Uluslararası Tarım Araştırmalarında Yenilikçi Yaklaşımlar Dergisi
International Journal of Innovative Approaches in Agricultural Research 2019, Vol. 3 (1), 25-52
https://doi.org/10.29329/ijiaar.2019.188.4

Original article

Estimation of Gene Action, Heritability and Pattern of Association among Different Yield Related Traits in Upland Cotton

Bilal Nawaz [a], Muhammad Naeem [a, *], Tanwir Ahmad Malik [a],
Ghulam Muhae-Ud-Din [b], Qadeer Ahmad [c] & Saira Sattar [a]

[a] Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad-38040, Pakistan
[b] State key Laboratory for Biology of Plant Diseases and Insect Pest, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, China
[c] PMAS-Arid Agriculture University Rawalpindi, Pakistan

Abstract

A random mating design comprising 6 varieties (FH-142, MS-DK, IUB-63, KZ-189, FB-3159, and VH-300) and F1 crosses was used to check gene action for yield contributing traits in upland cotton. Heritability and correlation were calculated from F3 populations of the cross CRS-456×Jumbo okra. The randomized complete block design was used in both experiments with three replication at the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan during 2015-2017. In both experiments, analysis of variance indicated significant variation present among the accessions of the upland cotton for all the traits (plant height, sympodial and monopodial branches, nodes number of 1st sympodial branch, height of 1st sympodial branch, bolls per plant, boll weight, lint weight, seed cotton yield, seed index, lint percentage, lint index, seeds per boll, fiber fineness, fiber strength, fiber length and fiber uniformity) under study. Mean values of all genotypes were significantly different from each other for all the traits studied. All the parameters manifested positive correlation with seed cotton yield except plant height, monopodia per plant, nodes number of 1st sympodia, height of 1st sympodia, bolls per plant, seed index and lint index. The inheritance of all the traits in F1 crosses was generally controlled by overdominance gene action except monopodial branches, nodes number of 1st sympodial branch, height of 1st sympodial branches, boll weight, fiber length and fiber uniformity that were partially controlled under additive gene action. Epistasis was not found to be involved in any of the traits. Estimation of broad sense heritability (h2 b. s) in F3 populations were high (60-97%) for all the traits under study. Results suggested form heritability and correlation that these traits can be improved either through appropriate selection method or hybrid breeding programme.

Keywords: Correlation, Heritability, Gene action, Yield related traits, Upland cotton (*Gossypium hirsutum*. L).

Received: 27 July 2018 * **Accepted:** 02 February 2019 * **DOI:** https://doi.org/10.29329/ijiaar.2019.188.4

---

* **Corresponding author:**

Muhammad Naeem, Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad-38040, Pakistan.
Email: naeem_plant_scientist@outlook.com

List of abbreviations used: Plant height(PH,), Sympodial branches per plant(SB), Monopodial branches per plant(MB), Nodes no. of 1st sympodial branch(NFSB), Height of 1st sympodial branch(HFSB), Bolls per plant(BPP), Boll weight(BW), Lint weight(LW), Seed cotton yield(SCY), Seed index(SI), Lint percentage(LP), Lint index(LI), Seeds per boll(SPB), Fiber fineness(FF), Fiber strength(FS), Fiber length(FL), Fiber uniformity(FU), Partial dominance (PD), over dominance (OD), Dominance (D), Additive (A)

INTRODUCTION

Pakistan is an agricultural country whose economy depends upon agriculture directly and indirectly. Agriculture sector is playing an important role in socio-economic development of the country and alleviating poverty. Cotton is known as white gold due to its importance as industrial and cash crop. Cotton is not only the most important fiber crop but also a second most important oilseed crop of the world (Cherry and Loffler, 1984). It plays a vital role in improving our national economy being the principal source of earning foreign exchange, therefore, it is considered to be the backbone of the economy of Pakistan. In Pakistan, millions of families are associated with cotton and textile industry for their livelihood (Hussain et al., 2014). Any fluctuation in its production and fiber quality can affect the economic growth of the country (Khan et al., 2009). Cotton is perennial plant having intermediate growth habit. It is a short day plant which fixes carbon in C3 form. It belongs to Gossypium Genus and Malvaceae family (Brubaker et al., 1999a). This genus consists of 50 species having 13 basic chromosome number (Poehlman and Sleeper, 1995). There are 45 diploid species and five are allotetraploid in nature (Fryxell, 1979). The new world species of cotton (Upland cotton and Egyptian cotton) are now leading the world in cotton production. Due to best agronomic properties and yield, Gossypium hirsutum is cultivated on 90% of the total cultivated area of the world. In Pakistan, 99% area is under cultivation of Gossypium hirsutum and less than 1% is cultivated with Gossypium arboreum. Among largest cotton producing countries, Pakistan is on the 4th position after China, USA and India while in consumption of cotton, Pakistan is on 3rd position in the world. The economy of Pakistan heavily depends on cotton. A huge amount of foreign exchange is earned by exporting cotton and its byproducts. Cotton crop contributes 1% in the GDP and 5.1 % in the value addition of agriculture in Pakistan. It is cultivated on 2.917 million hectares with a production of 10.074 million bales. The average seed cotton yield is 587 kg/ha in Pakistan (Anonymous, 2015-16).

A thorough knowledge about the correlation, gene action and heritability of plant traits is necessary to breed cotton varieties with higher yield and better fiber quality. Heritability predicts selection response for the traits to suggest the structure of a population. It also predicts the degree to which a given character would be transmitted to the next generation and the magnitude of genetic improvement that is possible through selection.

Correlation provides the information of association among different traits being helpful in selection of plants with a good combination of yield and quality related traits (Salahuddin et al., 2010). The association among yield related traits play a significant role toward improvement and to produce promising genotypes with high yield and quality. Correlation analysis also predicts direction of relationship among desirable plant traits. Suinaga et al. (2006), Taohua and Haipeng (2006), Khan et al. (2007) and Meena et al. (2007) studied the adaptability and stability of upland cotton cultivars and found varied values for different morphological, agronomic and yield contributing traits. Iqbal et al. (2013) and Wang et al. (2004) reported genetic variability and positive correlation among yield contributing traits in Upland cotton. Khan et al. (1999) and Khan (2003) observed high genetic variability for yield and yield related components among various genotypes of upland cotton. Vineela et al. (2013) reported that it is obligatory to understand the gene action pattern of inheritance of yield related traits to select a suitable breeding method for crop improvement.

So present research work was undertaken to determine correlation, gene action and heritability for the traits, plant height, sympodial branches per plant, monopodial branches per plant, nodes no. of 1st sympodial branch, height of 1st sympodial branch, bolls per plant, bolls per plant, boll weight, lint weight, seed cotton yield, seed index, lint percentage, lint index, seeds per boll, fiber fineness, fiber strength, fiber length and fiber uniformity. This information might be useful for cotton breeders to breed high yielding cotton varieties.

Materials and Methods

Plant material and experimental design

During the winter season of the year 2015-16, six varieties provided by the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad were planted in pots and placed in the greenhouse. Hybrids were developed by crossing six varieties (FB-3159, FH-142, KZ-189, VH-300, IUB-63, and MS-DK) during February-March, 2016.

The F_1 hybrids along with the parents were planted in a randomized complete block design with three replications to calculate gene action. Another experiment involving F_3 populations of the cross CRS-456 × JAMBO- OKRA and the parents was established on the randomized complete block design with three replications to compute heritability and correlation. The experiments were conducted in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the normal growing season of the year 2016. Each replication consisted of a single row for each entry containing 10 plants. Row-to-row and plant-to-plant distances were maintained at 75 and 30cm, respectively. In the first experiment, 5 plants were randomly selected from each F_1 progeny and the parents from each replication. In the second experiment, 25 plants of F_3 population and 5 plants from each parent were selected at random from each replication. All the agronomic practices and inputs including fertilizer, hoeing and irrigation were followed from sowing to harvest to minimize environmental variations. Different types of insecticides were also sprayed to minimize and control attacks of sucking and chewing insect pests with respect to prevailing conditions. Date of following traits was collected at maturity. The data was recorded on plant height (cm), sympodial branches per plant, monopodial branches per plant, nodes number of 1st sympodial branch, height of 1st sympodial branch (cm), bolls per plant, boll weight (g), lint weight (g), seed cotton yield (g), seed index (g), lint percentage (%), lint index (%), seeds per boll, fiber fineness(µg/inch), fiber strength (g/tex), fiber length(mm) and fiber uniformity (%).

At the time of maturity, the height of selected plants was recorded from cotyledonary node (zero node) to ceased apical bud with the help of measuring tape in centimeters. Then the average of these measurements was calculated for each genotype in a replication. Sympodial branches are direct fruit bearing branches and these are generally short appearing towards the top of the stem. At maturity, sympodial branches were counted from all the selected plants in each replication and the average number of sympodial branches from each replication was calculated. These are vegetative branches which are generally located at the base of the main stem. These are also named as indirect fruit bearing branches. At maturity, monopodial branches from the selected plants of parental genotypes and their progeny were counted in each replication and the average number of monopodial branches for each genotype from each replication was calculated at the time of full maturity. Nodes number of 1st sympodial branch from selected plants of parental genotypes and their progeny was counted in each replication and the average number of nodes of 1st sympodial branch for each genotype from each replication was calculated. At the time of full maturity, the height of 1st sympodial branch from the selected plants of parental genotypes and their progeny was counted in each replication and the average number of height of 1st sympodial branch for each genotype from each replication was calculated. The number of bolls per plant picked at each picking was recorded from individual plants. When final picking was over, picking record was summed up and the average number of bolls per plant was calculated. Five bolls of each selected plant were harvested at random. These bolls were weighed separately. Then average boll weight was calculated for each plant and then for each genotype in a replication. Total seed cotton yield of five selected plant of each genotype was weighed and ginned with a single roller electrical gin. All lint of each plant was weighted with the help of electrical balance than summed and divided by five to take the average lint weight of each genotype in a replication. The mature bolls were picked from each selected plant and weighed separately with the help of electrical balance. The average seed cotton yield of each parent and its population in a replication was calculated. Seed index is a weight of 100-seeds obtained from each plant. A random sample of one hundred seeds was taken from the lot obtained after ginning a sample and were weighted on balance. The mean seed index of each genotype was calculated. Total seed cotton yield of each selected plant was weighed and ginned with a single roller electrical gin. A random sample from the lint of each plant was weighed and lint percentage was calculated by using following formula.

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

Mean value was calculated for each parental its population in a replication. Lint index is calculated by dividing the seed index into the lint percentage, as follows:

$$\text{Lint index} = \frac{\text{Seed index}}{\text{Lint Percentage (\%)}} \times 100$$

For seeds per boll, five bolls of each selected plant were harvested at random. After ginning these bolls with help a single roller electrical gin, total seeds of each boll was counted, summed and divided by five to take average seeds per boll for each genotype in a replication. Fiber characteristics like fiber fineness (FF), fiber strength (FS), fiber length (FL) and fiber uniformity (FU) from the lint of selected plants were recorded using Ustar HVI-900 S.A in the Department of Fiber Technology, University of Agriculture Faisalabad. The computerized instrument recorded fiber length (mm), fiber strength (g/tex), fineness (µg/inch) and Fiber uniformity (%) according to international standards.

Statistical analysis

The collected data were subjected to analysis of variance (ANOVA) by using the method described by Steel et al. (1997) to establish genotypic differences for the various plant traits under study. Correlation coefficients were calculated from the F_3 population data by using the formula as outlined by Dewey and Lu (1959) using the computer Minitab program. Gene action was calculated using the hybrids and the parents. Heritability was calculated by the method used by Majeedano et al. (2014).

Result and Discussion

ANOVA of both experiments calculated by using the method described by Steel *et al.* (1997) revealed that F_3 populations of the cross CRS-456 × Jambo okra and F_1 hybrids with parents showed significant differences for all the observed traits like plant height, sympodial branches, monopodial branches, nodes number of 1st sympodial branch, height of 1st sympodial branch, bolls per plant, boll weight, lint weight, seed cotton yield, seed index, lint percentage, lint index, seeds per boll, fiber fineness, fiber strength, fiber length and fiber uniformity (Table 1). Frequency distribution graphs for all recorded traits of F_3 populations are given in Fig. 1-17.

Table 1. F-ratio for various traits in F_3 populations and F_1 hybrids of upland cotton

Parameters	**F_3 populations F-ratio**	**F_1 populations F-ratio**
PH	9.99*	222.90**
SB	12.28*	18.84**
MB	75.32**	17.93**
NFSB	7.16*	9.00**
HFSB	46.00**	155.75**
BPP	192.89**	191.02**
BW	46.87**	383.01**
LW	170.86**	233.18**
SCY	218.80**	761.67**
SI	977.57**	1245.79**
LP	29.01**	5.36**
LI	6.73*	7.36**
SPB	15.92**	10.10**
FF	46.45**	223.10**
FS	26.44**	846.71**
FL	183.86**	364.74**
FU	153.14**	2095.92**

*, ** Significant at $p \leq 0.05$ and highly significant $p \leq 0.01$.

Table 2. Mean values of the parents and F_3 populations for various agronomic traits in F_3 populations of the cross CRS-456 × Jambo okra

Population	PH	SB	MB	NFSB	HFSB	BPP	BW	LW	SCY	SI	LP	LI	SPB	FF	FS	FL	FU
CRS-456	97.458	13.826	6.0804	15.463	32.75	44.690	2.760	34.498	79.85	6.766	44.261	16.599	25.564	5.3500	27.433	25.533	50.500
Gumbo-Okra	94.160	11.994	3.6419	16.097	45.58	27.290	2.349	17.655	45.36	5.927	43.958	14.309	22.339	4.1600	26.533	27.600	48.237
CRS-456 x G. Okra	98.370	10.470	4.8897	17.812	41.43	31.941	2.875	26.126	63.65	6.528	41.577	16.112	24.131	4.1720	26.556	26.664	48.155
Population Effects	*	*	**	*	**	**	**	**	**	**	**	*	**	**	**	**	**
Heritability	70.522	89.852	60.764	91.515	96.370	89.737	80.273	72.667	77.880	64.980	60.311	88.297	75.726	89.297	96.429	86.513	88.723

* $p<0.05$ **$p<0.01$

Table 3. Correlation matrix for F_3 population and parents among the various agronomic traits in F_3 populations of the cross CRS-456 × Jambo okra

	PH	**SB**	**MB**	**NFSB**	**HFSB**	**BPP**	**BW**	**LW**	**SCY**	**SI**	**LP**	**LI**	**SBP**	**FF**	**FS**	**FL**
SB	0.2727**															
MB	0.3011**	-0.3938**														
NFSB	0.4118**	-0.3814**	0.6623**													
HFSB	0.4632**	-0.4729**	0.7113**	0.8133**												
BPP	0.5351**	0.0641	0.6085**	0.4391**	0.4701**											
BW	-0.3304**	0.0173	-0.2792**	-0.3528**	-0.2974**	-0.4781**										
LW	0.1452	0.2788**	0.0806	-0.1245	-0.0185	0.1924	0.5693**									
SCY	0.1527	0.2631**	0.0775	-0.1109	-0.0210	0.1871	0.6111**	0.9751**								
SI	0.0883	0.0879	-0.0999	-0.0244	-0.0480	-0.1279	0.1359	0.1054	0.1584							
LP	0.3177**	0.0391	0.1326	0.1535	0.2465*	0.2868**	0.0751	0.3740**	0.3764**	-0.2082*						
LI	0.1853	-0.0323	0.0211	0.0754	0.1657	0.0860	0.0471	0.1994	0.1973	-0.0835	0.6948**					
SPB	0.2176*	0.0148	0.0819	0.0102	0.1469	0.1519	0.1266	0.3676**	0.3620**	-0.0747	0.7620**	0.8817**				
FF	0.3435**	0.1129	0.1124	0.0512	0.2260*	0.2967**	0.1181	0.4229**	0.4267**	-0.0708	0.8735**	0.6591**	0.8268**			
FS	0.3040**	0.0801	0.0910	0.0418	0.2092*	0.2508*	0.1325	0.4116**	0.4210**	-0.0747	0.8938**	0.7417**	0.8847**	0.9843**		
FL	0.3063**	0.1047	0.1043	0.0030	0.1824	0.2773**	0.1230	0.4331**	0.4327**	-0.1003	0.8611**	0.7212**	0.8988**	0.9792**	0.9821**	
FU	0.3245**	0.0860	0.1038	0.0606	0.2208*	0.2714**	0.1112	0.4018**	0.4048**	-0.1139	0.9075**	0.7800**	0.8898**	0.9785**	0.9875**	0.9811**

*p<0.05 **p<0.01

Table 4. Gene action in the F_1 crosses in upland cotton for various agronomic traits

Traits	**Gene action**
Plant height	OD+PD
Sympodial branches per plant	OD+PD+A
Monopodial branches per plant	OD+A
Nodes no. of 1st smpodial branch	D+OD+PD+A
Height of 1st sympodial branch	OD+PD+A
Bolls per plant	OD+PD
Boll weight	OD+A
Lint weight	D+OD+PD
Seed cotton yield	D+OD
Seed index	D+OD
Lint percentage	D+OD
Lint index	D+OD
Seeds per boll	D+OD
Fiber fineness	OD+PD
Fiber strength	OD
Fiber length	OD+A
Fiber uniformity	D+OD+A

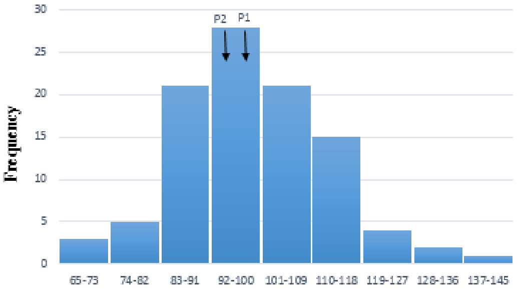

Fig.1 Plant height

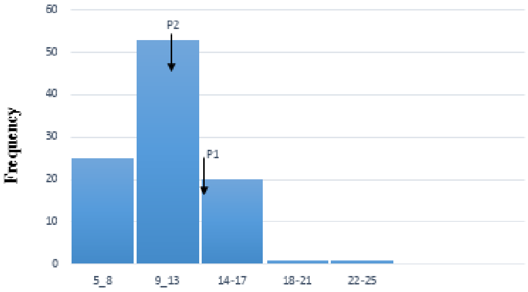

Fig.2 Sympodial branches

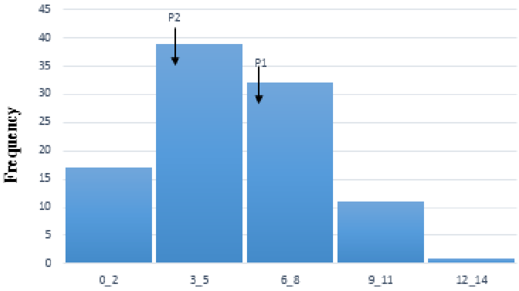

Fig.3Monopodial branches

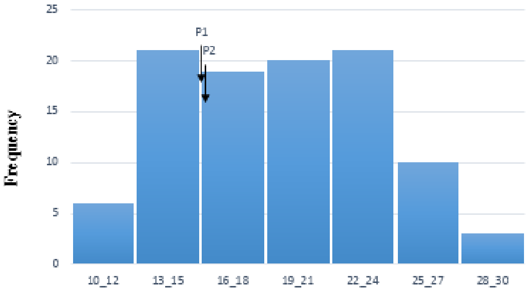

Fig.4 Nodes no. of 1st sympodial branch

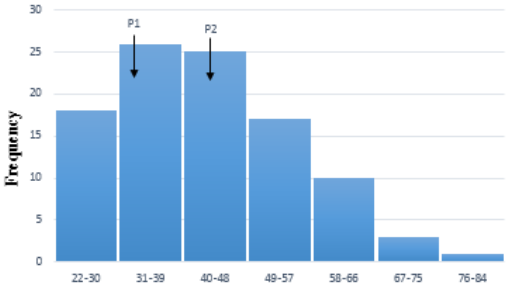

Fig.5 Height of 1st sympodial branch

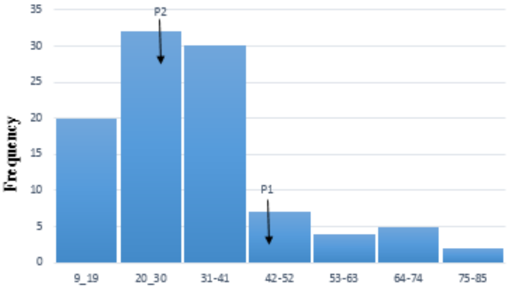

Fig.6 Bolls per plant

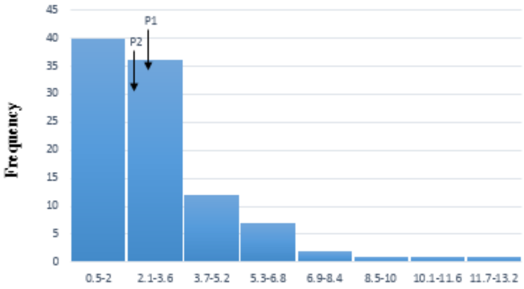

Fig.7 Boll weight

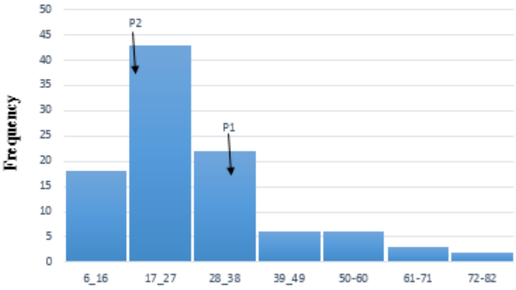

Fig.8 Lint weight

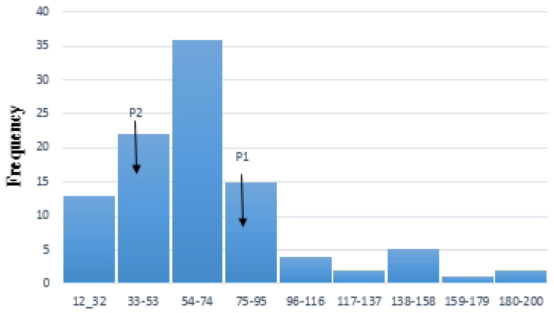

Fig.9 Seed cotton yield

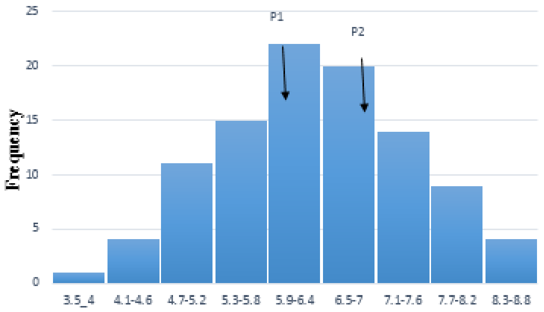

Fig.10 Seed index

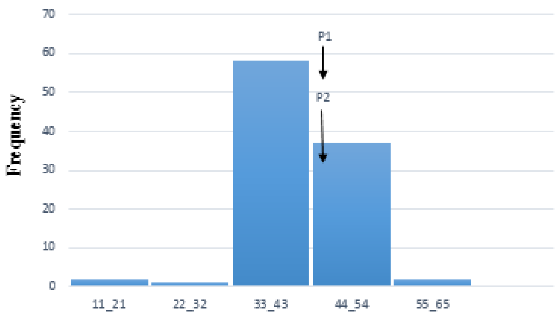

Fig.11 Lint percentage

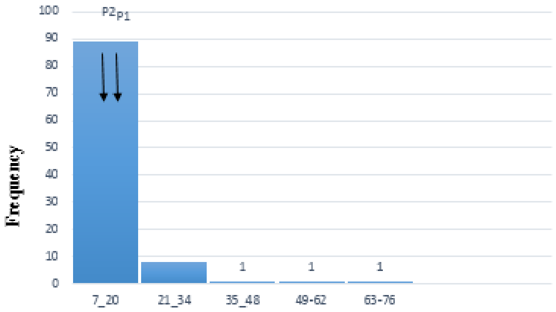

Fig.12 Lint index

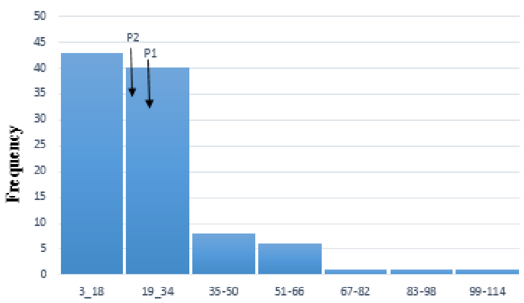

Fig.13 Seeds per boll

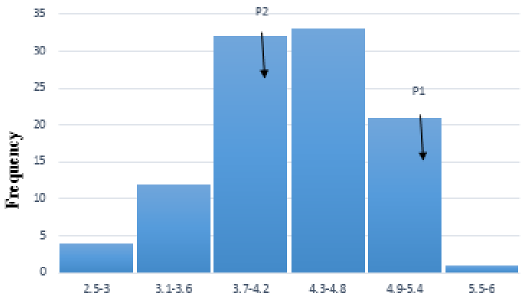

Fig.14 Fiber fineness

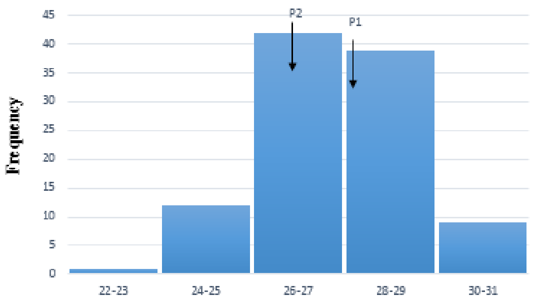

Fig.15 Fiber strength

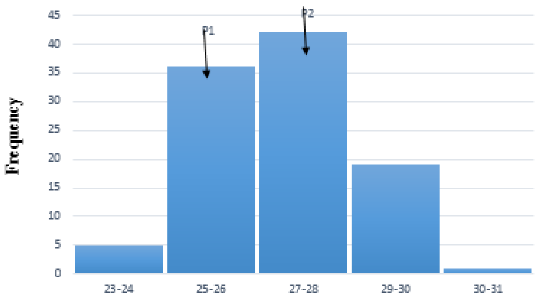

Fig.16 Fiber length

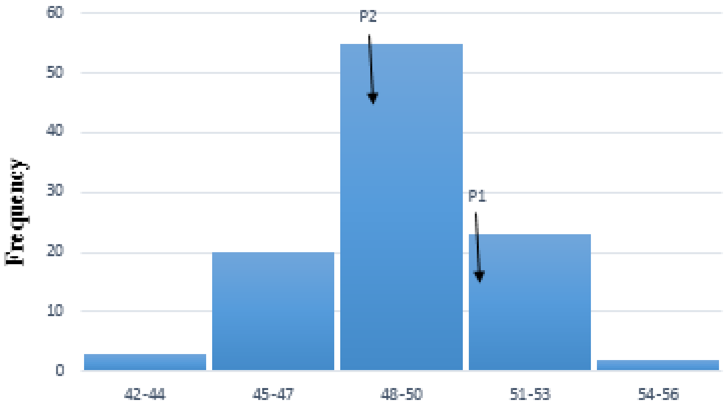

Fig.17 Fiber uniformity

Correlation and inheritance studies

Plant height

Mean data in Table 2 showed that the parent CRS-456 had 97.458 cm plant height and the other parent, Jambo okra, exhibited 94.160 cm plant height. The result depicted that F_3 population produced 98.370cm average plant height that was higher than both of the parents.

Correlation analysis in Table 3 indicated that plant height positively associated with sympodial branches per plant, monopodial branches per plant, nodes no. of 1st sympodial branch per plant, height of 1st sympodial branch, bolls per plant, lint percentage, seeds per boll, fiber fineness, fiber strength, fiber length and fiber uniformity, while it had a negative association with boll weight. This significant and positive correlation of plant height with different agronomic traits showed that sympodial branches, monopodial branches, nodes no. of 1st sympodial branch per plant, height of 1st sympodial branch, bolls per plant, lint percentage, seeds per boll, fiber fineness, fiber strength, fiber length and fiber uniformity can be improved with increasing plant height. As plant height had non-significant association with seed cotton yield that indicates that there will be no improvement in seed cotton yield with increasing in plant height. Broad sense heritability for plant height was 70.522% (Table 2). Due to high value of broad sense heritability, this trait had over dominance gene action in mostly crosses while in a few crosses partial dominance gene action was also expressed (Table 4). So it is suggested that plant height can be used in hybrid breeding programme.

Magadum et al. (2012) and Farooq et al. (2013) reported same results that plant height showed positive linkage with sympodial branches per plant and bolls per plant while it had a negative association with seed cotton yield. This different results may be due to a different genetic makeup of the experimental materials. Nachnani and Abro (1980), Akbar et al. (1994) and Azhar and Ajmal (1999) also studied that plant height positively correlated with monopodial branches per plant and ginning out turn. Kapoor and Kaushik (2003) and Kalim-Ullah et al. (2015) also found that plant height possessed 94% and 87% broad sense heritability. Ranganatha et al. (2011) reported that plant height was controlled under dominance gene action due to high broad sense heritability while Sarwar et al. (2011) studied that plant height possessed an additive type of gene action with partial dominance.

Sympodial branches per plant

For sympodial branches (Table 2), CRS-456 showed the highest mean performance 13.826 and the other parent, Jambo okra, possessed lower mean performance 11.994. While F_3 population produced 10.470 average performance for sympodial branches that was lower from both of the parents.

Correlation analysis showed in Table 3 that sympodial branches positively associated with lint weight and seed cotton yield while it had a negative association with monopodial branches, nodes no. of 1st sympodial branch and height of 1st sympodial branch. Sympodial branches had a significant effect on seed cotton yield and lint weight that indicated that seed cotton yield can be improved with increasing sympodial branches. Result enunciated that a unit increase in the number of sympodia will lead to a matching increase in the seed cotton yield. For this trait, broad sense heritability value was 89.852% (Table 2). This trait had a high value of broad sense heritability that showed that this trait has less environmental effects. The inheritance study depicted in table IV that sympodial branches possessed partial dominance gene action in mostly crosses but in a few crosses additive type of gene action with overdominance was also exhibited. It is concluded that this fruitful association between seed cotton yield and sympodial branch can be helpful in selection programmes for the improvement of diverse genotypes of upland cotton towards the yield.

Annapurve et al. (2007), Zeng et al. (2007) and Mustafa et al. (2007) found similar results that sympodial branches per plant showed a positive correlation with seed cotton yield. Baloch et al. (2015) reported that sympodial branches had positive correlation with seed cotton yield and ginning out turn. Bibi et al. (2011) and Magadum et al. (2012) investigated that sympodial branches positively associated with seed cotton yield. Ahmad et al. (2011), Vineela et al. (2013), Joshi et al. (2006) and Farooq et al. (2014) and Baloch et al. (2015) investigated 92%, 88%, 79%, 43% and 79.17% broad sense heritability for this trait respectively. Ali et al. (2009) reported that sympodial branches per plant possessed a high value of narrow sense heritability due to additive gene action.

Monopodial branches per plant

For monopodial branches parent (table II), CRS-456 showed highest mean performance 6.0804 as compared to the other parent, Jambo okra, and F_3 population that showed 3.6419 and 4.8897 mean performance for monopodial branches per plant respectively.

Correlation matrix indicated in table III that monopodial branches showed positive linkage with nodes no. of the 1st sympodial branch, height of 1st sympodial branch, bolls per plant while it had negative association with boll weight. Monopodial branches had non-significant association with seed cotton yield that reveals that there is no change in seed cotton yield with increasing monopodial branches. For this trait heritability value was 60.764% (table II). The gene action for this trait (table IV) was over dominance in half crosses and additive in remaining half crosses. So it is suggested that this trait can be improved either through appropriate selection or hybrid breeding programme.

Baloch et al. (2014) also found non-significant correlation between monopodial branches and seed cotton yield. Azhar et al. (1999) reported that monopodial branches per plant had positive correlation with bolls per plant. Iqbal et al. (2006) studied that monopodial branches per plant positively correlated with bolls per plant. Hussain et al. (2010) studied that monopodial branches per plant positively correlated with bolls per plant. Ekinci et al. (2010) reported that monopodial branches had positive linkage with bolls per plant. Kapoor and Kaushik (2003) estimated 99% broad sense heritability for this trait. Killi et al. (2005) observed 61% broad sense heritability for monopodial branches. Vineela et al. (2013) estimated 56% broad sense heritability for this trait. Baloch et al. (2015) reported 86% broad sense heritability for this trait. Ali et al. (2009) reported that monopodial branches per plant possessed low value of narrow sense heritability estimates due to the presence of more dominant genes. Heterosis would be necessary to attain the genetic advancement in monopodial branches per plant. Hence it is concluded that the relationship of monopodial branches per plant with seed cotton yield is weak and it could not be a criterion for selection.

Nodes number of 1st sympodial branch

Nodes number of 1st sympodial branch basically determines the early maturity of cotton. Theoretically, it is assumed that lower nodes number of the 1st sympodial branch is highly correlated with earliness and heat tolerance and resistance (Baloch and Veesar, 2007). This trait is one of the most reliable and practical morphological measures of earliness in various genotypes of upland cotton.

For nodes number of 1st sympodial branch parent (Table 2), CRS-456 showed 15.463 performance and Jambo okra exhibited 16.097 average performance. While F_3 population produced 17.812 average performance for this trait that was higher from both of the parents.

Correlation analysis indicated (Table 3) that nodes number of 1st sympodial branch positively correlated with height of 1st sympodial branch and bolls per plant while it had a negative association with boll weight. This trait had no effect on seed cotton yield. For this trait heritability value was 91.515% (Table 2). This high value of broad sense heritability depicted that environment had very less effect on transmission of this trait from parents into progeny. The inheritance pattern (Table 4) showed that over dominance gene action was found in mostly crosses but in a few crosses additive type gene action with partial dominance was also exhibited. So it is suggested that appropriate breeding methodology can be used advantageously for improvement of this trait. Hence it is concluded that selection of this trait could not be helpful in breeding cotton varieties towards yield.

Height of 1st sympodial branch

For height of 1st sympodial branch parent (table II), Jambo okra possessed 45.582cm highest average performance as compared to other parent CRS-456 (32.758cm) and F_3 population (41.431cm).

Correlation matrix indicated (Table 3) that height of 1st sympodial branch showed positive linkage with bolls per plant, lint percentage, fiber fineness, fiber strength, and fiber uniformity while it had negative association with boll weight and sympodial branches per plant. As this trait had significant effect on fiber quality traits and bolls per plant but showed non-significant correlation with seed cotton yield. For this trait heritability value was 96.370% (Table 2). This trait had the additive type of gene action with over dominance in mostly crosses but in a one cross partial dominance gene action was also expressed (Table 4). This trait is basically used in developing early maturing varieties. As result reveals that this trait has a non-significant association with seed cotton yield. So it concluded that selection of this trait could not be helpful in improving yield but fiber quality traits can be improved through this trait thanks to their positive connection.

Bolls per plant

For bolls per plant parent (Table 2), CRS-456 produced 44.690 highest average bolls while other parent Jambo okra and F_3 population produced 27.290 and 31.941 average bolls.

Correlation analysis revealed (Table 3) that bolls per plant positively correlated with lint percentage, fiber fineness, fiber length, fiber strength, and fiber uniformity while it had negative association with bolls weight. There was found non-significant correlation between bolls per plant and seed cotton yield that indicates that selection of this trait may be not useful in improvement of seed cotton yield. Although in many studies results contradict to author’s research which may be due to different genetic makeup of germplasm. For this trait heritability value was 89.737% (Table 2). The inheritance study showed that over dominance gene action with partial dominance was expressed in most crosses (Table 4).

Ashokkumar and Ravikesavan (2010) reported that bolls per plant had positive correlation ginning out turn percentage, boll weight, and lint index. Desalegn et al. (2009) studied a positive correlation of bolls per plant with ginning out turn percentage. So it is concluded that selection on the basis of the number of bolls per plant can be effective for improving ginning out turn percentage. Thiyagu et al. (2010) observed that bolls per plant positively correlated with fiber length and fiber fineness. Abbas et al. (2013) studied that fiber length had positive linkage with bolls per plant. Arshad et al. (1993) also reported that bolls per plant had positive correlation with monopodial branches per plant. Butany et al. (1966) studied that bolls per plant had negative association with boll weight. Wu et al. (2004) reported that bolls per plant had positive linkage ginning out turn while it had negative association with boll weight. Ahmad et al. (2011) estimated 88% heritability for this trait. Baloch et al.

(2015) investigated that bolls per plant possessed 93% broad sense heritability. Desalegn et al. (2009) observed 59% broad sense heritability for this trait.

Ahmad et al. (2001) and Sarwar et al. (2011) studied gene action of yield contributing traits in upland cotton. The result showed an additive type of gene action with partial dominance for the number of bolls per plant. While additive gene action due to high value of narrow sense heritability was recorded by Murtaza (2005). Ranganatha et al. (2011) also reported that bolls per plant possessed dominance gene action. Ma et al. (1983) reported over dominance type of gene action for the number of bolls per plant.

Boll weight

Boll weight plays important role in enhancement in yield of seed cotton. Mean data showed that the parent (Table 2), CRS-456 had 2.7601g boll weight and Jambo okra exhibited 2.3493g boll weight. The result depicted that F_3 population produced 2.8752g average boll weight that was higher than bother both of the parents.

Correlation matrix indicated (Table 3) that boll weight positively correlated with lint weight and seed cotton yield. Seed cotton yield can be increased by increasing boll weight. For this trait, broad sense heritability value was 80.273% (Table 2). Boll weight had a direct influence on seed cotton yield because it is assumed that boll weight increases, seed cotton yield would also increase. Hence it is concluded that boll weight should be kept in mind while breeding for seed cotton yield. Gene action for boll weight was exhibited over dominance in mostly crosses while in a few crosses the additive type of gene action was also indicated in Table 4. The inheritance study reveals that this trait can be improved through appropriate selection or can be used in hybrid breeding programmes.

Jatt et al. (2007), Abbas et al. (2008), Soomro et al. (2008) and Desalegn et al. (2009) reported same results that boll weight had positive linkage with seed cotton yield. Bibi et al. (2011), Alkuddsi et al. (2013), Farooq et al. (2014) and Erande et al. (2014) observed that boll weight positively correlated with seed cotton yield. Ahasn et al. (2015) and Baloch et al. (2015) concluded from their experiment that boll weight positively correlated with seed cotton yield. Khan and Azhar (2000) estimated 61% broad sense heritability for boll weight. Kapoor and Kaushik (2003), Naveed et al. (2004), Joshi et al. (2006), Lu and Myers (2011) and Baloch et al. (2015) reported 95%, 22%, 66%, 57%, and 93.58% broad sense heritability for boll weight respectively. Ahmad et al. (2001) studied the additive type of gene action with partial dominance for boll weight in upland cotton while only additive gene action was observed by Murtaza (2005) and Ali et al. (2010). Ranganatha et al. (2011) analyzed dominance gene action for boll weight.

Lint weight

Lint weight is a necessary trait in seed cotton yield improvement. Mean data revealed that parent (Table 2), CRS-456 had highest lint weight 34.498g as compared to Jambo okra (17.655g) and F_3 population (26.126g).

Correlation analysis depicted (Table 3) that lint weight positively correlated with seed cotton yield, lint percentage, lint index, seeds per boll, fiber fineness, fiber strength, fiber length, and fiber uniformity. The significant relationship between seed cotton yield, fiber quality traits, and lint weight shows that we can improve seed cotton yield and fiber quality traits by increasing lint weight. For this trait, broad sense heritability was 72.667% (Table 2). The inheritance study depicted that over dominance gene action was found in mostly crosses but in a few crosses partial dominance and dominance gene action was also expressed (Table 4). Due high value of broad sense heritability, this trait can advantageously use in hybrid breeding program. Hence it is concluded that lint weight should be kept in mind while breeding for seed cotton yield.

Seed cotton yield

Mean data revealed that parent, CRS-456 had the highest seed cotton yield 79.854g as compared to Jambo okra (45.361g) and F_3 population (63.657g) (Table 2).

Correlation analysis showed (Table 3) that seed cotton yield had positive linkage lint percentage, seeds per boll, fiber fineness, fiber strength, fiber length, and fiber uniformity. This trait had significant association with lint percentage, seeds per boll and fiber quality traits that indicated that we can improve fiber quality traits by increasing seed cotton yield. As seed cotton yield is primary criteria of breeder during breeding for improvement in various agronomic traits that have positive association with yield. So correlation study indicates that fiber quality traits can be improved with increasing seed cotton yield because seed cotton has positive effect on fiber quality traits. For this trait, broad sense heritability was 77.880% (Table 2). Gene action for seed cotton yield was found over dominance in mostly crosses but in a few crosses dominance gene action was also expressed.

Salahuddin et al. (2010) studied that seed cotton yield positively correlated with lint percentage. Baloch et al. (1992) and Bibi et al. (2011) reported that seed cotton yield had positive linkage with sympodial branches per plant. Ashokkumar and Ravikesavan (2010), Magadum et al. (2012) and Farooq et al. (2013) observed that seed cotton yield can be increased by increasing sympodial branches per plant. Hussain et al. (2010) reported that seed cotton yield positively correlated with fiber length and fiber fineness. Ahsan et al. (2015) studied that seed cotton yield showed positive linkage with boll weight. Baloch et al. (2015) reported that seed cotton yield positively correlated with boll weight and sympodial branches per plant. Iqbal and Nadeem (2003), Kapoor and Kaushik (2003), Joshi et al. (2006), Hussain et al. (2010a), Ahmad et al. (2011), Reddy and Sharma (2014), Kalim-Ullah et al. (2015) and

Baloch et al. (2015) observed 91%, 89%, 85%, 50%, 76%, 80%, and 98% for seed cotton yield respectively. Ahmad et al. (2001) and Sarwar et al. (2011) and studied gene action of yield contributing traits in upland cotton. The result showed that additive type of gene action with partial dominance was found for seed cotton yield. Ali et al. (2009) reported dominant gene action for seed cotton yield due to high estimates of broad sense heritability while additive type of gene action was observed for seed cotton yield by Ali et al. (2010) and Iqbal et al. (2011).

Seed index

Mean values depicted that parent (Table 2), CRS-456 showed 6.7665g maximum average seed index as compared to Jambo okra (5.9275g) and F_3 population (6.5283g).

Correlation analysis revealed (Table 3) that seed index negatively correlated with lint percentage while it had non-significant association with other yield related traits. Broad sense heritability for seed index was 64.980% (Table 2). Overdominance gene action was found in mostly crosses for seed index but in a few crosses dominance gene action was also found (table IV). So it concluded that this trait could not be helpful in breeding of cotton varieties towards yield.

Soomro et al. (2010) also reported low heritability for seed index. Sarwar et al. (2011) observed dominant gene action for seed index.

Lint percentage

Lint percentage is a complex polygenic trait which has high effects of the various environmental factors. This trait basically depends on lint weight which had a direct effect on seed cotton yield. So selection for higher lint percentage could often result in an increase in the production per plant and per unit area. Mean values of lint percentage indicated that parent (Table 2), CRS-456 had maximum 44.261% lint percentage as compared to Jambo okra (43.958%) and F_3 population (41.577%).

Correlation analysis indicated (Table 3) that lint percentage had positive linkage with lint index, seeds per boll, fiber fineness, fiber strength, fiber length, and fiber uniformity while it had negative association with seed index. Broad sense heritability value for lint percentage was 60.311% (Table 2). Non-significant association between lint percentage and seed cotton yield indicates that selection of this could not be helpful in improving seed cotton yield. Overdominance gene action was found in mostly crosses for lint percentage but in a few crosses dominance gene action was also found (Table 4).

Selim et al. (1978) studied that ginning out turn percentage showed positive linkage with seeds per boll and fiber strength. Waldia et al. (1979), Giri and Updhayay (1980) and Soomro et al. (1982) also reported that ginning out turn percentage positively correlated with seeds per boll. Bing et al. (1996) also studied that lint percentage had positive correlation with fiber fineness and seed cotton yield. Tian et al. (1993) conducted experimentation on 10 lines of Upland cotton to investigate correlation. Results indicated that lint percentage and number of bolls per plant had positive correlation with GOT%. Baloch et al. (2015) reported that ginning out turn had positive linkage with plant height. Naveed et al. (2004), Joshi et al. (2006), Desalegn et al. (2009), Reddy and Sharma (2014) reported 23%, 95%, 72% and 46% broad sense heritability for this trait respectively. Baloch et al. (2015) reported 91.48% broad sense heritability for this trait. Berdymuradov et al. (1990) and Ali et al. (2009) also reported that dominance gene action for lint percentage. Ali et al. (2010) and Iqbal et al. (2011) reported that lint percentage possessed additive type of gene action. Sarwar et al. (2011) studied genetics of seed cotton yield and its contributing traits to estimate gene action for different agronomic and fiber related traits in upland cotton. They reported that additive type of gene action with partial dominance was found for lint percentage.

Lint index

Mean values of lint index indicated that parent (Table 2), CRS-456 had maximum 16.599% lint index as compared to other parent Jambo okra (14.309%) and F_3 population (16.112%).

Correlation matrix exhibited (Table 3) that lint index positively correlated with seeds per boll, fiber fineness, fiber strength, fiber length, and fiber uniformity. Broad sense heritability for lint index was 88.297% (Table 2). This trait had non-significant association with seed cotton yield so this trait could not be helpful in breeding for yield. The inheritance study depicted that over dominance gene action was found in mostly crosses for lint index but in a few crosses dominance gene action was also expressed (Table 4).

Ahsan et al. (2015) estimated heritability in upland cotton. The traits such as lint index, bolls per plant and seed cotton yield per plant possessed high heritability estimates. Sarwar et al. (2011) reported dominance gene action for lint index.

Seeds per boll

Seeds per boll play a significant role in the improvement of seed cotton yield. Mean values of seeds per boll indicated that parent (Table 2), CRS-456 had maximum 25.564 seeds per boll as compared to other parent Jambo okra (22.339) and F_3 population (24.131).

Correlation matrix showed (Table 3) that seeds per boll had positive association with seed cotton yield, fiber fineness, fiber strength, fiber length, and fiber uniformity. Broad sense heritability for seeds per boll was 75.726% (Table 2). Hence it is concluded from correlation study that seeds per boll should be kept in mind while during breeding of various genotypes of upland cotton towards yield. Gene action for seeds per boll was found over dominance in mostly crosses but dominance gene action was also expressed in a few crosses (Table 4).

Turner et al. (1976) studied that seeds per boll positively correlated with seed cotton yield. Azhar et al. (2004) also observed that seeds per bolls showed positive linkage with seed cotton yield. Tang and Xio (2014) reported that seeds per boll had positive correlation with seed cotton yield. Batool et al. (2010) concluded from their experiment that seeds per bolls positively correlated with seed cotton yield and ginning out turn percentage. Ahmad et al. (2001) studied the additive type of gene action with partial dominance for seeds per boll. Sarwar et al. (2011) also reported over dominance gene action for seeds per boll.

Fiber fineness

A micronaire reading is a defined measurement of the degree of cotton fiber fineness by means of an airflow instrument known as the Micronaire. Mean values of fiber fineness indicated that parent (Table 2), CRS-456 had maximum 5.3500 µg/inch fiber fineness as compared to other parent Jambo okra (4.1600 µg/inch) and F_3 population (4.1720 µg/inch).

Correlation analysis depicted (Table 3) that fiber fineness positively correlated seed cotton yield, fiber strength, fiber length, and fiber uniformity. Significant positive correlation between seed cotton yield and fiber fineness indicated that seed cotton yield can be improved. Broad sense heritability for fiber fineness was 89.297% (Table 2). Gene action for fiber fineness was found over dominance in mostly crosses but in a few crosses partial dominance gene action was also expressed (Table 4).

Turner et al. (1976) studied that fiber fineness showed positive linkage with seed cotton yield. Azhar et al. (2004) also observed that fiber fineness had positive correlation with seed cotton yield. Chao-Zhu et al. (2007) and Tang and Xio (2014) studied that fiber fineness positively associated with seed cotton yield. Altaher and Singh (2003) depicted that fiber fineness showed positive linkage with bolls per plant. Asif et al. (2008) also found that fiber fineness had positive linkage with fiber strength. Natera et al. (2012) reported that broad sense heritability was higher for fiber fineness. Azhar et al. (2004) estimated 41% broad sense heritability for this trait. Killi et al. (2005) recorded 73% broad sense heritability for fiber fineness. Hendawy et al. (1999) and Sarwar et al. (2011) reported dominance gene action for fiber fineness. Yuan et al. (2002) studied genetic components and concluded that fiber fineness possessed additive type of gene action due to a high value of broad sense heritability.

Fiber strength

Mean values of fiber strength indicated that parent (Table 2), CRS-456 had maximum 27.433 g/tex fiber strength as compared to Jambo okra (26.533 g/tex) and F_3 population (26.556g/tex).

Correlation analysis revealed (Table 3) that fiber strength had positive linkage with seed cotton yield, fiber fineness, fiber length, and fiber uniformity. Significant association between fiber strength and seed cotton yield indicates that selection of fiber strength could be helpful in improving seed cotton yield. Broad sense heritability for fiber strength was 96.429% (Table 2). The inheritance study showed that fiber strength possessed over dominance gene action (Table 4). High value of broad sense heritability indicated that this trait can be used advantageously in hybrid breeding programme.

Rasheed et al. (2010) observed that fiber strength and fiber fineness associated positively with seed cotton yield. Rajarathinam et al. (1993) and Karadmir et al. (2010) also reported that fiber length and fiber strength had positive association. Iqbal et al. (2015) also reported that fiber strength had positive linkage with fiber fineness. Killi et al. (2005), Rasheed et al. (2009) and Reddy and Sharma (2014) estimated 73%, 97% and 21% broad sense heritability for this trait respectively. Shakeel et al. (2015) observed 93% heritability for fiber strength. Yuan et al. (2002) reported dominance gene action for fiber strength due to a high value of broad sense heritability. Saghir et al. (2003) and Ali et al. (2009) estimated additive type of gene action for fiber strength.

Fiber length

Mean data showed that the parent (Table 2), CRS-456 had 25.533mm fiber length and other parent, Jambo okra exhibited highest 27.600mm fiber length. The result depicted that F_3 population produced 26.664mm average length.

Correlation analysis depicted (Table 3) that fiber length positively correlated with seed cotton yield and fiber uniformity. Broad sense heritability for fiber length was 86.513% (Table 2). Due to significant and positive correlation of fiber length with seed cotton yield, selection of this trait could be helpful in breeding for yield. The inheritance study exhibited that fiber length possessed over dominance gene action in mostly crosses but in a few crosses additive gene action was also expressed (Table 4).

Swati et al. (1999) indicated that fiber length and strength associated positively. Similar results were reported by Rajarathinam et al. (1993). Larik et al. (1999) and Ping et al. (2005) reported that fiber length and fiber strength associated positively. Chao-Zhu et al. (2007) also reported that fiber length positively associated with fiber strength. Asif et al. (2008) and Hussain et al. (2010) also concluded that fiber length had positive association with fiber strength. Karadmir et al. (2010) observed that fiber length positively associated with fiber strength. Imran et al. (2011) reported that fiber length positively correlated with fiber strength. Batool et al. (2010) concluded that fiber length positively associated with seed cotton yield. Tang and Xio (2014) reported that positive association existed between fiber length and fiber strength. Fibre length and fiber strength had positive association in the experiment conducted by Farooq et al. (2014), Malagouda et al. (2014) and Khan et al. (2014). Abbas et al. (2013) they concluded that fiber length had positive association with fiber fineness and plant height. Mei et al. (2013) and Malagouda et al. (2014) concluded from studies that fiber length had positive association with fiber strength while it negatively associated with fiber fineness. For this trait heritability value was 78 %. Killi et al. (2005) estimated 94% broad sense heritability for fiber length. Abbas et al. (2013) determined 52% broad sense heritability for this character. Khan and Azhar (2000) found 96% broad sense heritability for fiber length. Baloch et al. (2015) observed that broad sense heritability for this trait fiber length is 97.89%. Yuan et al. (2002) and Sarwar et al. (2011) studied dominance gene action for fiber length. Ali et al. (2009) and Iqbal et al. (2011) reported additive gene action for fiber length.

Fiber uniformity

Mean data showed that the parent (Table 2), CRS-456 had maximum 50.500% fiber uniformity, and Jambo okra exhibited 48.237% fiber uniformity. The result depicted that F_3 population produced 48.155% average fiber uniformity.

Correlation matrix revealed (Table 3) that fiber uniformity positively correlated with seed cotton yield. Broad sense heritability for fiber uniformity was 88.723% (Table 2). Hence it is concluded that selection of fiber uniformity could be helpful in breeding program for seed cotton yield improvement. Gene action for this trait was found over dominance in mostly crosses but in a few crosses additive and dominance gene action was also expressed (Table 4).

Pujer et al. (2014) investigated correlation for various quantitative and fiber related traits in 8 different cotton genotypes. Correlation results predicted a positive association of seed cotton yield ginning out turn, lint index, bolls per plant and uniformity ratio. Abbas et al. (2008) reported high heritability for fiber uniformity. Yuan et al. (2002) studied genetic components and environment influence of fiber quality traits in four different environments. They reported low value of broad sense heritability for fiber uniformity due to presence of additive gene action.

Conclusion and recommendation

All the parameters manifested positive correlation with seed cotton yield except plant height, monopodia per plant, nodes no. of 1st sympodia, height of 1st sympodia, bolls per plant, seed index and lint index. Broad sense heritability was found maximum for height of 1st sympodial branch, fiber strength, nodes no. of 1st sympodial branch, sympodial branches per plant, bolls per plant, fiber fineness, fiber uniformity fiber length, lint index, boll weight, seed cotton yield, plant height, lint weight and seeds per boll. The inheritance of all the traits in F_1 crosses was generally controlled by over dominance gene action except monopodial branches, nodes no. of 1st sympodial branch, height of 1st sympodial branches, boll weight, fiber length and fiber uniformity that were partially controlled under additive gene action. Thus during future breeding programme these traits should also kept in mind during making selection as those traits had major contribution in yield.

Based on the present findings, it is recommended while breeding for higher seed cotton yield:

- Selection of sympodial branches per plant, boll weight, lint weight, lint percentage, seeds per boll, fiber fineness, fiber strength, fiber length and fiber uniformity should be practiced, as they were found positively associated with seed cotton yield.

- Higher plant height, monopodia per plant, nodes no. of 1st sympodial, height of 1st sympodia, bolls per plant, seed index and lint index should be discouraged as they were found to be declining in seed cotton yield.

REFERENCES

Abbas, A., M. A. Ali and T.M. Khan (2008). Studies on gene effects of seed cotton yield and its attributes in five American cotton cultivars. J. Agric. Soc. Sci., 4, 147-152.

Abbas, H.G., A. Mahmood and Q. Ali (2013). Genetic variability, heritability, genetic advance and correlation study in cotton (*Gossypium hirsutum* L.). Int. Res. J. Microbiol., 4, 156-161.

Ahmad, L., A. Ali, M. Zubair and I.A. Khan (2001). Mode of gene action controlling seed cotton yield and various components in (*Gossypium hirsutum* L.). Pak. J. Agri. Sci., 38, 19-21.

Ahmad, M., N.U. Khan, F. Mohammad, S.A. Khan, I. Munir, Z. Bibi and S. Shaheen (2011). Genetic potential and heritability study for some polygenic traits in cotton *(Gossypium hirsutum* L.). Pak. J. Bot., 43, 1713-1718.

Ahsan, M.Z., M.S. Majidano, H. Bhutto, A.W. Soomro, F.H. Panhwar, A.R. Channa and K.B. Sial (2015). Genetic variability, coefficient of variance, heritability and genetic advance of some (*Gossypium hirsutum* L.) accessions. J. Agric. Sci. 7(2), 9752-9760.

Akbar, M., J. Ahmad and F.M. Azhar (1994). Genetic correlation, path coefficient and heritability estimates of some important traits in upland cotton. Pak. J. Agric. Sci., 31(1), 47-50.

Ali, M.A., A. Abbas, M. Younas, T.M. Khan and H.M. Hassan (2009). Genetic basis of some quantitative traits in upland cotton (*Gossypium hirsutm* L.). Plant Omics J., 2(2), 91-97.

Ali. M.A., M.F. Bhatti. A. Abbas and I.A. Khan (2010). Assessment of inheritance pattern of some multigenic characters in cotton (*Gossypium hirsutum* L.). J. Agric. Res., 48, 1.

Alkuddsi, Y., S.S. Patil, S.M. Manjula and B.C. Patil (2013). Correlation studies on yield and its components in interspecific cotton hybrids (*G.hirsutum* × *G.barbadense*) for developing heterotic box. Mol. Plant Breed., 4(28), 228-237.

Altaher, A.F. and R.P. Singh (2003). Yield components analysis in upland cotton (*Gossypium hirsutum* L.). J. Ind. Soc. Cotton Improv., 28, 151-157.

Anapurve, S.N., G.S. Desmukh, S.P. Kausale, S.P. and U.V. Kale (2007). Correlation study of yield contributing characters in American cotton. J. Cotton Res. Dev., 21, 16-20.

Anonymous (2015-16). Govt. of Pakistan, Ministry of Finance, Economic Advisor's Wing, Islamabad.

Arshad, M., M. Hanif, I. Noor, S.M. Shah and N. Hani (1993). Correlation studies on some commercial cotton varieties of *Gossypium hirsutum* L. Sarhad J. Agric., 9, 49-53.

Ashokkumar, K. and R. Ravikesavan (2010). Genetic study of correlation and path coefficient analysis for seed oil, yield and fibre quality traits in cotton (*Gossypium hirsutum* L.). Aust. J. Basic Appl. Sci., 4, 5496-5499.

Asif, M., J.I Mirza and Y. Zafar (2008). Genetics analysis for fibre quality of some cotton genotypes. Pak. J. Bot., 40, 1209-1215.

Azhar, F.M. and S.U.K. Ajmal (1999). Diallel analysis of oil content in seed of *Gossypium hirsutum* L. J. Genet. Breed., 53, 19-23.

Azhar, F.M., M. Naveed and A. Ali (2004). Correlation analysis of seed cotton yield with fiber characteristics in *Gossypium hirsutum* L. Int. J. Agric. Biol., 6, 656-658.

Baloch, A., M.W. Baloch, M.K. Baloch, I.A. Mallano, A.M. Baloch, N.J. Baloch and S. Abro (2015). Association and Heritability Analysis for Yield and Fiber Traits in Promising Genotypes of Cotton (*Gossypium hirsutum* L.). Sindh Univ. Res. J., 47(2), 303-306.

Baloch, M.J. and N.F. Veesar (2007). Identification of plant traits for characterization of early maturing upland cotton varieties. Pak. J. Sci. & Ind. Res., 50, 128-132.

Baloch. M. J., C. Kumar, W.A. Jatoi and I.H. Rind (2014). Phenotypic correlation and regression analysis of yield and fiber quality traits in upland cotton (*Gossypium hirsutum* L.). Pak. J. Agri. Engg. Vet. Sci., 30, 135-146.

Batool, S.N,U. Khan, K. Makhdom, Z. Bibi, G. Hassan, K.B. Marwat, Farhatullah, F. Mohammad, Raziuddin and I.A. Khan (2010). Heritability and genetic potential of upland cotton genotypes for morpho-yeild traits. Pak. J. Bot., 42, 1057-1064.

Berdymuradov, R., R. Meredov and G. Novruzov (1990). Significance of backcrosses. Khlopok, 5, 42-43.

Bibi M., N.U. Khan, F. Mohammad, R. Gul, A.Z. Khakwani and O.U. Sayal (2011). Genetic divergence and association among polygenic characters in *Gossypium hirsutum* L. Pak. J. Bot., 43(6), 2751-2758.

Bing, T., J.N. Jenskins, C.E. Watson, J.C. McCarty and R.G. Grecer (1996). Evaluation of genetic variances and correlation for yield and fibre traits among cotton F_1 hybrid populations. Euphytica, 91, 315-322.

Brubaker, C.L., F.M. Bourland and J.E. Wendel (1999a).The origin and domestication of cotton. In: Smith, C.W. and J.T. Cothren, (Eds.), Cotton: Origin, History, Technology and Production. John Wiley and Sons, Inc., New York: 3-31.

Butany, W.Y., A.D. Munshi and A.S. Chopra (1966). Interrelationship between some characters in *Gossypium hirsutum* L. Ind. J. Genet., 26, 262-268.

Chao-zhu, X., Y. Shun-xun, G. Li-Ping, M. Cheng-duo, F. Wen-Juan, W. Hai-Lin and Z. Yun-Lei. (2007). Heterosis performance and correlation analysis on economic traits of upland cotton in different ecological environments. Cotton Sci., 19, 3-7.

Cherry, J.P. and Loffler, H.R. 1984. Seed. In: Kohel, R.J. and Lewis, C.F. (eds.), Cotton, ASA, Madison, WI: 511-569.

Desalegn D., N. Ratanadilok and R. Kaveeta (2009). Correlation and heritability for yield and fiber quality parameters of ethiopian cotton (*Gossypium Hirsutum* L.) estimated from 15 (diallel) crosses. Kasetsart J., 43, 1–11.

Ekinci, R., S. Basbag and O. Gencer (2010). Path coefficient analysis between seed cotton yield and some characters in cotton (*Gossypium hirsutum* L.). J. Envir. Biol., 31, 861-864.

Erande, C.S., H.V. Kalpande, D.B. Deosarkar, S.K. Chavan, V.S. Patil, J.D. Deshmukh, V.N. Chinchane, A. Kumar, U. Dey and M.R. Puttawar. 2014. Genetic variability, correlation and path analysis among different traits in desi cotton (*Gossypium arboreum* L.). Afric. J. Agri. Res., 9, 2278-2286.

Farooq, J., M. Anwar, M. Riaz, A. Farooq, A. Mahmood, M.T.H. Shahid, M. Rafiq, S. and F. Ilahi (2014). Correlation and path coefficient analysis of earliness, fiber quality, and yield contributing traits in cotton (*Gossypium hirsutum* L.). J. Animal Plant Sci., 24(3), 781-790.

Farooq, J., M. Anwar, M. Riaz, A. Mahmood, A. Farooq, M.S. Iqbal and M.S. Iqbal (2013). Association and path analysis of earliness, yield and fiber related traits under cotton leaf curl virus intensive condition in *Gossypium hirsutum* L. Plant Know. J., 2, 43-50.

Fryxell, P.A. (1979). The natural history of the cotton tribe. Texas A & M University Press, College Station, Texas, USA.

Giri, A.N. and U.C. Updhyay (1980). Correlation and regression studies in upland cotton under different patterns and intercropping systems. Inf. J. Agric. Sci., 50, 907-910.

Hendawy, F.A., M.S. Rady, A.M. Hamid and R.M. Esmail (1999). Inheritance of fibre traits in some cotton crosses. Egyptian J. Agron., 21, 35-36.

Hussain, A., F.M. Azhar, M.A. Ali, S. Ahmad, K. Mahmood (2010a). Genetic studies of fiber characters in upland cotton. Animal Plant Sci., 20(4), 234-238.

Hussain, S., N.N. Nawab, M.A. Ali, A. Hussain, M.A. Nawaz and T.A. Malik (2010). Evolution of performance, genetic divergence and character association of some polygenic traits in upland cotton. J. Agric. Soc. Sci., 6(4), 79-82.

Hussain, S.B., Z. Ali and H.N. Khan (2014). A-one: high yielding, CLCV tolerant and transgenic Bt cotton variety for irrigated areas of Pakistan. J. Ann. Plant Sci., 24, 543-549.

Imran, M., A. Shakeel, J. Farooq, A. Saeed, A. Farooq and M. Riaz (2011). Genetic studies of fiber quality parameter and earliness related traits in upland cotton *(Gossypium hirsutum* L.). AAB. J. Bioflux, 3, 151-159.

Iqbal, M., K. Hayat, R.S.A. Khan, A. Sadiq and Noor-ul-Islam (2006). Correlation and path coefficient analysis for earliness and yield traits in cotton (*Gossypium hirsutum* L.). Asian J. Plant Sci. 5(2), 341-344.

Iqbal, M., M.A. Chang, M.Z. Iqbal, M.U. Hassan, A. Nasir and N.U. Islam (2003). Correlation and path coefficient analysis of earliness and agronomic characters of upland cotton in Multan. Pak. J. Agron., 2(3), 160-168.

Iqbal, M.Z. and M.A. Nadeem (2003). Behavior of some polygenic characters in cotton (*Gossypium hirsutum* L.). Asian. J. Plant Sci., 2, 485-490.

Iqbal. M, M.A. Khan, M. Jameel, M.M. Yar, Q. Javaid, M.T. Aslam, B. Iqbal, S. Shakir, A. Ali (2011). Study of heritable variation and yield components in upland cotton. (*Gossypium hirsutum* L.). Afr. J. Agric. Res., 6, 4099-4103.

Jatt, T., H. Abro, A.S. Larik and Z.A. Soomro (2007). Performance of different cotton varieties under the climatic conditions of Jamshoro. Pak. J. Bot., 39, 2427-2430.

Joshi, H.J., P.K. Chovatia and D.R. Mehta (2006). Genetic variability, character association and component analysis in upland cotton. Ind. J. Agric. Res., 40, 302-305.

Kalim-Ullah, Z. Usman, N. Khan, Rehmant-Ullah, F.Z. Saleem, S.I. Khattak and M. Ali (2015). Genetic diversity for yield and related traits in upland cotton genotypes. Pak. J. Agric. Res., 28, 118-125.

Kapoor, C.J. and S.K. Kaushik (2003). Variability, heritability and genetic advance studies in cotton (*Gossypium hirsutum* L.). J. Cotton Res. Dev., 17, 242.

Karademir, E., C. Karademir, R. Ekinci and O. Gencer (2010). Relationship between yield, fiber length and other fiber related traits in advanced cotton strains. Not. Bot. Hort. Agrobot. Cluj., 38(3), 111-116.

Khan, A.I. and F.M. Azhar (2000). Estimates of heritabilities and pattern of association among different characters of *Gossypium hirsutum* L. Pak. J. Agri., 37, 7-10.

Khan, M.I., M.A. Dasti, Z. Mahmood, M.S. Iqbal (2014). Effects of fiber traits on seed cotton yield of cotton (*Gossypium hirsutum* L.). J. Agric. Res. 52(2), 159-166.

Khan, N.U. (2003). Genetic analysis, combining ability and heterotic studies for yield, its components, fibre and oil quality traits in upland cotton (*G. hirsutum* L.). Ph. D Dissert. Sindh Agric. Univ. Tandojam, Pakistan.

Khan, N.U., H.K. Abro, M.B. Kumbhar, G. Hassan and M. Khan (1999). Exploitation of heterosis can combat Cotton Leaf Curl Virus (CLCV) incidence in cotton (*G. hirsutum* L.). The Pak. Cottons., 43(3&4), 21-33.

Khan, N.U., K.B. Marwat, G. Hasssan, M.B. Kumbhar, Farhatullah, Z.A. Soomro, N. Khan, A. Parveen and U. Aiaman (2009). Study of fiber quality traits in upland cotton using additive-dominance model. Pak. J. Bot., 41, 1271-1283.

Killi, F., L. Efe and S. Mustafayev (2005). Genetic and environmental variability in yield, yield components and lint quality traits of cotton. Int. J. Agric. Biol., 7, 1007-1010.

Larik, A.S., A.A. Kakar, M.A. Naz and M.A. Shaikh (1999). Character correlations and path analysis in seed cotton yield (*G. hirsutum* L.). Sarahad J. Agric., 15, 269-274.

Lu, H. and G.O. Myers (2011). Combining abilities and inheritance of influential upland cotton varieties. Aust. J. Crop Sci., 5, 384-390.

Ma, r.c., Y.Y. Zhou, R.T. Wang and C.O. Liu (1983). Genetic analysis of characters in the progeny of an intervarietal hybrid of upland cotton. Acta Agri. Univ. Pekinansis (China) 9(4), 27-34 PI. Br. Abst. 54(4-5), 3321-1984.

Magadum, S., U. Baneijee, R. Ravikesavan, K. Thiyagu, N.M. Boopathi and S. Rajarathinam (2012). Association Analysis of Yield and Fibre Quality Characters in interspecific Population of Cotton (*Gossypium* spp.). J. Crop Sci. Biotech., 15, 239-243.

Majeedano, M.S., M.Z. Ahsaan, A.W. Somroo and A.R. Channa (2014). Heritability and correlation estimates for some yield traits of *Gossypium hirsutum.* Am. Res. Thoughts, 1, 781-790.

Malagouda, P., B.M. Khadi, K. Basamma and I.S. Katageri (2014). Genetic variability and correlation analysis for fiber quality traits in diploid cotton (*Gossypium* spp). American-Eurasian J. Agric. Environ. Sci., 14(5), 392-395.

Meena, R.A., D. Monga and R. Kumar (2007). Undescriptive cotton cultivars of north zone: an evaluation. J. Cotton Res. Dev., 21(1), 21-23.

Mei, Y., W. Hu, S. Fan, M. Song, C. Pang and S. Yu (2013). Analysis of decision-making coefficient of three main fibre quality traits for upland cotton (*Gossypium hirsutum* L.). Euphytica, 140, 946-961.

Murtaza, N. (2005). Study of gene effects for boll number, boll weight, and seed index in cotton. J. Central Eur. Agric., 6, 255-262.

Mustafa, A.M., Y.M.A. Elsheikh and E.A. Babikar (2007). Genetic variability and character association and selection criteria in cotton (*Gossypium hirsutum* L.). Sudan J. Agric. Res., 8, 43-50.

Nachnani, G.H. and H.K. Abro (1980). Correlation studies of yield with certain physical characteristics in F_3 generations of cross of Upland cotton. The Pak. Cottons, 24, 119-129.

Natera, J.R.M., A. Rondon, J. Hernandez and J.F.M. Pinto (2012). Genetic studies in upland cotton for genetic parameters, correlation and path analysis. SABRAO J. Breed. Genet., 44, 112-128.

Naveed, M., F.M. Azhar and A. Ali (2004). Estimates of heritabilities and correlations among seed cotton yield and its components in *Gossypium hirsutum* L. Int. J. Agric. Biol., 6, 712-714.

Ping, L.J., M.Y. Jun, Z.L. Li, H.S. Lin, G.W. Feng and X.R. Cinpek (2005). Analysis of heredity and correlation between boll traits and fibre quality traits in "0" plant type island cotton. Acta Agronomica Sinica, 31, 1069-1073.

Poehlman, J.M. and D. Sleeper (1995). Breeding field crops. 4th ed. Iowa State University Press, Ames, Iowa: 369-370.

Pujer, S., S.S.J. Deshmukh, R.S. Sangwan and O. Sangwan (2014). Genetic variability, correlation and path analysis in upland cotton (*Gossypium hirsutum* L.). Electron. J. Plant Breed., 5, 284-289.

Rajarathinam, S., N. Nadarajan, Sukanya and Subramaniam (1993). Genetic variability and association analysis in cotton. J. Ind. Soc. Cotton Improv., 18, 54-59.

Ranganatha, H.M., S.S. Patill, S.M. Manjula and B.N. Avinkumar (2011). Genetic variability studies in segregating generation of upland cotton (*Gossypium hirsutum* L.). Mol. Plant Breed., 4, 84-88.

Rasheed, A.,W. Malik, A.A. Khan, N. Murtaza, A. Qayyum and E. Noor (2009). Genetic evaluation of fiber yield and yield components in fifteen cotton (*Gossypium hirsutum*) genotypes. Int. Agri. Biol., 11(5), 581-585.

Reddy, Y.R. and A.S.R. Sharma (2014). Genetic variability for yield components and fiber characters in cotton (*Gossypium hirsutum* L.). Plant Arch., 14, 417-419.

Saghir, A., M.Z. Iqbal, A. Hussain, M.A. Sadiq and A. Jabbar (2003). Gene action and heritability studies in cotton (*Gossypium hirsutum* L.). Pak. J. Biol. Sci., 3, 443-450.

Salahuddin, S., S. Abro, M.M. Kandhro, L. Salahuddin and S. Laghari (2010). Correlation and path analysis of yield component of upland cotton (*Gossypium hirsutum* L.).World Appl. Sci. J., 8, 71-75.

Salahuddin, S., S. Abro. A. Rehman and K. Iqbal (2010). Correlation analysis of seed cotton yield with some quantitative traits in upland cotton (*Gossypium hirsutum* L.). Pak. J. Bot., 42, 3799-3805.

Sarwar, S., M. Baber, N. Hussain, I.A. Khan, M. Naeem, M.A. Ullah and A.A. Khan (2011). Genetic dissection of yield and its components in upland cotton (*Gossypium hirsutum* L.). Afr. J. Agri. Res., 6, 2527-2531.

Selim, A.K.A., A.M. Omar, A.M. El-Marakby and M.A. Mohamed (1978). Inheritance of lint percentage and its correlation with fibre strength in a cross between two varieties of Egyptian cotton. Aim. Shams Univ. Agric. Faculty. Res. Bull., 948.

Shakeel, A., I. Talib, M. Rashid, A. Saeed, K. Ziaf and M.F. Saleem (2015). Genetic diversity among upland cotton genotypes for quality and yield related traits. Pak. J. Agric. Sci., 52, 73-77.

Soomro, B.A., M.H. Channa and M. Ahmad (1982). Correlation studies in *Gossypium hirsutum* L. The Pak. Cottons, 26, 39-51.

Soomro, Z.A., A.S. Larik, M.B. Kumbhar, N.U. Khan and N.A. Panhwar (2008). Correlation and path analysis in hybrid cotton. SABRAO. J. Breed. Genet., 40, 49-56.

Soomro, Z.A., M.B. Kumbhar, A.S. Larik, M. Imran and S.A. Brohi (2010). Heritability and selection response in segregating generations of upland cotton. Pakistan J. Agri. Res., 23, 1-2.

Suinaga, F. A., C.S. Bastos and L.E.P. Rangel (2006). Phenotypic adaptability and stability of cotton cultivars in Mato Grosso State, Brazil. Pesquisa Agropecuaria Trop. (PAT), 36(3), 145-150.

Swati, B., L.D. Meshram and P.W. Khorgade (1999). Genetic variability and character association in naturally coloured cotton (*Gossypium hirsutum* L.). J. Ind. Soc. Cotton Improv., 24, 197-199.

Tang, F. and W. Xio (2014). Genetic association of with in boll yield components and boll morphological traits with fibre properties in upland cotton (*Gossypium hirsutum* L.). Plant Breed., 133, 521-529.

Taohua, Z. and Z. Haipeng (2006). Comparative study on yield and main agri-characters of five hybrids coloured cotton varieties. J. Anhui Agric. Univ., 33(4), 533-536.

Thiyague, K., N. Nadarajan, S. Rajarathinam, D. Sudhakar and K. Rajendran (2010). Association and path analysis for seed cotton yield improvement in interspecific crosses of Cotton. Electron. J. Plant Breed., 1, 1001-1005.

Tian, Z.G., X.Q. Haq and S.F. Zhang (1993). Inheritance analysis and selection strategies for earliness and yield component in short season cotton. Acta Agri. Borcali Sinica., 8, 18-22.

Turner, J.H., H.H. Ramey and S. Workley (1976). Influence of environment on seed quality of four cotton cultivars. Crop Sci., 16, 407-409.

Vineela, N., J.S.V.S. Murthy, P.V. Ramakumar and S.R. Kumari (2013). Variability studies for morphological and yield components traits in American cotton (*Gossypium hirsutum* L.). J. Agric. Vet. Sci., 4, 7-10.

Waldia, R.S., D.S. Jatasra and B.N. Dahiya (1979). Correlation and Path analysis of yield components in *Gossypium arboreum* L. Ind. J. Agri. Sci., 49, 32-34.

Wang, C., A. Isoda and P. Wang (2004). Growth and yield Performance of some cotton cultivars in Xinjiang, China, an arid area with short growing period. J. Agron. Crop Sci., 190 (3):177–183.

Wu, J., J.N. Jinkins, J.C. McCarty and J. Zhu (2004). Genetic association of yield with its components in recombinant inbred line population of cotton. Euphytica, 140, 171-179.

Yuan, Y.L., T.Z. Zhang, W.Z. Guo, J.J. Pan, Y.L. Yuan, T.Z. Zhang, W.Z. Guo and J.J. Pan (2002). Genetic stability of fibre qualities in Upland cotton. Cotton Sci., 14, 67-70.

Zeng, L., W.R. Meredith, L. Deborah, Boykin and E. Taliercio (2007). Evaluation of an exotic germplasm population derived from multiple cross among *Gossypium* tetraploid species. J. Cotton Sci., 11, 118-127.