lu, 1959). Principal component analysis is important tool to estimate genetic divergence

among various genotypes. The divergence was calculated by PCA by XLSTAT.

## RESULTS AND DISCUSSION

### Analysis of Variance

Analysis of variance was performed and found that all the treatments (different doses of radiations) were significantly different for all the yield and fiber related character i.e. plant height, number of sympodial branches, first fruiting branch number, total number of nodes, height to node ratio, number of bolls per plant, seed cotton yield, boll weight, seed index, lint index, got%, seeds per boll, fiber fineness, fiber strength, fiber maturity, uniformity index, fiber length and short fibers index. While non-significant differences were observed for number of monopodial branches.

These results showed that variation was created by different doses of mutagens within the same cotton variety for 19 different yield and fiber related parameters. Treatment 1 (control) had highest mean values for character like fiber strength. Treatment 2 (20 Kr) which had highest mean values for height to node ratio, lint index, seed index and MAT. Treatment 3 (25 Kr) had highest mean values for first fruiting branch number, total number of nodes, fiber maturity, uniformity index and seed cotton yield plant. Treatment 3 (25 Kr) had highest mean values for plant height and number of sympodial branches. Treatment 5 (35 Kr) which highest mean values for boll weight, GOT%, seeds per boll, short fibers index and fiber fineness. This variation is very important for the improvement and developing of new cultivars. (Rehman et al., 2020) reported that to get desired genotypes in the end of breeding experiment, maximal genetic variability should be present in amongst studied genotypes. The genotypes exhibiting high variability for yield and its contributing traits should be selected. (N. Kumar & Katageri, 2017) assessed considerable differences for the studied trait amongst all the genotypes thus it could be used as a potential resource of variability for future experiments. (C. P. S. Kumar et al., 2019) showed that the genotypes were genetically diverse for boll

weight. As boll weight is an important character that contributes highly to the yield therefore, the variability present among varieties should be exploited to get expected

results (Dhivya, Amalabalu, Pushpa, & Kavithamani, 2014). Similar results were obtained by (Abdullah et al., 2016) and (Raza et al., 2016).

Table 1 (a): ANOVA of cotton yield and fiber quality related traits

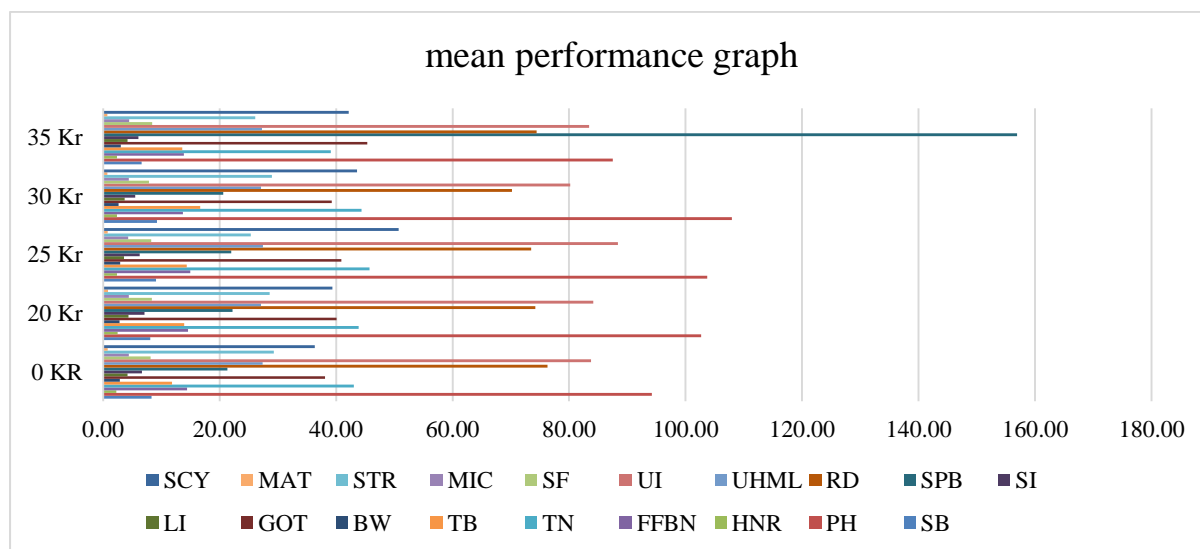
Source	df	MAT	HNR	LI	MB	Mic	RD	PH	SCY	SB	SF
replications	2	0.023	0.02024	0.0194	4.43289	0.009	0.0044	92.688	2.423	0.23674	0.00048
genotypes	4	0.00539	0.23453	0.28845	0.20283	0.02058	14.3343	136.219	161.986	2.97806	0.16521
error	6	4.76E-06	0.01983	0.00795	0.59384	0.00565	0.0582	18.978	2.284	0.2564	0.00808

Table 1 (b): ANOVA of cotton yield and fiber quality related traits

Source	df	SI	TN	SPB	STR	UHML	UI	FFBN	GOT	BW	TB
replications	2	0.18888	17.225	1785.48	0.0893	2.8244	0.2211	0.43819	2.4673	0.01754	0.5232
genotypes	4	1.02286	85.8798	7949.31	16.7625	0.52244	35.9883	2.60896	42.9712	0.37992	16.7356
error	6	0.02685	1.284	1866.06	0.0332	0.11919	0.0395	0.76064	0.2785	0.02672	0.545

Table 2: Mean performance of M2 population under different treatments

Treatments	SB	PH	HNR	FFBN	TN	TB	BW	GOT	LI	SI	SPB	RD	UHML	UI	SF	MIC	STR	MAT	SCY
0 KR	8.31	94.22	2.27	14.41	43.06	11.84	2.87	38.09	4.18	6.67	21.32	76.29	27.38	83.77	8.15	4.40	29.30	0.80	36.34
20 Kr	8.08	102.6	2.50	14.59	43.89	13.93	2.81	40.10	4.35	7.09	22.22	74.22	27.12	84.15	8.35	4.40	28.56	0.82	39.34
25 Kr	9.06	103.7	2.38	14.94	45.74	14.34	2.94	40.88	3.61	6.25	21.99	73.46	27.46	88.40	8.25	4.28	25.37	0.76	50.73
30 Kr	9.26	107.9	2.40	13.70	44.38	16.68	2.65	39.22	3.67	5.48	20.61	70.20	27.10	80.20	7.86	4.42	28.99	0.72	43.58
35 Kr	6.62	87.50	2.37	13.87	39.08	13.57	3.02	45.33	4.21	6.07	156.8	74.43	27.25	83.42	8.42	4.48	26.13	0.75	42.19



**Correlation Analysis**

Table 3 showed the results of the correlation analysis of the M2 population of cotton. The Sympodial branches were found positively associated with plant height, first fruiting branch number, number of bolls per plant and seed cotton yield. Plant height was negatively associated with seeds per boll and reflectance.

The height to node ratio was positively correlated with number of bolls per plant, boll weight, seed index, fiber strength and seed cotton yield. There was found a positive association between seed index and seed cotton yield. The total number of bolls were found positively correlated with boll weight. There was found a positive correlation

between lint index and seed index. Mic value and short fiber index were negatively correlated. Seed cotton yield showed positive association with number of sympodial branches, first fruiting branch number, height to node ratio, number of bolls per plant, boll weight and negatively correlated with GOT%, and fiber maturity. (Reddy, Reddy, Ahamed, Naidu, & Srinivasarao, 2015) had found similar results for correlation between plant height and sympodial branches, lint index, height to node ratio, seed index, and boll weight. (Rehman et al., 2020) found similar

results for a positive correlation between plant height, boll weight, and the number of bolls. (Khokhar et al., 2017) however found similar results as in that study the number of bolls was negatively correlated with boll weight. (Nawaz, Sattar, & Malik, 2019) also found a positive correlation between boll weight, number of bolls, and seed cotton yield. (Kumbhar et al., 2020) found opposite results, a negative correlation between the number of bolls per plant, and ginning out turn was recorded.

**Table 3: Correlation analysis of cotton yield and fiber quality related traits**

	SB	PH	HNR	FFBN	TN	TB	BW	GOT	LI	SI	SPB	RD	UHML	UI	SF	MIC	STR	MAT
<b>PH</b>	0.738* *																	
<b>HNR</b>	0.273	0.10																
<b>FFBN</b>	0.445*	0.19	0.46*															
<b>TN</b>	0.013	0.37	-0.74**	-0.18														
<b>TB</b>	0.626* *	0.42	0.71**	0.33	-0.57**													
<b>BW</b>	0.338	-0.13	0.49*	0.57**	-0.59**	0.45*												
<b>GOT</b>	-0.65**	-0.24	-0.33	-0.57**	0.14	-0.32	-0.52*											
<b>LI</b>	-0.283	-0.384	0.353	0.171	0.591* *	0.018	0.409	-0.082										
<b>SI</b>	-0.025	-0.185	0.446*	0.24	-0.475*	0.055	0.294	-0.202	0.705* *									
<b>SPB</b>	-0.61**	0.537* *	-0.082	0.061	-0.151	-0.213	0.13	0.341	0.125	-0.248								
<b>RD</b>	-0.446*	-0.491*	-0.466*	0.092	0.328	0.815* *	0.03	-0.018	0.285	0.249	0.248							
<b>UHML</b>	0.04	0.29	-0.454*	0.002	0.68**	-0.398	-0.126	0.209	-0.281	-0.433*	0.046	0.347						
<b>UI</b>	-0.174	-0.039	0.599* *	0.069	0.71	0.665* *	-0.185	0.136	-0.383	-0.128	0.084	0.637* *	0.485*					
<b>SF</b>	-0.171	-0.338	0.193	0.665* *	-0.214	-0.066	0.638* *	-0.217	0.479*	0.323	0.49*	0.497*	0.032	0.308				
<b>MIC</b>	-0.187	-0.336	0.522* *	-0.053	0.761* *	0.338	0.418*	-0.129	0.561* *	0.254	0.13	-0.246	-0.51* *	0.683* *	0.075			
<b>STR</b>	0.225	0.147	0.506* *	-0.121	-0.527* *	0.417	-0.042	-0.111	0.4	0.426	-0.394	-0.444* *	-0.394	-0.82**	-0.464* *	0.42		
<b>MAT</b>	-0.315	-0.299	-0.121	-0.25	-0.149	-0.305	-0.316	0.134	0.385	0.586* *	-0.26	0.223	0.563* *	0.045	-0.076	0.091	0.237	
<b>SCY</b>	0.554* *	0.252	0.514* *	0.593* *	-0.305	0.644* *	0.714* *	-0.502* *	-0.177	-0.008	0.019	-0.297	-0.153	-0.004	0.411	0.093	-0.268	-0.453* *

### Principal Components

The Principal Component Analysis is a multivariate statistical technique, to extract the important information from the data table and simplify the description of the data set (Malaquias et al., 2017). To discern patterns of variation, PCA was performed on all variables simultaneously. The Eigen values, variability (%) and cumulative (%) are presented in Table 4. Out of six principal components, four components had extracted Eigen value of >1. This contributed for 80.93% of the variation

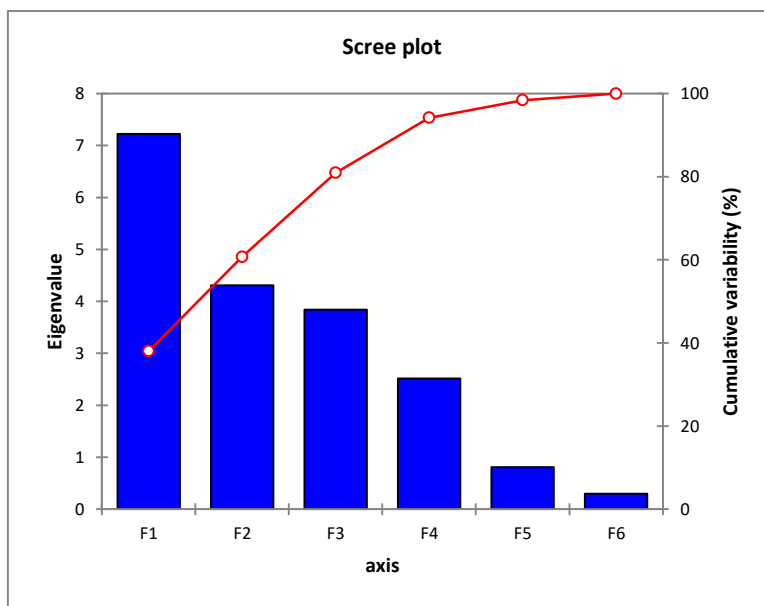
among the treatments. Principal component 1, contributed for 38.03%, to the total variability. The variation on principal component 1 was mainly attributed due to HNR, TB, BW, MIC, STR and SCY. The PC2 contributed for 22.68% to the total variability and was depicted mainly by SB and PH. The PC3 contributed for 20.21% of the total variability and was mainly attributed to STR and MAT. The first three PCs exhibited high variation for the traits under study and therefore good cotton improvement may be accomplished

through inter varietal development. The principal component scatter plot depicted that the treatments those were close together were

perceived as being similar when rated based on the variables.

**Table 4: Eigen values of PC'S**

	PC1	PC2	PC3	PC4	PC5	PC6
Eigenvalue	7.2265	4.3093	3.8417	2.5166	0.8083	0.2976
Variability (%)	38.0342	22.6805	20.2194	13.2452	4.2542	1.5664
Cumulative %	38.0342	60.7147	80.9342	94.1794	98.4336	100.0000



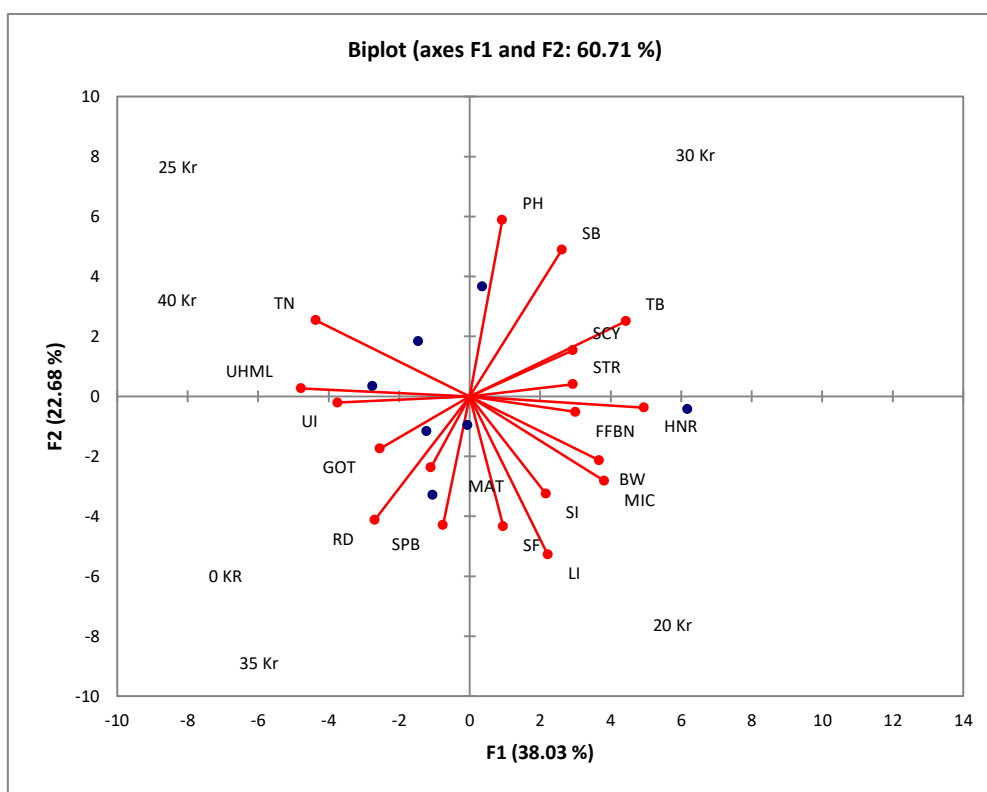
**Table 5: Factor loadings**

	PC1	PC2	PC3	PC4	PC5	PC6
SB	0.5132	0.7405	-0.2621	0.3044	-0.1189	-0.1130
PH	0.1815	0.8912	-0.0186	0.2701	0.1186	0.2922
HNR	0.9692	-0.0565	0.0352	0.0529	0.2312	-0.0037
FFBN	0.5880	-0.0788	-0.7219	0.3549	-0.0089	-0.0285
TN	-0.8562	0.3845	-0.1776	0.1875	-0.0865	0.2119
TB	0.8691	0.3799	0.0142	-0.2594	0.1604	0.0844
BW	0.7197	-0.3229	-0.6009	-0.0175	-0.0465	-0.1197
GOT	-0.4994	-0.2640	0.4865	-0.4098	0.5212	-0.0682
LI	0.4351	-0.7986	0.2139	0.2510	-0.1200	0.2232
SI	0.4242	-0.4915	0.1345	0.7138	0.2255	0.0103
SPB	-0.1488	-0.6490	-0.2511	-0.6975	0.0155	0.0821
RD	-0.5273	-0.6235	-0.3360	0.3890	-0.2446	-0.0957
UHML	-0.9368	0.0400	-0.3213	0.0472	-0.1239	-0.0059
UI	-0.7350	-0.0313	-0.5624	0.2657	0.2627	-0.0540
SF	0.1861	-0.6556	-0.6867	0.0834	0.1372	0.1954
MIC	0.7492	-0.4274	0.2619	-0.3423	-0.2545	0.0742
STR	0.5746	0.0610	0.7548	0.2422	-0.1718	-0.0903
MAT	-0.2160	-0.3591	0.5594	0.6771	0.2285	-0.0271
SCY	0.5738	0.2327	-0.7339	-0.1646	0.2112	-0.0791

### Biplot

These variables were super imposed on the plot as vectors in the biplot, the relative length of the vector represents the relative proportion of variability in each variable. The relative distance of the variables from the origin regarding PC-1 and PC-2 depicts the share of each variable to the total variation of the germplasm (I. Ali et al., 2017). The distance covered from origin to the tip of the plot provide information about the diversity present among the genotypes (Farias, De Carvalho, Da Silva Filho, & Teodoro, 2016). The variety that is at maximum distance from the origin had higher variation as compared to other varieties. The line joining the character to the

origin is called traits vector while the angle that represent the association amongst all the characters is cosine angle. Characters with less than  $90^\circ$  cosine angle had positive correlation while characters with more than  $90^\circ$  angle were negatively correlated. The extant variety distant from origin showed more variation and less similarity with other varieties (Latif, Bilal, Hussain, & Ahmad, 2015). Traits such as PH, SB, TB and HNR were well represented with high amount of variability, while remaining traits showed the lowest variability. The range of variability in each trait, among the varieties under study, exhibited greater divergence which may be useful for an effective cotton breeding program.



### CONCLUSION

M2 population exhibited highly significant differences for all the traits except number of monopodial branches. Seed cotton yield had positive association with number of sympodial branches, first fruiting branch number, height to node ratio, number of bolls per plant, boll weight and negatively correlated with GOT%, and fiber maturity. Traits such as plant height, number of sympodial branches, number of bolls per plant and height to node ratio were

well represented with high amount of variability as these traits were far from origin, while remaining traits showed the lowest variability. The range of variability in each trait of M2 population under study exhibited greater divergence which may be useful for an effective cotton breeding program. Therefore, these populations can be used in future breeding programs to enhance the seed cotton yield.

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