INNSPUB

RESEARCH PAPER   OPEN ACCESS

Assessment of genetic variability and association in yield and quality parameters of upland cotton (*Gossypium hirsutum* L.)

Ameer Hussain Jarwar[1,4], Muhammad Shahid Iqbal[1,3], Xiaoyan Wang[2], Long Wang[1], Qifeng Ma[1], Fan shuli[1*]

[1]*State Key Laboratory of Cotton Biology, Institute of Cotton Research of CAAS, Anyang 455000, China*

[2]*Anyang Institute of Technology, College of Biology and Food Engineering, Anyang, 455000, China*

[3]*Cotton Research Station, Ayub Agricultural Research Institute, Faisalabad, Pakistan*

[4]*Oil Seeds Section, Agriculture Research Institute, Tandojam, Sindh, Pakistan*

Abstract

A research experiment was executed to investigate the presence of genetic variation existing as components of variation, correlations and path-coefficient analysis of yield and fiber quality traits *viz.* plant height, sympodial branches per plant, bolls per plant, boll weight, ginning outturn percentage, seed index, fiber length, fiber fineness and seed cotton yield. The research experiment was conducted comprising of 12 cotton cultivars planted under randomized complete blocked design (RCBD) at the experimental field of Cotton Research Institute Anyang Henan, China, during the cotton crop season 2017-18. The cultivars included 705230, 705240, 705242, 705244, 705252, 705360, 705366, 705368, 705398, 705441, 705482, and 705542 accessions of upland cotton (*Gossypium hirsutum* L). The results in analysis of variance revealed that plant height, sympodial branches, bolls per plant, fiber fineness, and seed cotton yield shown highly significant differences, whereas ginning outturn percentage, boll weight, fiber length and seed index exhibited significant differences. High heritability with moderate genetic advance for the number of sympodial branches, Micronaire value, Number of bolls per plant, and seed cotton yield provide a sound ground for improvement in these through selection. In conclusion results showed that genotype 705244 has the highest plant height whereas genotype 705244 produced a maximum number of sympodial branches per plant similarly and genotype 705244 exhibited as, as a superior variety for cotton with reference to seed production and can be commercialized as a high yielding variety.

* **Corresponding Author:** Fan shuli ✉ fsl427@126.com

Introduction

Upland Cotton (*Gossypium hirsutum* L.) is the most significant cash and fiber crop of the world (Wang *et al.,* 2012; Ameer *et al.*, 2019)**.** China is the second largest country producing cotton in the world (Statista, 2017). The cotton crop is an important source of foreign exchange earnings and plays a significant role in the economy of the cotton producing countries. Besides talking about the cotton fiber cotton seed cake and cotton seed oil produced are extensively used for animal feed and as and edible oil for human consumption. Before starting any breeding, program aimed at improvement of cotton yield it is necessary to understand the different factors/components influencing cotton yield (Nizamani *et al.*, 2017). It is necessary for a breeder to have knowledge about the nature of yield and yield contributing factors; but is difficult to have exact knowledge regarding the association and importance of the indirect or direct effects all the contributing traits to yield (Reta Sanchez and Fowler, 2002). Information relating to the association between yield components and helps a plant breeder in the selection of desirable genotypes. The correlation investigation provides an index to forebode the corresponding variation that prevails in a related trait at the expense of the harmonious variation in the others (Ahmed *et al.*, 2011; Khan *et al.*, 2007). Upland cotton contains is a fluffy, soft fiber that matures in a cover case called boll and surround the cotton seeds of plants (Soomro, 2000). The genus *Gossypium* is a member of family Malvaceae and the fiber is considered as cellulose in and listed among natural fibers. Cotton bolls will look after to grow the diffusion of the seeds. The adaptability and consistency of upland cotton genotypes discovered different values for agronomic, physiological, morphological, yield and fiber-related traits (Wang *et al.*, 2004; Iqbal *et al.*, 2003). An establish genetic variability and direct and indirect association in fiber related traits as well as cotton seed yield and yield related factors in cotton has been earlier reported by (Meena *et al.*, 2007; Rahman *et al.,* 2013; Rahman *et al.*, 2008).

Upland cotton (*Gossypium hirsutum* L.) plays an important role in the mainland economy being among the basic sources of earning foreign exchange. Cotton has also been enlisted as the backbone of the national economy most of the cotton producing countries of the world. Synonymously the term white gold has also been quoted mostly due to its prominent value as a cash and textile/industrial crop. Development of cotton cultivars/ genotypes with improved capacity of having superior fiber quality and higher yield potential are the basic objectives for any cotton plant breeder (Iqbal, *et al.*, 2006). Seed cotton yield is affected by environment as well as genetics of the variety. The association between these two components makes the choice dissimilar for a cotton breeder. Inter controvertible correlation between seed cotton yield with other yield and fiber factors was discovered in *Gossypium hirsutum* genotypes/varieties by (Méndez-Natera *et al.*, 2012). A high genetic variation for fiber and yield factors in upland cotton has been reported by (Khan *et al.*, 2009a; Khan *et al.*, 2010). To know the nature of component affected by yield is a pre-requisite for implementing an efficient cotton breeding strategy and can help to unleash characteristics and nature of yield and fiber traits that are still undiscovered. Investigation of direct and indirect effects can also help to explore exact knowledge regarding the association and importance of directly or indirectly affected traits (Kempthorne, 1957; Reta-Sanchez and Fowler, 2002).

Cotton is one of the fundamental and renewable sources of natural industrial fibers that is considered as 6th largest producers of edible oil worldwide. It belongs to the kingdom Plantae and genus *Gossypium* that places at almost five allotetraploid and 45 diploids species (Ulloa *et al.*, 2006). The cotton yield is contributed by traits i.e. boll weight, lint percentage and number of bolls per plant etc. selection for high yielding cultivars/lines is mainly based on these yield contributing traits. Nature of yield and yield contributing traits is very complex and the existence of association among these complex traits is a mainly the recognition of genes, factors and their relationship as described by (Dilday *et al.*, 1990;

and Kebede *et al.*, 2001). Correlation analysis, linear regression analysis and path co-efficient analysis are the basic techniques which are mainly being used to explore the relationships among complex traits (Akbar *et al.*, 1994; Azhar *et al.*, 1999; Hassan *et al.*, 2013). Manifestation of different traits is often executed with minor modification in breeding methods. Thus, the knowledge of direct and indirect relationship among different traits especially those contributing yield is essential for the cotton breeding program that suggests the selection for better or improved genotypes (Taohua, and Haipeng *et al.*, 2006). Basically, correlation among cotton seed yield and its related traits is reflected from the direct effect of those traits which will useful for indirect selection of the traits that provide a forward direction to increase seed cotton yield as described by (Fonseca and Paterson, 1968). Correlation analysis provides a great index to anticipate the corresponding modification that occurs in single trait at the cost of the harmonious modification in the others related traits as reported by (Ahmed *et al.*, 2008; Khan *et al.*, 2007; Rahman *et al.*, 2013).

The current study was designed to explore the genetic relationship of cotton seed yield with different yield and yield contributing factors as well as fiber-related traits.

Materials and methods

The research experiment was conducted comprising of 12 Chinese cotton cultivars planted under randomized complete blocked design (RCBD) at the experimental field of Cotton Research Institute Anyang Henan, China, during the cotton crop season 2017-18. Plant to plant distance was maintained as 30 cm while among row to rows distance was 75 cm with a plot size of 600x450 cm. All agronomic and cultural practices were followed as recommend in a uniformly for the entire experimental unit.

Data was collected for yield and fiber quality related traits at the time of maturity from 10 tagged guarded plants from each replication from each variety was selected. The parameters were collected such as

number of bolls per plant, Plant height (PH) and number of sympodial branches was taken from the standing crop before picking. Picking was carried out from tagged plants in the month of November. Boll weight and seed cotton yield per plant was estimated by weighing the picked bolls from tagged plants with the help of digital weighing balance. The ginning outturn percentage% was carried out with the help of swaging and the ginning out turn percentage% (GOT %) was calculated by the formula as follows.

GOT%= total lint weight/ total cotton seed weight
Seed index was measured by dividing the seed weight to the total number of seeds. Then lint of 10 guarded plants was subjected to the fiber quality analysis by HV1-900 to find out the fiber length and fiber fineness.

The results were subjected to analysis of variance (ANOVA) with the help of computer software package MSTAT-C (Freed, Russell, D. Michigan state university. USA, 1984). Comparison of means was carried out using Fishers methods and least significant difference methods (LSD) at $P> 0.05$. Phenotypic and genotypic co-efficient of variability (PCV and GCV), Phenotypic and genotypic co-efficient of variation, herebility in (broad sense) were calculated according to the method of (Burton and Devane, 1953). Genetical advance was estimated at 20% select intensity using the methods suggested by (Poehlman and Sleper, 1995). Total correlation (genotypic and phenotypic) was calculated to following the statistical methods given by (Kowon, and Torrie *et al.*, 1964).

The genotypic correlations were calculated following the methods of (Lotherop *et al.*, 1985). Statistical important of phenotypic correlation was calculated by T-test as previously presented by (Steel *et al.*, 1997) and the path co-efficient analysis was done through the method proposed by (Dewy and Lu, 1959).

Phenotypic and genotypic co-efficient of variation (PVC and GVC), were calculated by the equation propose by Devane and Burton as given below:

Genotypic co-efficient of variability (GCV) =σg/X̄×100

Whileas σg = Phenotypic Standard deviation, X̄ = population mean.0

Similarlary, the phenotypic co-efficient (PVC=σg/X̄×100

Herebility: Heritability in wide sense was calculated following to Johnson.

%H= σ²g/σ² ᴾ×100

Genetic advance =σ²g/σ² ᴾ KX×100

Where,

K= choice for differential, the values of which is 2.06 at 5% choice intensity,

OP= Phenotypic standard deviation.

Results and discussion

As shown in (Table 1), all traits showed highly significant differences except GOT% which shows a significant. Comparisons of means as shown in (Fig. 1) the means sharing letters have significant differences among different genotypes related to corresponding trait.

Table 1. Components of variation for different yield and fiber quality parameters of cotton (*Gossypium hirsutum* L.).

Trait	Symp	BW	GOT	MiC	No.B	PH	SL	S.Index	YLD
GMean	11.0486	573.7167	40.11	5.2417	15.0444	86.3556	28.95	11.3583	297.825
Fratio	23.4744**	3.8411*	2.8297*	9.1387**	8.9531**	14.1916**	3.1473*	4.8603*	31.1515**
PV	4.0112	6526.28	9.811	0.2669	15.6547	31.6762	6.1955	3.9251	8573.251
GV	3.5388	3174.363	3.7168	0.195	11.367	25.8072	2.5845	2.2087	7797.427
PCV	18.1272	14.0811	7.8091	9.857	26.2995	6.5174	8.5978	17.4426	31.0893
GCV	17.0264	9.8204	4.8065	8.4256	22.4102	5.8827	5.5532	13.0844	29.6493
h2	88.2235	48.6397	37.8838	73.0669	72.6104	81.4719	41.7167	56.2704	90.9506
GA	3.6399	80.9452	2.4444	0.7777	5.9182	9.4459	2.139	2.2965	173.4785
GAM	32.9444	14.1089	6.0943	14.8365	39.338	10.9383	7.3887	20.219	58.2485
S.E.	0.3968	33.4261	1.4253	0.1548	1.1955	1.3987	1.0971	0.7564	16.0813
C.D.(5%)	1.1616	97.8524	4.1724	0.4532	3.4998	4.0946	3.2117	2.2143	47.0767
CV(%)	6.2207	10.0913	6.1547	5.1155	13.7639	2.8054	6.5639	11.5345	9.3523

GMean= General mean, Fratio=Fraction Ratio, PV= Phenotypic variance, GV= Genotypic variance, PCV= Phenotypic co-efficient variance, GCV= Genotypic co-efficient variance, h2= Herebility, GA= Genetic Advance, GAM= Genetic Advance Mean, S.E= Standard Error, CV= Co-efficient of variance,

Symp=Sympodial Branches, BW=Boll weight (g), GOT=Ginning out turn (%age), MIC=Micronaire value (micrgram/inch), NOB=Number of Boll, PH=Plant Height (cm), SL= Staple length (mm), SI=Seed Index, YLD=Yield (g).

The maximum range of variability was observed in boll weight with a range 3174.363-6526.28, followed by seed cotton yield per plant (8573.251-7797.427), number of sympodial branches per plant (3.53-4.01) and GOT % (3.71-9.81). Heritability in broad sense was recorded 88.22, 48.63, 37.88 and 73.06 in respect manners between the traits (Table 1). A range of variability in the number of bolls was 11.36-15.65 with the GAM of 39.33 (Saleem *et al.*, 2016). The remaining contribute characters had specified range of variability indicating the small range between the genotypic traits.

Phenotypic and genotypic variability, heritability, phenotypic coefficient of variability, genotypic co-efficient of variability and genetic advance of six economic traits of 12 Chinese cotton cultivars are presented in (Table 1). Selection in early generations with moderate to high GCV and PCV were also recommended by (Ahsan *et al.*, 2015; Shao *et al.*, 2016; Adsare *et al.*, 2017) for seed cotton yield and yield contributing traits.

Table 2. Genotypic, Phenotypic, Environmental and simple correlations of different yield and fiber quality parameters of cotton.

Character		Genotypic r	Pheno r	Env
SYMP	BW	0.427 N.S	0.3397 N.S	-0.2389**
SYMP	GOT	-0.8554**	-0.476 N.S	0.0684 N.S
SYMP	MIC	0.5354 N.S	0.4319 N.S	0.0115 N.S
SYMP	BNO	0.7206**	0.6019*	0.1401*
SYMP	PH	0.7467*	0.6783*	0.3057**
SYMP	SL	0.6434*	0.4217 N.S	0.1197*
SYMP	SL	0.7188*	0.4264 N.S	-0.3527**
SYMP	YLD	0.5114 N.S	0.4573 N.S	-0.0073 N.S
BW	GOT	-0.1795 N.S	-0.1865	-0.2811 N.S
BW	MIC	0.1182 N.S	0.1568 N.S	0.3207*
BW	BNO	0.8003**	0.6173*	-0.0672 N.S
BW	PH	0.0027 N.S	-0.0209	-0.141**
BW	SL	0.032 N.S	0.0876 N.S	0.2356**
BW	SL	0.2882 N.S	0.1999 N.S	0
BW	YLD	1.037 N.S	0.8953**	-0.168**
GOT	MIC	-0.2574 N.S	-0.2423N.S	-0.2613**
GOT	BNO	-0.7704**	-0.4641 NS	-0.1454**
GOT	PH	-0.5073 N.S	-0.2738 NS	0.0238 N.S
GOT	SL	-1.086 N.S	-0.6108*	-0.2976**
GOT	SL	-0.7055**	-0.3899 NS	-0.1232**
GOT	YLD	-0.4104 N.S	-0.2694 NS	-0.1202**
MIC	BNO	0.2436 N.S	0.1687 N.S	-0.0322 N.S
MIC	PH	0.4287 N.S	0.4447 N.S	0.5103 N.S
MIC	SL	0.2077 N.S	0.1894 N.S	0.1887 N.S
MIC	Sl	0.8064**	0.5833*	0.1931 N.S
MIC	YLD	0.1653 N.S	0.1845 N.S	0.3187 N.S
BNO	PH	0.4617 N.S	0.4211 N.S	0.2928 N.S
BNO	SL	0.5951*	0.5804*	0.6329*
BNO	SL	0.7322**	0.4316 N.S	-0.1052 N.S
BNO	YLD	0.8801**	0.6923**	-0.1453 N.S
PH	SL	0.7296*	0.408 N.S	-0.053 N.S
PH	SL	0.6485*	0.4218 N.S	-0.0608 N.S
PH	YLD	0.0633 N.S	0.1057**	0.3954**
SL	SI	0.9434**	0.3632 N.S	-0.186**
SL	YLD	0.2474 N.S	0.1471 N.S	-0.0228 N.S
SL	YLD	0.3695 N.S	0.3007 N.S	0.1827**

Symp= Sympodial Branches, BW=Boll weight (g), GOT=Ginning out turn (%age), MIC=Micronaire value (micrgram/inch), NOB=Number of Boll, PH=Plant Height (cm), SL= Staple length (mm), SI=Seed Index, YLD=Yield (g).

High to low genetic advance values ranging from 10.93% to 58.24 % for different traits as shown in (Table 1). Highest value was recorded for seed cotton yield while lowest for plant height. High heritability with high genetic advance for the number of sympodial branches, micronaire value, number of bolls per plant, and seed cotton yield provides a sound ground for improvement in these characters through selection. High heritability estimated for seed cotton yield and yield contributing traits. More genetic influence with lower environmental factors predicted that most of the traits were controlled by additive type of gene action. Thus, phenotypic selection is recommended for the improvement of these traits under investigation except fiber quality reported by (Batool *et al.*, 2010; Aziz *et al.*, 2014;

Raza *et al.*, 2016).

Highest genotypic and phenotypic coefficient of variance for seed cotton yield (29.64, 3108) followed by number of bolls per plant (22.41, 26.29) while the lowest value for GOT% as (4.80, 7.80), as shown in (Table 1).

The phenotypic and genotypic correlation ranged from 0.9434 and 0.8003 to 0.427 and 1.037 (Table 2). Calculation of phenotypic and genotypic correlation was significant for the number of sympodial branches boll weight and yield related traits. Phenotypic and genotypic correlation for the number of bolls exhibited by yield was (0.2474 and 0.3695).

Table 3. Path coefficient analysis for yield and fiber quality parameters of Cotton.

	Symp	BW	GOT	MiC	Bno	PH	SL	SI	YLD
Symp	0.4815	0.0985	-0.0565	-0.1998	0.5832	-0.3206	-0.3067	0.2317	0.5114
BW	0.3019	0.1572	-0.019	-0.2934	0.5739	-0.2503	-0.2759	0.3774	0.5718
GOT	-0.4119	-0.0451	0.0661	0.096	-0.6236	0.2178	0.5176	-0.2274	-0.4104
MiC	0.2578	0.1236	-0.017	-0.3731	0.1972	-0.1841	-0.099	0.2599	0.1653
Bno	0.347	0.1114	-0.0509	-0.0909	0.8094	-0.1982	-0.2837	0.236	0.8801
PH	0.3596	0.0916	-0.0335	-0.16	0.3737	-0.4293	-0.3478	0.209	0.0633
SL	0.3098	0.091	-0.0718	-0.0775	0.4817	-0.3133	-0.4766	0.3041	0.2474
SI	0.3461	0.184	-0.0466	-0.3009	0.5926	-0.2784	-0.4496	0.3223	0.3695

Symp=Sympodial Branches, BW=Boll weight (g), GOT=Ginning out turn (%age), MIC=Micronaire value (micrgram/inch), NOB=Number of Boll, PH=Plant Height (cm), SL= Staple length (mm), SI=Seed Index, YLD=Yield (g).

The results presented in (Table 2), represents that genotypic correlation was significant and positive for number of sympodial branches with number of bolls per plant, plant height, staple length and boll weight while significant but negative correlation with ginning outturn%. GOT% has significant and negative correlation with number of bolls while significant and positive directly with seed index. Genotypic correlation for micronaire value was significant and positive for seed index, whereas number of bolls per plant has significant and positive with staple length, seed index and seed cotton yield per plant. Correlation significant of plant height with staple length and seed index has been observed. Staple length has significant and positive correlation with seed index.

Phenotypic correlation as represented in (Table 2) depicted that positive and significant correlation was observed for number of sympodial branches per plant with number of bolls per plant and plant height, similarly for boll weight with number of bolls per plant and seed cotton yield per plant. GOT% has

significant negative correlation with staple length. Micronaire value exhibited significant and positive phenotypic correlation within seed index and similar positive significant correlation was exhibited for number of bolls per plant with staple length and seed cotton yield per plant. Seed cotton yield also represented similar pattern with plant height.

Genotypic correlation of seed cotton yield was further subdivided to direct and indirect effects with the help of path coefficient analysis as presented in (Table 3).

The information regarding the relationship between different traits effecting on seed cotton yield is imperative to reach possibility impression on the selection index.

The path-coefficient analysis revealed that yield exhibit their direct effects through boll weight and number of bolls per plant. The correlation analysis is a method of statistical development used to investigate the extent of correlation between two quantitative variables traits.
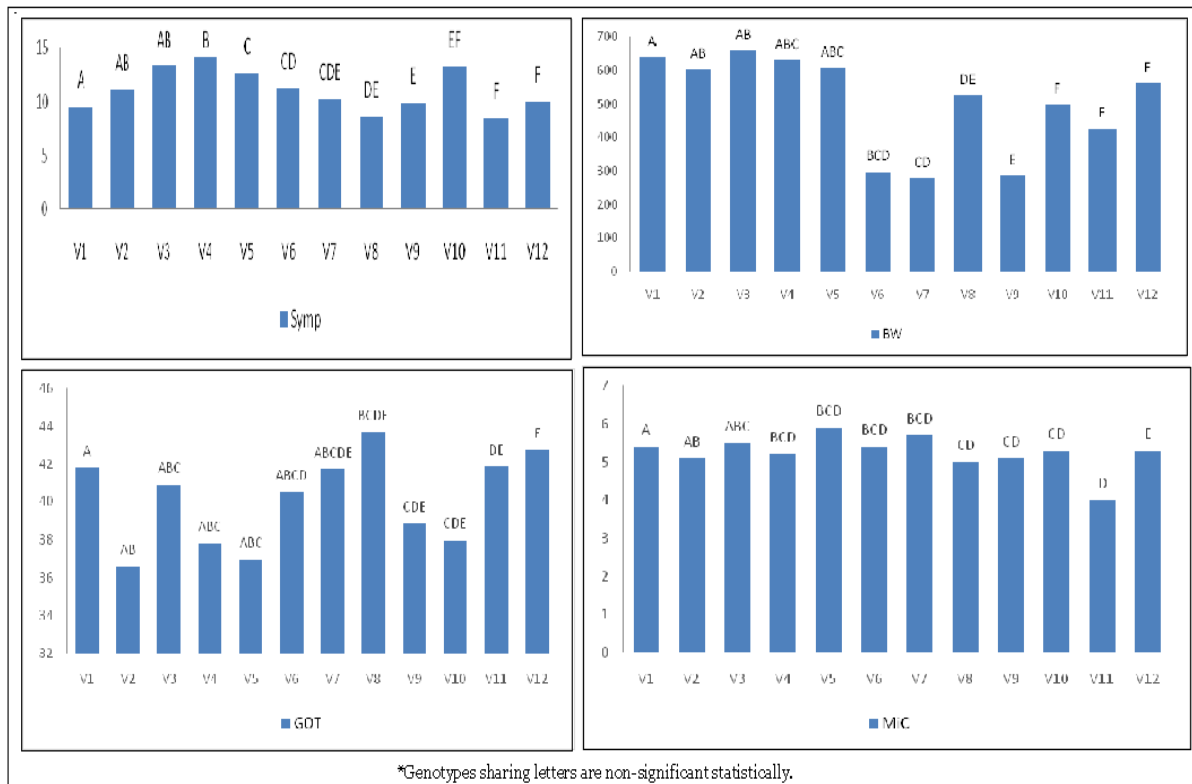
Fig. 1. Diagrammatical results of four parameters, for sympodial branch, Boll weight, ginning out percentage,and micronaire value.
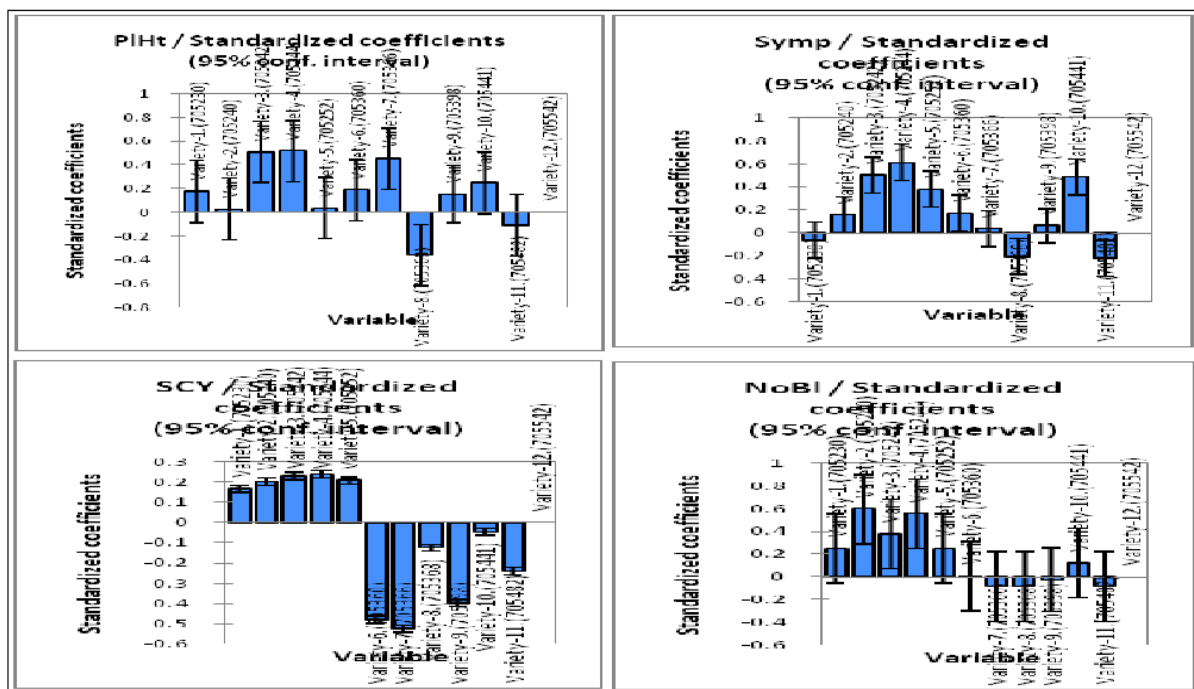

Fig. 2. Standardized co-efficient Variable results of four parameters, for plant height, sympodial branch, yield components, and number of bolls per plant.

This type of analysis is used when a scientist needs to find if there is a potential relationship among visibilities. It is offently misunderstood that the correlation analysis ascertains effect because whenever that is not the variations that do not appear in the study may have played an impact on the

results. When the correlation is discovered among two variables means that there is a systematic change in the variable.

It is also imperative change in the other variable which can be modified in the specific time period. A correlation discovered depends upon the numerical values which can be negative or positive. Negative correlation is represented in its extant if one variable dropdown the other variable progresses inversely with enhancement in its values. Positive correlation is described as if the value of single variable is increased the value of other variable is also increased. The

correlation between seed cotton yield and ginning outturn percentage% was seen constructive but non-significant, unhelpful and non-momentous between micronaire values along with staple length encouraging, but significant with seed index and boll weight.

It enlightens that ever-increasing of seed cotton yield (kg ha^{-1}) gives an approving result for GOT% and micronaire value but eventually decrease another character. These results of variation were back up by determination of previous studies by (Ahmad *et al.*, 2011; Hassan *et al.*, 2013; Rahman *et al.*, 2013).
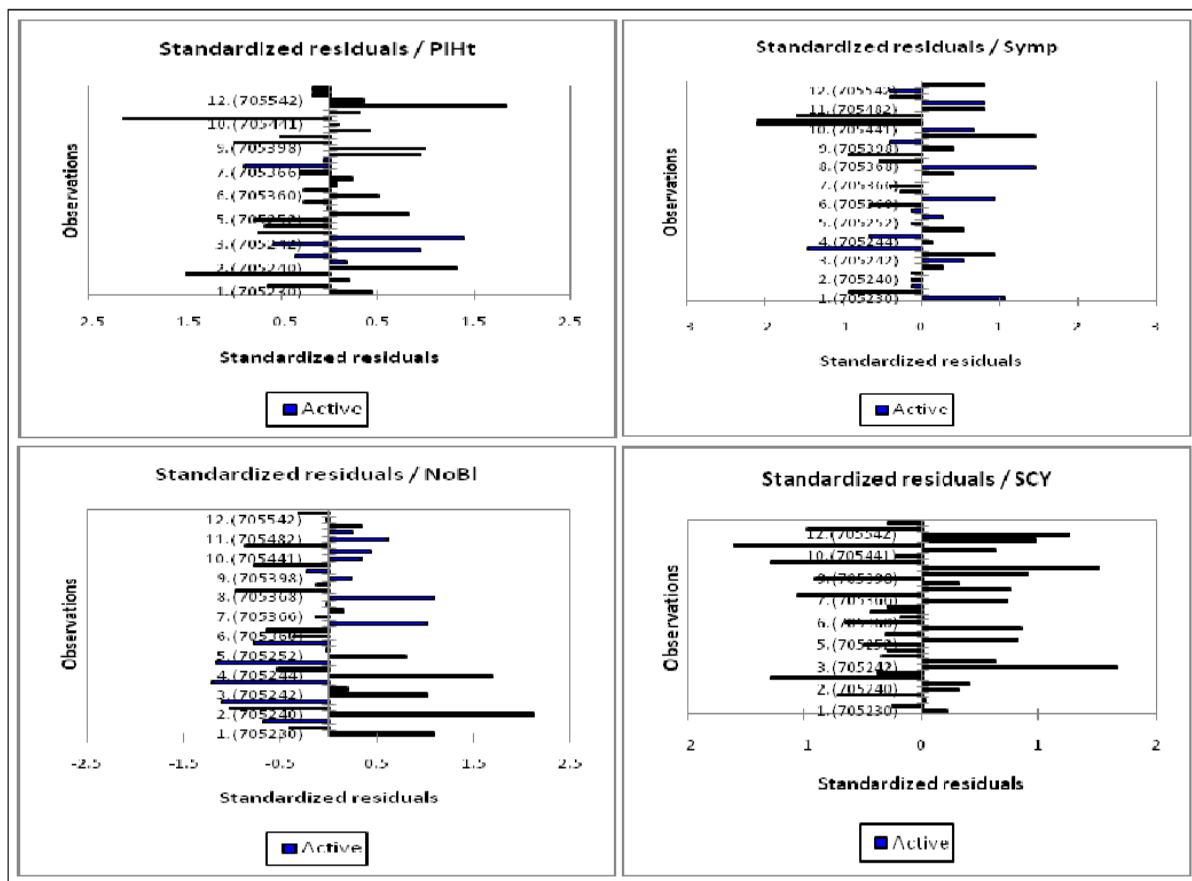

Fig. 3. Standardized residual observations results of all nine parameters, for plant height, sympodial branch, number of bolls per plant, and seed cotton yield components.

The interaction between sympodial branches per plant with staple length and number of bolls per plant was observed unhelpful but considerable helpful and highly significant with cotton seed yield (kg ha-1) and negative but non-significant by means of ginning outturn percentage%, seed index, boll weight and micronaire value. This suggests that amplify in the

number of sympodial branches per plant would ultimately bring a decrease in seed index, boll weight, GOT% and micronaire value but fruitful results for number of bolls, staple length and positive results for cotton seed yield (kg ha-1). The results were according to the observations by (Mendez-Natera *et al.*, 2012; Rahman *et al.*, 2013), positive but

significant affiliation was examined between seed cotton yield and number of bolls per plant pessimistic but non-significant through micronaire value and

staple length highly considerable but negative with seed index and boll weight. In addition, a non-significant interaction was observed through GOT%.
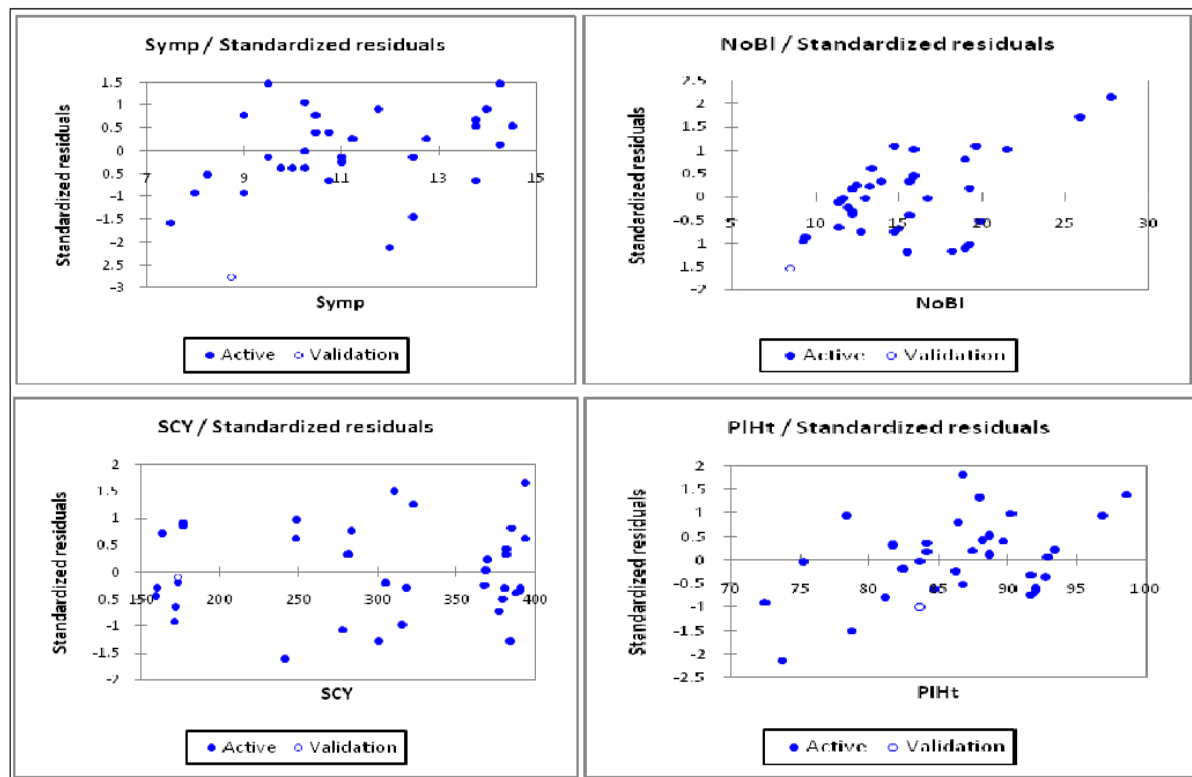

Fig. 4. Standardized residuals results of all nine parameters, for sympodial branch, number of bolls per plant, seed cotton yield components, and plant height.

These results further illustrate that increasing the number of bolls per plant will support to boost up seed cotton yield (kg ha⁻¹) but remaining other characters may not get positive change. Similar results were reported by (Afiah and Ghoneim, 2000; Rahman *et al.*, 2013). For path analysis results indicates in the Table 3, the direct and indirect effect displays on different parameters.

The path coefficient analysis results revealed that the traits like sympodial branches per plant (0.74), plant height (-0.43) and boll weight (1.10). GOT% (0.39) demonstrates direct effect on cotton seed yield as represented in (Table 3), whereas all the remaining traits demonstrates negative values (Natera-Mendez *et al.*, 2012), discovered the highest direct effect of number of sympodial branches with seed cotton yield. Whereas in the path correlation studies as previously described by (Alkuddsi, *et al.*, 2013) that highest

direct effects were imposed by boll weight and number of sympodial branches per plant. Whereas, for staple length, plant height exhibits non significant. However, other traits shown negative indirect effect on seed cotton yield these results are in accordance with (Azhar *et al.*, 1999).

The indirect effects of monopodial branches per plant determines the cotton seed yield positively through number of bolls per plant, staple length, seed index, micronaire vale and other related traits showed negative values by (Iqbal *et al.*, 2003), described the negative direct effect of sympodial branches on seed cotton yield.

Sympodial branches per plant demonstrate non-significant and direct effect on cotton seed yield. It also demonstrates nonsignificant indirect effects on yield, boll weight and plant height accordingly.

The standardized co-efficient is also known as beta co-efficient are used for to estimate the resulting from a regression analysis. Which has been standardized so that the variances of dependent and independent variables as shown in (Fig. 2). Whereas a standardized residual is a quotient resulting from the partition of a residual by an estimate of its standard deviation. Typically, the standard deviation of residuals in a sample varies greatly from one data point to another even the error all have the same standard deviations as mentioned in (Fig. 3).

Genotypes sharing letters are non-significant statistically. The coloums which proceed upwards are positively significant. Where as the columns which proceed downword which are shown negative significant as described in the diagrams (Fig. 4). The coloumns which proceed upwords which are shown positive and highly significant as shown in the (Fig. 5), phenotypical results of five parameters, including, plant height, sympodial branches per plant, seed cotton yield components, number of bolls per plant, and ginning outturn% as shown in (Fig. 5).
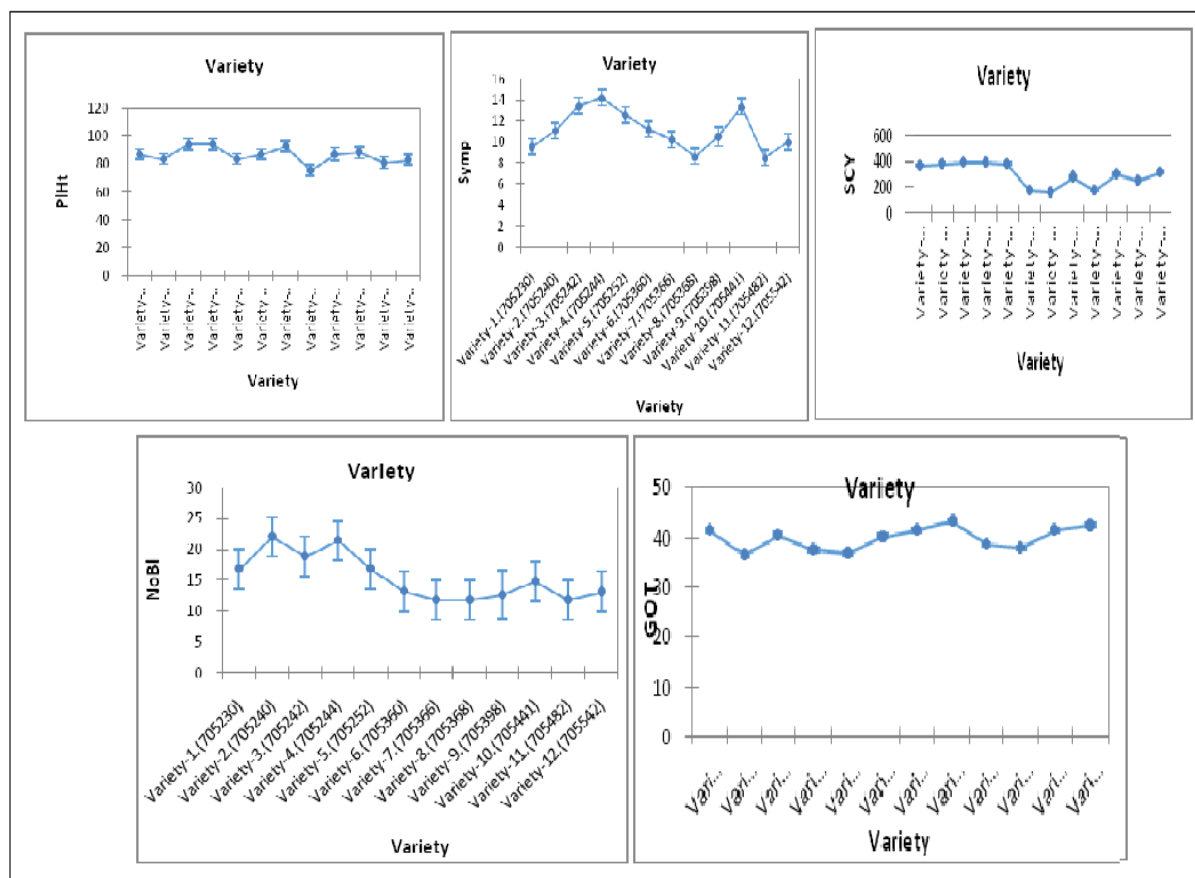

Fig. 5. Diagrammatical results of five parameters, for plant height, sympodial branch, seed cotton yield components, number of bolls per plant, and ginning out percentage.

Conclusion

Different traits are interrelated to each other and have a scope of promoting any changes corresponding trait through indirect selection of correlated traits. So, we can make a selection of desirable cultivars for yield and other traits simultaneously by considering correlation and path coefficients while considering direct and indirect relationship of traits with dependent trait which is seed cotton yield. Similarly, we have a great scope of cotton improvement for yield and fiber quality indirectly considering other corelated traits based on direct and indirect influence on yield considering it dependent variable.

Conflict of interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

References

Adsare AN, Abhay NS. 2017. Study on genetic variability for the quantitative traits in some genotypes of upland cotton (*Gossypium hirsutum* L.). Biosciences, Discovery **8(3),** 365-368.

Afiah SAN, Ghoneim EM. 2000. Correlation, stepwise and path co-efficient analysis in Egyptian cotton under saline condition. Arab. University of Agricultural Sciences **8(2),** 607-618.

Ahmad W, Khan NU, Khalil MR, Parveen AE. Aiman U, Samiullah MS, Shah SA. 2008. Genetic variability and correlation analysis in upland cotton. Sarhad Journal of Agriculture **24(4),** 573-580.

Ahmad M, Khan NU, Mohammad F, Khan SA, Munir I, Bibi Z, Shaheen S. 2011. Genetic potential and heritability studies for some polygenic traits in cotton (*G. hirsutum* L.). Pakistan Journal of Botany **43,** 1713-1718.

Ahsan MZ, Majidano MS, Bhutto H, Soomro AW, Panhwar FH, Channa AR, Sial KB. 2015. Genetic Variability, coefficient of variance, heritability and genetic advance of some *Gossypium hirsutum* L. accessions.

Akbar M, Ahmad J, Azhar FM. 1994. Genetic correlation, path-coefficient and heritability estimates of some important plant traits in Upland cotton. Pakistan Journal of Agriculture Sciences **31(1),** 47-50.

Alkuddsi Y, Rao M.R, Patil SS, Joshi M, Gowda TH. 2013. Correlation and path coefficient analysis between seed cotton yield and its attributing characters in intra hirsutum cotton hybrids. Molecular plant Breeding **4,** 214-219.

Ameer HJ, Wang X, Iqbal MS, Sarfaraz Z, Wang L, Qifeng Ma, Shuli F. 2019. Genetic divergence on the basis of principle component, correlation and cluster analysis of yield and quality traits in cotton cultivars. Pakistan Journal of Botany. **51(3),** 1143-1148.

Azhar FM, Khan AI Mahmood I. 1999. Path coefficient analysis of some advanced progenies of *G. hirsutum* L. International Journal of Agriculture Biology **1(3),** 85-87.

Aziz U, Afzal J, Iqbal M, Naeem M. 2014. Selection response, heritability and genetic variability studies in upland cotton. Journal of Applied and Environmental Biological Sciences. **4(8S),** 400-412.

Batool S, Khan NU, Makhdoom K, Bibi Z, Hassan G, Marwat KB, Farhatullah F, Raziuddin M, Khan IA. 2010. Heritability and genetic potential of upland cotton genotypes for morpho-yield traits. Pakistan Journal of Botany. **42(6),** 1057-1064.

Burton GW, Devane EH. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. **45(10),** 478–481.

Dewey DR, Lu KH. 1959. A correlation and path coefficient analysis of components of crested wheat

grass seed production. Agronomy Journal **51,** 515-518.

Dilday RH, Mgonja MA, Amonsilpa SA, Collins FC, Wells BR. 1990. Plant height vs. mesocotyl and coleoptile elongation in rice: Linkage or pleiotropism. Crop Science **30,** 815– 818.

Fonseca S, Paterson FL. 1968. Yield components heritability and interrelationship in winter wheat. Crop Science **8,** 614-617.

Freed R. 1984. MSTAT: A Multipurpose Computer Program for Agricultural Research. IRRI Microcomputer Workshop. Sept. 1984.

Hassan SMF, Iqbal MS, Rabbani G, Naeem-ud-Din, Shabbir G, Riaz M, Noorka IR. 2013. Correlation and path analysis for yield and yield components in sunflower (*Helianthus annus.* L). African Journal of Biotechnology **12(16),** 1968-1971.

Iqbal MK, Rao H, Khan SA, Attique S, Islam N. 2006. Correlation and path coefficient analysis for earliness and yield traits in cotton. American Journal of Plant Sciences **52,** 341-344.

Iqbal M, Chang MM, Iqbal MM, Hassan M, Nasir A, Islam N. 2003. Correlation and path coefficient analysis of earliness and agronomic characters of upland cotton in Multan. Journal of Agronomy **23,** 160-168.

Kebede H, Subudhi PK, Rosenow DT, Nguyen HT. 2001. Quantitative trait loci influencing drought tolerance in grain sorghum (*Sorghum bicolor* L. *Moench*). Theory Applied Genetics. **103,** 266–276.

Kempthorne O. 1957. An introduction to genetic statistics. Wiley, New York.

Khan NU, Hassan G, Kumbhar MB, Parveen A, Aiman U, Ahmad W, Shah SA, Ahmad S. 2007. Gene action of seed traits and oil content in upland cotton (*G. hirsutum* L.). Sabrao Journal of

Breeding & Genetics **39,** 17-30.

Khan NU, Hassan G, Marwat KB, Farhatullah S, Batool Makhdoom K, Khan I, Khan IA, Ahmad W. 2009a. Genetic variability and heritability in upland cotton. Pakistan Journal of Botany **41(4),** 1695-1705.

Khan NU, Marwat KB, Hassan G, Farhatullah, Batool S, Makhdoom K, Ahmad W, Khan HU. 2010. Genetic variation and heritability for cottonseed, fiber and oil traits in *G. hirsutum* L. Pakistan Journal of Botany **42,** 615-625.

Kwon SH, Torrie JH. 1964. Heritability and interrelationship of two soybean (*Glycine max* L.) populations. Crop Sciences **4,** 196-198.

Lotherop JE, Akins RE, Smith OS. 1985. Variability of yield and yield components in IAPIR grain sorghum random mating population means variance components and heritabilities. Crop Science, **25,** 235-240.

Meena RA, Monga D, Kumar R. 2007. Un-descriptive cotton cultivars of north zone: an evaluation. Journal of Cotton Research. Dev. **211,** 21-23.

Méndez-Natera JR, Rondón A, Hernández J, Merazo-Pinto JF. 2012. Genetic studies in upland cotton. III. Genetic parameters, correlation and path analysis. Sabrao Journal of Breeding & Genetics. **44(1),** 112-128.

Nizamani F, Baloch MJ, Buriro AW, Nizamani M, Nizamani GH, Baloch IA. 2017. Genetic distance, heritability and correlation analysis for yield and fibre quality traits in upland cotton genotypes. Pakistan Journal of Biotechnology **14,** 29-36.

Poehlman JM, Sleper DA. 1995. Breeding field crops. 4th Edn. Panima Publishing Corporation. New Dehli. India.

Rahman S, Malik TA. 2008. Genetic analysis of fibre traits in cotton. International Journal of Agriculture Biology **10,** 209-212.

Rahman SA, Iqbal MS, Riaz M, Mahmood A, Shahid MR, Abbas G, Farooq J. 2013. Cause and effect estimate of morphological and yield traits in cotton. Journal of Agriculture Research. **51(4),** 395-400.

Raza H, Khan NU, Khan SA, Gul S, Latif A, Hussain I, Khan J, Raza S, Baloch M. 2016. Genetic variability and correlation studies in F4 populations of upland cotton. Journal of Animal and Plant Sciences **26(4),** 1048-1055.

Reta-Sanchez Fowler JL. 2002. Canopy Light Environment and Yield of Narrow-Row Cotton as Affected by Canopy Architecture. Agronomy Journal. **94,** 1317-1322.

Saleem S, Kashif, Hussain M, Khan A, Saleem FA. 2016. Genetic behavior of morpho-physiological traits and their role for breeding drought tolerant wheat. Pakistan Journal of Botany **48(3),** 925-93.

Shao D, Wang T, Zhang H, Zhu J, Tang F. 2016. Variation, heritability and association of yield, fiber and morphological traits in a near long staple upland cotton population. Pakistan Journal of Botany. **48(5),** 1945-1949.

Soomro ZA. 2000. Genetic architecture of quantitative and qualitative traits in *Gossypium hirsutum* L. M.Phil. Thesis, Dept. Plant Breeding and Genetics, Sindh Agriculture University Tandojam, Sindh, Pakistan.

Statista. 2017. http://www.statista.com/statistics/263055/cotton-production-worldwide -by -top-countries/.

Steel RGD. Torrie JH, Dickey DA. 1997. Principles and Procedures of Statistics: A Biometrical Approach, 3rd edition. McGraw Hill Book Co. Inc. New York.

Taohua Z, Haipeng Z. 2006. Comparative study on yield and main agri-characters of five hybrids colored cotton varieties. Journal of Anhui Agriculture University **33,** 533-536.

Ulloa M, Hutmacher RB, Davis RM, Wright SD, Percy R, Marsh B. 2006. Breeding for fusarium wilt race 4 resistances in cotton under field and greenhouse conditions. Journal of Cotton Science **10,** 114-127.

Wang C, Isoda A, Wang P. 2004. Growth and yield performance of some cotton cultivars in Xinjiang, China, an arid area with short growing period. Journal of Agron & Crop Science **190,** 177-183.

Wang K, Wang Z, Li F, Ye W, Wang J, Song G, Yu S. 2012. The draft genome of a diploid cotton *Gossypium raimondii*. Nature Genetics **44(10),** 1098-1103.