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# Correlation studies among Morphological traits providing Natural Resistance against Insect, pest and yield in Upland Cotton *(Gossypium hirsutum* L.)

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Cotton production worldwide faces challenges from numerous insect pest species, resulting in significant yield losses in Pakistan due to 93 identified pest species. Widespread use of insecticides and pesticides raises concerns about human and animal health, environmental pollution, and insect resistance, necessitating environmentally friendly and cost-effective alternative pest control methods in cotton farming. This study evaluated 50 upland cotton genotypes for genetic diversity using cluster and principal component analysis at Cotton Research Station, AARI, Faisalabad. Thirteen traits associated with cotton's genetic defense mechanism against insect pests, including foliage density, stem tip hairiness, leaf type, gossypol content, and others, were analyzed for correlation. Traits such as leaf hairiness, stem tip hairiness, gossypol content, and okra leaf type were found to positively correlated with higher yield and resistance against insect pests. Cluster and principal component analysis identified specific genotypes and elite traits with potential for breeding programs aimed at developing cotton genotypes with improved insect tolerance and higher yield potential. This study contributes to identifying desirable traits for cotton breeding programs that enhance natural resistance against insect pests while reducing reliance on chemical insecticides and pesticides, promoting sustainable and environmentally friendly cotton production practices.

**Keywords: Cotton pest, Correlation study, Principal component analysis, Natural resistance.**

## INTRODUCTION

Worldwide the cotton crop production is handicapped by more than 1326 insect species and in Pakistan 93 insect pest species were discovered which disturb cotton crop (Atwal and Dhaliwal, 2002). Insect pest attack drops crop production from 30 to 45 percent and yield losses are greater than 70 percent in the absence of preventive measures (Din et al. 2016; Kanher et al. 2016). There are two types of insect species like chewing and sucking which are mainly responsible for yellowing, ragging and mining of leaves and foliage consumption. Mostly farmers prefer to use insecticides and pesticides because of their quick action (ud Din, 2015) but extensive use is becoming the source of human and animal health problems, environmental pollution, resistance in insects, disturbance of natural equilibrium and rebirth of secondary pests (Razaq et al. 2013). Therefore, it is essential to adopt alternative method which is compatible with environment and cost effective for farmers. Plant breeders are trying their best to improve and identify the genetic pool to develop better yielding varieties with greater insect pest resistance. The success of any breeding effort depends on the availability of genetic diversity in gene pool and inheritance of a trait that is docile to selection (Costa et al. 2003). No doubt breeders have made remarkable progress to breed the cotton varieties with high resistance and yield by using naturally available morphological traits which impart natural resistance and yield by effecting the feeding preferences of insect pest species to meet the growing challenges of international market (Ali and Awan, 2009; Kanher et al. 2016). There is immense diversity of traits present in cotton cultivars which ward off insect pest species and these traits are collectively known as defence umbrella. These traits include absence of nectars, red stem colour, okra leaf shape, fregobracts and hair on different plant parts. These natural morphological traits provide defensive mechanism by affecting the feeding preferences of chewing and sucking insect pest species and ultimately sustaining yield output (Rahman et al. 2013; Majeedano et al. 2014). These natural trait genotypes are cost effective, no issue of cross contamination, affordable for small land holding farmers, safe for human and animal health and significantly improve seed cotton yield. The correlation is a parameter which is useful to identify the strength and magnitude between two variables. It is helpful to identify the positive or negative association and direction between two desirable traits and provides information that highly inherited trait can be used to improve low inherited trait like yield. Therefore, a complete set of knowledge is demanded about correlation and inheritance mechanism of morphological traits to develop cotton varieties with high insect pest resistance and cotton seed yield (da Silva et al. 2008). The proposed research was carried out to govern the relationship among morphological traits such as foliage density, stem tip hairiness, leaf type, gossypol content, monopodia per plant, sympodia per plant, plant height (cm), bolls per plant, boll weight (g), leaf hairiness, bracteole length and width and seed cotton yield (g). The provided knowledge would be an easing element for plant breeders to develop or improve the cotton varieties with high insect pest resistance and yield.

## MATERIALS AND METHODS

### Experiment Location

During the winter season of 2020-2021 year, the research was carried out at the experimental area of Cotton Research Station, Ayub Agricultural Research Institute, Faisalabad. Seeds of fifty cotton genotypes, all belonging to American cotton (*G. hirsutum* L.) were provided by Cotton Research Station to assess the genetic potential of morphological traits against insect pest species and yield.

### Experimental Material

During the Kharif season of 2020-2021, a randomized complete block design (RCBD) was used to sow seeds of fifty different genotypes (as listed in Table 1). The experiment was conducted with three replications in a bed that was fifteen feet in size. Within the bed, the distance between rows was maintained at 2.2 feet, while the distance between individual plants within a row was kept at 1.5 feet. P×P and R×R distance was kept at 45cm and 75cm, correspondingly. There were ten plants in each of three replications and five plants were arbitrarily selected from each genotype in a replication for data collection. For data collection, at the maturity stage, five plants were randomly selected from each replication, and from each selected plant, three leaves were chosen. The soil of experimental area was sandy loam and acclaimed agronomic techniques and cultural practices such as doses of fertilizers, use of chemicals, seed bed preparation, weed control and number of irrigations were carried out according to recommendation and requisite from sowing to harvest stage.

### Data Collection of qualitative and quantitative traits

The data for the qualitative parameters such as leaf type, stem tip hairiness, foliage density, leaf hairiness, gossypol content, bracteole length and width and quantitative traits viz., plant height (cm), number of sympodia and monopodia per plant, number of bolls per plant, boll weight (g) and seed cotton yield (g) were recorded at the stage of plant maturity. The scoring criterion for qualitative traits was given in table 2.

**Table 1: List of cotton genotypes used in experiment**

| Sr.No. | Accession | Sr.No. | Accession | Sr.No. | Accession |
|---|---|---|---|---|---|
| 1 | MP-1 | 18 | W-1103 | 35 | FH-324 |
| 2 | MS-40 | 19 | NIAB-BT-1 | 36 | FH-341 |
| 3 | IR-NIBGE-901 | 20 | KZ-389 | 37 | 2660 |
| 4 | N-999 | 21 | RH-510 | 38 | 2663 |
| 5 | PAK-22 | 22 | GN-2085 | 39 | FH-312 |
| 6 | PRS-72 | 23 | FRN-55 | 40 | VH-363 |
| 7 | PMDWARF | 24 | FRN-59 | 41 | SAIM-32 |
| 8 | REBAB-55 | 25 | FRN-60 | 42 | SAHARA-150 |
| 9 | FH-114 | 26 | CEMB-55 | 43 | 2651 |
| 10 | RH-1 | 27 | AGC-999 | 44 | 2658 |
| 11 | RH-512 | 28 | VH-305 | 45 | 2659 |
| 12 | RIM-2-65 | 29 | CIM-616 | 46 | 2553 |
| 13 | ROW NO.32 | 30 | GH-142 | 47 | 2554 |
| 14 | CIM-598 | 31 | FH-4243 | 48 | 2602 |
| 15 | CIM-595 | 32 | FH-942 | 49 | 2610 |
| 16 | SLH-41 | 33 | FH-312 | 50 | 2611 |
| 17 | TADLA-3 | 34 | FH-330 | | |

Table 2: All qualitative characters are scored in data collection

| Characters | | | | | | | Score ↓ |
|---|---|---|---|---|---|---|---|
| Leaf type | Stem tip hairiness | Foliage density | Leaf hairiness | Gossypol content | Bract length | Bract width | |
| State | | | | | | | |
| Normal | Sparse | Sparse | Sparse | Low | Short | Narrow | 1 |
| Semi-okra | Medium | Intermediate | Medium | Normal | Medium | Medium | 2 |
| okra | profuse | Dense | Absent | High | Long | Wide | 3 |

## Statistical analysis

To determine the differences among the genotypes, the analysis of variance (ANOVA) was estimated using the approach proposed by Steel et al. (1997). The correlation coefficient was calculated using the formula described by Dewey and Lu (1959). Genetic diversity was assessed by cluster analysis and principal component analysis (Neyman and Pearson, 1928). Furth, heritability was calculated as used by Falconer and Mackay (1996).

## RESULTS

Plant breeders utilize many statistical ways to evaluate genetic variability and potential in genotypes that show significantly different results from one another and ensure promising output. Correlation analysis examines the strength of the relationship between traits on paired bases while other components are kept fixed. The value of association can be positive or negative. Cluster analysis indicated the cluster of genotypes which show similar results for any particular trait. Clusters are preferred based on genetic divergence from one another. PCA shows the positive association of traits in a specific quadrate and helps in selecting the elite traits. It is essential for a breeder to evaluate the cotton genotypes to select the promising traits against biotic and abiotic stress to ensure stable output. Results of ANOVA (Table 3) indicated that all cotton accessions demonstrated significant differences for all observed traits during the two-year study of 2020 and 2021. Estimation of genetic variability and heritability for both years is mentioned in table 4. Correlation parameters of both years are given in table 5 and 6. Principal component analysis of both years is given in table 7 and 8. Cluster analysis is mentioned in table 9 and 10 for both year of 2020 and 2021, respectively.

### Genetic variability

In 2020, Broad heritability for plant height was 0.825% and genetic advance was 59.99 which is shown in table 4. Phenotypic, genotypic, and environmental coefficient of variance was 17.50, 15.90 and 7.32 respectively. Phenotypic and genotypic variance is approximately equal and environmental coefficient is less from both. Broad heritability for sympodial branches per plant was 0.939% and genetic advance was 14.28. The values of PCV, GCV and ECV was 30.02, 29.09 and 7.40 respectively. PCV and GCV are approximately equal and environmental coefficient is less from both. The broad sense heritability of monopodial branches per plant was 0.800% and genetic advance was 2.353. The values of PCV, GCV and ECV were 57.06, 51.06 and 25.46 respectively as given in table 4 and PCV and GCV are approximately equal and environmental coefficient of variation is less from both. The broad heritability for bolls per plant was 0.651% and genetic advance was 49.70. The values of PCV, GCV and ECV were 54.60, 44.06 and 32.24 respectively. PCV and GCV are approximately equal and the environmental coefficient is less for both. Broad heritability was 0.869% and genetic advance was 1.769 which shows that the boll weight is under non- additive gene action and character is inclined to favorable environmental factors. The variance was 35.56, 33.15 and 12.86 respectively. PCV and GCV are approximately equal and environmental coefficient of variation is less from both. Broad sense heritability was 0.751% and genetic advance was 72.45 which shows additive genes action and selection may be helpful in future program. The values of PCV, GCV and ECV was 30.80, 26.70 and 15.35 respectively as in table 4. Phenotypic and genotypic variance is approximately equal and the environmental coefficient is less from both.

In 2021, broad heritability was 0.73% and genetic advance was 54.48 for plant height as which is shown in table 4. The values of PCV, GCV and ECV were 18.18, 15.55 and 9.422, respectively. Broad heritability was 0.974% and genetic advance was 74.31 which shows that bolls per plant is under additive gene control. The values of PCV, GCV and ECV were 53.85, 53.15 and 8.65 respectively. Broad heritability was 0.595% and genetic advance was 10.20 which shows that the sympodial branches is highly affected by environmental factors. Phenotypic, genotypic and environmental variance was 33.41, 25.78 and 21.25 respectively. Broad heritability for monopodial branches per plant was 0.803% and genetic advance was 2.021 The values of PCV, GCV and ECV were 49.63, 44.49 and 21.98 respectively. Broad heritability was 0.855% and genetic advance was 1.632 for boll weight. The values of PCV, GCV and ECV was 32.56, 30.11 and 12.38 respectively. Broad sense heritability was 0.936% and genetic advance was 1.632 for Seed cotton yield. The value of PCV, GCV and ECV was 29.88, 28.91 and 7.54 respectively.

### Estimation of correlation

### Quantitative Traits

During the year 2020, a correlation analysis (as shown in Table 5) revealed several significant associations among various cotton plant traits. Plant height was found to be positively correlated with leaf hairiness, gossypol content, bolls per plant, sympodial branches per plant, and boll weight, but negatively correlated with monopodial branches per plant and stem tip hairiness. Sympodia per plant showed significant positive correlations with boll weight, bolls per plant, seed cotton yield, and leaf type, but had a negative correlation with monopodia per plant and leaf hairiness. Monopodia per plant were significantly correlated with bolls per plant and foliage density, but negatively correlated with boll weight. The correlation matrix in table 5 also showed that bolls per plant was positively correlated with boll weight, seed cotton yield, leaf hairiness, and gossypol content. Boll weight was positively correlated with seed cotton yield, but negatively correlated with bract length, leaf type, and gossypol content. Seed yield was positively correlated with boll weight, plant height, and sympodial branches per plant, but negatively correlated with bract length.

During the year 2021, correlation analysis given in table 6 indicated that plant height was correlation (positive) with boll weight, seed cotton yield, leaf type and sympodial branches per plant while negatively linked with number of monopodia and bract width. Positive correlation of sympodial branch with seed cotton yield, leaf type, boll weight, bolls per plant and gossypol content but negatively correlated with monopodial branches. Monopodial branches per plant were significantly related to bolls per plant and foliage density but negatively linked with boll weight and leaf type. Bolls per plant were associated with seed cotton yield, gossypol content and boll weight. Boll weight was significantly associated with seed cotton yield and bract length while negatively correlated with foliage density. Seed cotton yield was positively associated with sympodial branches per plant and plant height while negatively correlated with bract length.

### Qualitative Traits

Two-year correlation analysis overall depicted that stem tip hairiness was significantly related with bolls per plant and seed yield and highest frequency distribution range indicated that 25 plants had medium scoring level. Leaf types such as okra and semi-okra type showed linkage with sympodial branches and plant height but negative relation with boll weight and monopodial branches per plant. The highest frequency distribution range for this trait was that almost 49 plants were normal type. Analysis of variance results showed that leaf type character was significant and showed great differences. The correlation matrix showed a positive association of foliage density with monopodial branches per plant. Correlation analysis depicted that gossypol content was linked with plant height, bolls per plant but negative linkage with boll weight and leaf hairiness was correlated with bolls per plant and plant height. Bract length was found to have a positive association with sympodial branches per plant, but a negative relationship with boll weight and seed cotton yield. Bract width showed a significant association with sympodial branches per plant and foliage density.

### Principal Component Analysis

Principal component analysis (PCA) was used as a statistical method to analyze and gain valuable insights into how different genotypes can be grouped based on specific trait associations, with the goal of guiding breeding purposes. Biplot depicts the relationship between different characters i.e., if between two vector parameters the angle is less than 90° then there will be a positive association between the two parameters and vice versa.

Principal component analysis of genotypes (sown in 2020) showed total thirteen PCs but first five PCs (PC1 to PC5) showed eigen values greater than one (>1.0) and cumulatively variation was 63.95% but variability reduced from PC6 to PC13 in table 7. The first PC axes was noted 21.26% of total variation while PC2 axes accounted for 13.28% of total variation, whereas third and four PC axes accounted for 10.89% and 9.75% of total variation and variation in all these PC axes showed great variability for observed traits. The variation in PC1 was largely related to seed cotton yield, leaf type, bolls per plant, plant height, gossypol content, sympodial branches and leaf hairiness while in PC2 variation was associated with bolls per plant, seed cotton yield, and foliage density while variation in PC3 was associated with sympodial branches per plant, plant height, foliage density bolls per plant and bract length. Variation in PC4 was related with traits such as plant height, monopodial branches per plant, seed cotton yield, boll weight, leaf type, leaf hairiness and bract length while variation in PC5 was linked with plant height, leaf type, seed cotton yield, boll weight, bolls per plant, gossypol content and leaf hairiness. PC1 showed great variability as compared to other PCs and it shows high contribution in selection program.

Principal component analysis of genotypes (sown in 2021) showed first five PCs (PC1 to PC5) showed eigenvalues greater than one (>1.0) and cumulatively variation was 61.77% and variability reduced from PC6 to PC13 in table 8. The PC1 axes were noted as 18.38% of total variation while PC2 axes accounted for 13.57% of total variation, whereas third, four and five PC axes accounted for 10.86%, 9.78% and 9.15% of total variation, respectively. The variation in PC1 was largely positively related with plant height, leaf type, bolls per plant, gossypol content and leaf hairiness while in PC2 variation was associated with leaf hairiness, boll weight, bract length and seed cotton yield while variation in PC3 was linked with traits such as seed cotton yield, leaf type, monopodial branches, leaf hairiness, bolls per plant and gossypol content (Table 8). Variation in PC4 was related with traits such as plant height, boll weight, bolls per plant and leaf type while variation in PC5 was linked with leaf type, plant height, foliage density, monopodial and sympodial branches and leaf hairiness.

## Biplot

Scatter plot of first year (2020) data traits depicted that variables were executed on the plot as vectors. The First vector is best for selecting the elite traits which are positively correlated with each other as in figure 1.

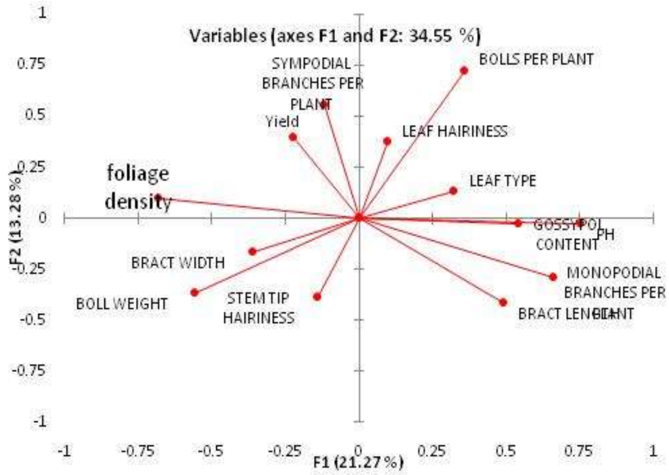

**Figure 1: Two-dimensional orientation of twelve cotton traits during year 2020**

Leaf hairiness, leaf type and bolls per plant but it was negatively correlated with 4th vector traits such as bract width, boll weight and stem tip hairiness which shows poor selection criteria. Second vector is better for selection as compared to 3rd vector and it showed positive relationship of seed cotton yield, foliage density and sympodia per plant but these traits showed negative association with 3rd vector traits such as monopodial branches per plant, bract length and gossypol content. The best scattered traits were stem tip hairiness, boll weight, bolls per plant and foliage density with greater variability.

Meanwhile second year data evaluation showed that first quadrate depicted elite traits positive association of leaf hairiness, stem tip hairiness, gossypol content and bract length while negative linkage with 4th vector traits such as bract width and foliage density (Figure 2).

The second vector depicted a significant association of boll weight and yield while negative relation with 3rd vector traits such as leaf type, monopodial and sympodial branches per plant, plant height and bolls per plant. The best scattered traits were boll weight, bolls per plant and sympodial branches per plant with high variability. The first vector is preferred for desirable and elite trait selection and fourth vector shows poor selection criteria for trait selection because they show poor performance.

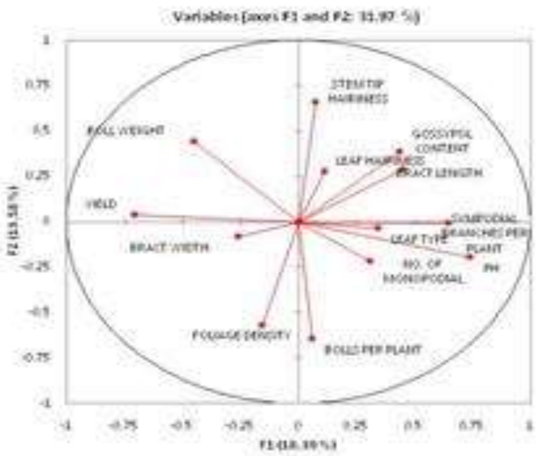

**Figure 2: Two-dimensional orientation of twelve cotton traits during year 2021**

## Cluster Analysis

Cluster analysis is a statistical method which is used to make groups of genotypes which belong to the same order having similarity in most of aspects as in contrast to other clusters. It is a useful tool which aids to disclose the association among genotypes which came from different origins and helps to identify genotypes which have desirable and valuable traits in various clusters which can be further used for hybridization purpose. The 50 cotton genotypes were categorized into three major clusters based on relative magnitude, with each cluster exhibiting distinct trait patterns. Cluster-2 was the largest, consisting of 28 genotypes, while cluster-1 and cluster-3 contained 11 genotypes each. Traits within each cluster had smaller values compared to those between clusters, highlighting specific trait associations within each cluster for further breeding purposes. In cluster-1, genotype-6 (PRS-72) had maximum plant height while genotype-46 (2553) from cluster-2 had great boll weight, sympodial branches per plant, seed cotton yield and genotype-31 (FH-4243) from cluster-3 had high bolls per plant, stem tip hairiness, foliage density and leaf hairiness as mentioned in table 9.a. Minimum distance within cluster-1, cluster-2 and cluster-3 from each cluster was 14.21, 11.75 and 26.22, correspondingly.

All observed traits represent minimum and maximum values in table 9. Genotypes in cluster-1 elucidated maximum genetic divergence against cluster-2 and 3 whereas cluster-3 depicted minimum genetic divergence. Dendrogram depicted that genotypes which fall under same cluster for a particular trait are homogenous in nature, but they show variability in comparison with other clusters. During 2021, 50 cotton genotypes were also grouped into three major clusters. According to the cluster pattern analysis, cluster-2 was found to be the largest group, consisting of 38 genotypes.

**Table 3: Mean square of fifty cotton genotypes for various quantitative and qualitative traits during year 2020-2021**

| Parameters | Replications | | Genotypes | | Error | |
|---|---|---|---|---|---|---|
| | 2020 | 2021 | 2020 | 2021 | 2020 | 2021 |
| | DF= 2 | DF= 2 | DF= 49 | DF= 49 | DF= 98 | DF= 98 |
| **Plant height** | 714.3* | 629.40 | 3302.9** | 3219.9** | 218.20 | 351.00 |
| **Sympodial branches** | 159.20 | 52.34 | 156.80** | 151.55** | 3.32 | 27.98 |
| **monopodial branches** | 2.16** | 12.06** | 5.29** | 3.88** | 0.40 | 0.29 |
| **bolls per plant** | 103.15 | 74.60 | 3161.01** | 4047.11** | 478.79 | 35.40 |
| **Boll weight** | 0.57* | 0.02 | 2.67** | 2.33** | 0.12 | 0.12 |
| **Seed cotton yield** | 2609.9* | 0.03 | 5484.3** | 6414.8** | 544.70 | 142.30 |
| **Stem tip hairiness** | 2.93 | 1.54 | 1.34** | 1.22** | 3.97 | 3.50 |
| **Leaf type** | 1.20 | 4.82 | 0.06** | 0.12** | 2.99 | 4.44 |
| **Foliage density** | 3.16 | 3.30 | 1.05** | 0.98** | 3.69 | 4.13 |
| **Gossypol content** | 0.01 | 2.60 | 0.58** | 0.83** | 0.01 | 2.44 |
| **Leaf hairiness** | 0.01 | 2.60 | 0.85** | 0.83** | 0.01 | 2.44 |
| **Bract length** | 4.14 | 1.14 | 1.44** | 1.50** | 5.53 | 4.69 |

** Highly Significant = ($P<0.01$) * Significant= ($P<0.05$)

**Table 4: Estimation of genetic parameters of 50 cotton genotypes for various qualitative traits during year 2020-2021**

| Characters | Year | σ2p | σ2g | σ2e | PCV | GCV | ECV | $H_2$(%) | GA | GA% |
|---|---|---|---|---|---|---|---|---|---|---|
| Plant height | 2020 | 126.40 | 108.24 | 118.16 | 17.50 | 15.90 | 7.32 | 0.83 | 59.99 | 29.75 |
| | 2021 | 130.30 | 95.29 | 35.01 | 18.18 | 15.15 | 18.18 | 0.73 | 54.48 | 27.04 |
| Sympodial branches per plant | 2020 | 54.50 | 51.18 | 3.31 | 30.02 | 29.09 | 7.40 | 0.94 | 14.28 | 34.56 |
| | 2021 | 69.17 | 41.19 | 27.97 | 33.41 | 25.78 | 21.25 | 0.59 | 10.20 | 40.99 |
| monopodial branches per plant | 2020 | 2.03 | 1.63 | 0.40 | 57.06 | 51.06 | 25.46 | 0.80 | 2.35 | 94.14 |
| | 2021 | 1.49 | 1.20 | 0.29 | 49.63 | 44.49 | 21.98 | 0.80 | 2.02 | 82.17 |
| bolls per plant | 2020 | 132.86 | 94.07 | 78.78 | 54.60 | 44.06 | 32.24 | 0.65 | 49.70 | 73.25 |
| | 2021 | 137.20 | 13.22 | 35.42 | 53.85 | 53.15 | 8.65 | 0.97 | 74.35 | 108.07 |
| Boll weight | 2020 | 0.97 | 0.84 | 0.12 | 35.56 | 33.15 | 12.86 | 0.87 | 1.77 | 63.68 |
| | 2021 | 0.85 | 0.73 | 0.12 | 32.56 | 30.11 | 12.38 | 0.86 | 1.63 | 57.37 |
| Seed cotton yield | 2020 | 219.20 | 166.51 | 544.70 | 30.80 | 26.70 | 15.35 | 0.75 | 72.45 | 47.68 |
| | 2021 | 221.40 | 290.80 | 142.30 | 29.88 | 28.91 | 7.54 | 0.93 | 91.14 | 57.63 |

**σ2p:** Phenotypic variance; **σ2e:** Environmental variance; **σ2g:** Genotypic variance; **PCV:** Phenotypic coefficient of variance; **ECV:** Environmental coefficient of variance; **GCV**: Genotypic coefficient of variance; **GA:** Genetic advance; **$H_2$ %:** Broad sense heritability percentage; **GA %:** Genetic advance percentage of mean

**Table 5: Correlation matrix among the traits various quantitative and qualitative traits during year 2020**

| Traits | PH | MB | SB | B/P | BW | GC | STH | FD | LH | LT | BL | BW |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **MB** | **0.0566** | | | | | | | | | | | |
| **SB** | 0.976** | -0.2153 | | | | | | | | | | |
| **B/P** | 0.9987** | 0.8653** | 0.9815** | | | | | | | | | |
| **BW** | 0.9345** | -0.2378 | 0.8674** | 0.8674** | | | | | | | | |
| **GC** | 0.6548* | 0.2727 | 0.0314 | 0.6458* | 0.0453 | | | | | | | |
| **STH** | -0.4567 | 0.2340 | 0.0514 | 0.0346 | 0.0674 | -0.0197 | | | | | | |
| **FD** | 0.0324 | 0.5435* | 0.2259 | 0.1545 | -0.0763 | 0.0639 | -0.0103 | | | | | |
| **LH** | 0.5678* | 0.0234 | -0.2322 | 0.5638* | -0.1146 | 0.0423 | 0.4211 | -0.1009 | | | | |
| **LT** | 0.2008 | 0.2091 | 0.5632* | 0.0578 | 0.6781* | -0.1875 | 0.0431 | 0.0292 | 0.4536* | | | |
| **BL** | 0.0221 | 0.0346 | 0.0552 | -0.0845 | 0.0342 | -0.3315 | -0.6530 | -0.1567 | 0.0762 | 0.0750 | | |
| **BW** | 0.0346 | 0.0567 | -0.0946 | -0.1821 | 0.0571 | 0.0616 | -0.0260 | 0.1440 | 0.0346 | -0.0494 | 0.0235 | |
| **SCY** | 0.8845** | 0.8945** | 0.749** | 0.9756** | 0.9975** | 0.9975 | 0.8766* | -0.0765 | 0.1232 | 0.1132 | -0.0450 | 0.0234 |

* = Significant ($P<0.05$); ** = Highly significant ($P<0.01$); Plant height (PH), Sympodial branches per plant (SB), Monopodial branches per plant (MB), Bolls/plant (B/P), Boll weight (BW), Gossypol content (GC), Stem tip hairiness (STH), Foliage density (FD), Leaf hairiness (LH), Leaf type (LT), Bract length and width (BL/W)

**Table 6: Correlation matrix among the traits various quantitative and qualitative traits during year 2021**

| Traits | PH | MB | SB | B/P | BW | GC | STH | FD | LH | LT | BL | BW |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **MB** | 0.0467 | | | | | | | | | | | |
| **SB** | 0.8765** | 0.0313 | | | | | | | | | | |
| **B/P** | 0.7899** | 0.6789* | 0.9876** | | | | | | | | | |
| **BW** | 0.9876** | -0.3450 | 0.8234** | 0.8732** | | | | | | | | |
| **GC** | 0.0345 | 0.2311 | 0.3411* | 0.4321* | 0.764** | | | | | | | |
| **STH** | 0.0678 | 0.0457 | 0.0765 | -0.3508 | 0.2390 | -0.1442 | | | | | | |
| **FD** | 0.0345 | 0.764** | 0.0843 | 0.0124 | -0.1291 | -0.0285 | -0.0821 | | | | | |
| **LH** | 0.0567 | 0.0654 | 0.1121 | 0.3460 | 0.0765 | 0.0705 | 0.1220 | 0.4321 | | | | |
| **LT** | 0.2054 | -0.1817 | 0.4568* | 0.1215 | 0.4532* | -0.1816 | 0.4321* | 0.0353 | 0.1687 | | | |
| **BL** | 0.0567 | 0.1896 | 0.1123 | 0.0430 | 0.0235 | -0.3483 | 0.1236 | -0.207 | 0.1121 | 0.0612 | | |
| **BW** | -0.1729 | 0.2340 | -0.0877 | -0.1654 | 0.1231 | 0.0178 | -0.0662 | 0.0855 | -0.167 | -0.049 | -0.037 | |
| **SCY** | 0.764** | 0.6754** | 0.9347** | 0.9764** | 0.8763** | 0.4321* | 0.1235 | -0.314 | 0.2016 | 0.0398 | 0.1459 | -0.211 |

* = Significant ($P<0.05$); ** = Highly significant ($P<0.01$); Plant height (PH), Sympodial branches per plant (SB), Monopodial branches per plant (MB), Bolls/plant (B/P), Boll weight (BW), Gossypol content (GC), Stem tip hairiness (STH), Foliage density (FD), Leaf hairiness (LH), Leaf type (LT), Bract length and width (BL/W)

**Table 7: Principal component analysis on correlation matrix for twelve characters in 50 cotton genotypes during year 2020**

| Traits | PC1 | PC2 | PC3 | PC4 | PC5 |
|---|---|---|---|---|---|
| Plant height | 0.4792 | -0.1457 | 0.2195 | 0.9881 | 0.7309 |
| Sympodial branches per plant | 0.4198 | -0.0040 | 0.2182 | 0.3850 | 0.6410 |
| monopodial branches per plant | 0.2012 | -0.1627 | 0.4146 | 0.5387 | 0.5544 |
| Bolls per plant | 0.384 | 0.4862 | 0.4464 | 0.5579 | 0.6285 |
| Boll weight | -0.2903 | 0.7325 | -0.2364 | 0.5713 | 0.4251 |
| Seed cotton yield | 0.4566 | 0.721 | 0.5551 | 0.3970 | 0.0060 |
| Stem tip hairiness | 0.0501 | 0.4933 | -0.1133 | -0.2015 | 0.3527 |
| Foliage density | -0.1006 | 0.4277 | 0.3126 | -0.2724 | 0.3972 |
| Leaf hairiness | 0.726 | 0.6081 | 0.5258 | 0.4457 | 0.6793 |
| Leaf type | 0.2217 | -0.0284 | 0.3338 | 0.5416 | 0.4198 |
| Bract length | 0.2915 | 0.5182 | 0.3207 | -0.0243 | -0.3569 |
| Gossypol content | 0.2823 | 0.2875 | 0.5865 | -0.0308 | 0.2701 |
| **Eigenvalues** | 2.7649 | 1.7269 | 1.4165 | 1.2679 | 1.1378 |
| **Variability (%)** | 21.2686 | 13.2836 | 10.8964 | 9.7528 | 8.7526 |
| **Cumulative %** | 21.2686 | 34.5522 | 45.4486 | 55.2014 | 63.9540 |

**Table 8: Principal component analysis on correlation matrix for twelve characters in 50 cotton genotypes during year 2021**

| Traits | PC1 | PC2 | PC3 | PC4 | PC5 |
|---|---|---|---|---|---|
| Plant height | 0.4529 | -0.0225 | 0.1908 | 0.2363 | 0.1427 |
| Sympodial branches per plant | 0.3968 | -0.2247 | 0.1558 | 0.1896 | 0.3587 |
| monopodial branches per plant | -0.0701 | 0.4233 | -0.1750 | 0.2860 | -0.3227 |
| Bolls per plant | 0.2146 | 0.5496 | 0.1587 | -0.1130 | 0.2232 |
| Boll weight | -0.3348 | -0.2791 | -0.0737 | 0.3108 | 0.4350 |
| Seed cotton yield | -0.4103 | 0.0738 | -0.1258 | 0.0084 | 0.4842 |
| Stem tip hairiness | -0.0852 | -0.2982 | -0.2037 | 0.5141 | -0.3675 |
| Foliage density | -0.1356 | 0.2994 | 0.4575 | 0.2926 | -0.1533 |
| Leaf hairiness | 0.0576 | 0.2837 | -0.4214 | 0.2917 | 0.0431 |
| Leaf type | 0.1936 | 0.0980 | 0.1110 | 0.4790 | 0.2085 |
| Bract length | 0.2951 | -0.3149 | 0.0594 | 0.0049 | -0.2296 |
| Gossypol content | 0.3255 | -0.0208 | -0.4073 | -0.2203 | 0.0403 |
| **Eigenvalues** | 2.3907 | 1.7651 | 1.4127 | 1.2716 | 1.1901 |
| **Variability (%)** | 18.3898 | 13.5777 | 10.8666 | 9.7813 | 9.1549 |
| **Cumulative %** | 18.3898 | 31.9675 | 42.8341 | 52.6154 | 61.7703 |

**Table 9.a: Cluster analysis of 50 genotypes; class centroid during year 2020**

| Class | PH | SB | MB | B/P | BW | SCY | STH | FD | LH | LT |
|---|---|---|---|---|---|---|---|---|---|---|
| 1(obs6) | 236 | 18 | 1.53 | 54.7 | 1.7 | 92 | 1 | 2 | 1 | 1 |
| 2(obs46) | 189.3 | 27 | 2.6 | 45.6 | 3.8 | 173 | 1 | 2 | 1 | 1 |
| 3(obs31) | 225.3 | 25.3 | 2.3 | 105 | 1.2 | 128 | 2 | 3 | 2 | 1 |

Plant height (PH), Sympodial branches (SB), Monopodial branches (MB), Bolls per plant (B/P), Boll weight (BW), Gossypol content (GC), Stem tip hairiness (STH), Foliage density (FD), Leaf hairiness (LH), Leaf type (LT), Bract length and width (BL/W)

**Table 9.b: Cluster analysis of 50 genotypes; Distance between the class centroids during year 2020**

| | 1 | 2 | 3 |
|---|---|---|---|
| **1** | 0 | | |
| **2** | 96.41 | 0 | |
| **3** | 92.15 | 83.8 | 0 |
| **Genotypes** | 1,2,5,7,9,10,13,15,17,32,48 | 3,5,11,12,14,16,19,20,22,24,25,26,27,28,29,33,34 | 4,8,18,21,23,30,31,35,36,37,39 |

**Table 9.c: Cluster analysis for 50 genotypes exhibiting range values during year 2020**

| Variable | Minimum | Maximum | Mean |
|---|---|---|---|
| Plant height | 114.3000 | 276.7000 | 201.6526 |
| Sympodial branches per plant | 12.0000 | 40.0000 | 25.0954 |
| monopodial branches per plant | 2.3000 | 6.3000 | 2.4766 |
| Bolls per plant | 12.3300 | 151.3000 | 67.8872 |
| Boll weight | 1.2000 | 9.3000 | 2.8540 |
| Seed cotton yield | 55.0000 | 234.0000 | 151.6800 |
| Stem tip hairiness | 1.0000 | 3.0000 | 1.8000 |
| Foliage density | 1.0000 | 3.0000 | 1.8800 |
| Leaf hairiness | 1.0000 | 3.0000 | 1.4066 |
| Leaf type | 1.0000 | 2.0000 | 1.0200 |
| Bract length | 1.0000 | 3.0000 | 1.6400 |
| Gossypol content | 1.0000 | 3.0000 | 1.9800 |

**Table 10.a: Cluster analysis of 50 genotypes; class centroid during year 2021**

| Class | PH | SM | MB | B/P | BW | SCY | STH | FD | LH | LT | BL | BW | GC |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1(obs6) | 231 | 18.7 | 17 | 55.7 | 1.9 | 88 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| 2(obs19) | 195 | 19.3 | 2.3 | 81 | 2.3 | 108.3 | 2 | 3 | 1 | 1 | 1 | 3 | 1 |
| 3(obs43) | 185.3 | 25.3 | 1.3 | 357 | 2.8 | 151.0 | 1 | 2 | 1 | 1 | 2 | 2 | 1 |

Plant height (PH), Sympodial branches (SB), Monopodial branches (MB), Bolls per plant (B/P), Boll weight (BW), Gossypol content (GC), Stem tip hairiness (STH), Foliage density (FD), Leaf hairiness (LH), Leaf type (LT), Bract length and width (BL/W)

**Table 10.b: Cluster analysis of 50 genotypes; Distance between the class centroids during year 2021**

| | 1 | 2 | 3 |
|---|---|---|---|
| 1 | 0 | | |
| 2 | 96.67 | 0 | |
| 3 | 317.92 | 282.34 | 0 |
| Genotypes | 1,2,6,7,9,10,13,15,17,32,48 | 3,4,5,8,11,12,14,16,18,20,21,22,23,24,25,26,27,28,29,30,31,33,34,35,36,37,38,39,40,41,42,44,45,46,47,49,50 | 43 |

**Table 10.c: Cluster analysis for 50 genotypes exhibiting range values during year 2021**

| Variable | Minimum | Maximum | Mean |
|---|---|---|---|
| Plant height | 115.7000 | 275.0000 | 198.8140 |
| Sympodial branches per plant | 0.3000 | 40.7000 | 24.9540 |
| monopodial branches per plant | 0.3000 | 37.0000 | 3.6554 |
| Bolls per plant | 12.3000 | 357.0000 | 75.2140 |
| Boll weight | 1.4000 | 5.1000 | 2.8220 |
| Seed cotton yield | 52.0000 | 244.0000 | 158.1267 |
| Stem tip hairiness | 1.0000 | 3.0000 | 1.7860 |
| Foliage density | 1.0000 | 3.0000 | 1.8600 |
| Leaf hairiness | 1.0000 | 3.0000 | 1.3800 |
| Leaf type | 1.0000 | 2.0000 | 1.0200 |
| Bract length | 1.0000 | 3.0000 | 1.7000 |
| Gossypol content | 1.0000 | 3.0000 | 1.8800 |

Cluster-1 contained 11 genotypes, and cluster-3 had only 1 genotype, as indicated in Table 10. In cluster-1 genotype-6 (PRS-72) had high plant height, and monopodial branches per plant while genotype-19 (NIAB-BT-1) from cluster-2 had high boll weight, stem tip hairiness, foliage density, bract width and seed cotton yield and genotype-43 (2651) from cluster-3 had high boll weight, sympodial branches per plant, and bolls per plant as mentioned in table 10.b Minimum distance within cluster-1 from each cluster was 18.31 and in cluster-2 was 11.97. All traits show variation in values from minimum to maximum value in Table 10.c. Genotypes in cluster-1 elucidated maximum genetic divergence against cluster-3 whereas cluster-3 depicted minimum genetic divergence.

## DISCUSSION

Statistical analysis showed that all the selected traits showed great differences and were significant enough to study them further. The correlation matrix showed the association of each character with other characters to depict every scenario that how a single character association can be helpful for better yield results. Promising traits such as number of bolls per plant, stem tip hairiness, sympodial branches per plant, leaf hairiness, seed cotton yield, gossypol content and okra leaf type are desirable for high yield production and provide resistance against insect pest population. It was found that gossypol content showed resistance against thrips attack (Javed et al. 2016; Miyazaki et al. 2017). Plant height was found to have a positive relationship with sympodial branches and bolls per plant (Magadum et al. 2012; Farooq et al. 2012), boll weight (da Silva et al. 2008) but negatively correlated with SCY (Yan et al. 2019), number of monopodia and bract width (Din et al. 2016; Rauf et al. 2019). A non-significant relation between seed cotton yield with monopodial branches was reported (Sarwar et al. 2011). There was a direct relationship observed between monopodial branches and bolls per plant (Shahid et al. 2012; Yaqoob et al. 2016). sympodial branches per plant were related to seed cotton yield (Baloch et al. 2015). Leaf hairiness leads to low whitefly attacks (Shahid et al. 2012). Shaheen et al. (2021) also found an association of bolls per plant with boll weight and GOT. Sarwar et al. (2011) evaluated different genotypes to determine the genetic inheritance mechanism of yield-attributing traits and the findings revealed that plant height, number of bolls per plant, and seed cotton yield exhibited additive gene action. Additionally, seed yield showed significant positive associations with boll weight (Kumar et al. 2019), plant height, and sympodial branches per plant (Thiyagu et al. 2010; Rehman et al. 2020), but the negative association with bract length (Zafar et al. 2009; Pujer et al. 2014). Boll weight was also found to be significantly linked with seed cotton yield (Khan et al. 2009; Shahid et al. 2012; Rehman et al. 2020).

During the study of 2020, Broad heritability of plant height, sympodial branches, bolls per plant is under the effect of additive genes and character is least influenced by environmental factors and selection is helpful in the future while monopodial branches per plant show that the character is under non-additive gene action and character is highly under the effect of environment and selection will not be helpful in the future program. boll weight is under non- additive gene action and character is inclined to favorable environmental factors and selection may not be helpful in the future programs (Jatt et al. 2007; Desalegn et al. 2009). It was observed by another researcher that bolls per plant were under additive gene action (Sarwar et al. 2011) and broad heritability reported 95%, 22% and 93.58% (Baloch et al. 2015). Previous researchers concluded 88% and 93% broad sense heritability (Desalegn et al. 2009; Sarwar et al. 2011; Baloch et al. 2015). During 2021, broad heritability was of plant height, is under additive gene action and character is least inclined to environmental factors and selection is helpful in the future. PCV and GCV for plant height are approximately equal and the environmental coefficient is less from both. Monopodial branches, boll weight, sympodial branches, bolls per plant and Seed cotton yield are highly affected by environmental factors and selection will be ineffective.

Principal component analysis showed that elite traits with positive or negative relations with other traits can be selected for breeding purposes. Seed yield was associated with boll weight and sympodial branches per plant during both year of data evaluation.

Cluster analysis depicted that the genotypes which show the same performance belong to one cluster and each cluster had a difference in grouping of genotypes it also showed that in each cluster a specific genotype is responsible for the better performance of a typical character. The minimum distance within cluster-1 from each cluster was 18.31 and in cluster-2 was 11.97 during 2020 evaluation. The minimum distance within cluster-1 from each cluster was 14.21 and cluster-2 was 11.75 and cluster-3 was 26.22 during 2021 evaluation. Genotypes in cluster-1 elucidated maximum genetic divergence against cluster-3 whereas cluster-3 depicted minimum genetic divergence. Similar cluster studies on cotton genotypes in the same manner were also reported by Gopinath et al. (2009) and Rathinavel et al. (2017).

## CONCLUSION

The study estimated genetic diversity and identified desirable traits, such as leaf hairiness, stem tip hairiness, gossypol content, and okra leaf type, that are positively correlated with higher yield and resistance against insect pests. These findings could assist cotton breeders in developing superior cotton genotypes with desirable traits for stable yield, environmental resilience, and better insect pest resistance.

## CONFLICT OF INTEREST

The authors declared that present study was performed in the absence of any conflict of interest.

## AUTHOR CONTRIBUTIONS

The experimental work and manuscript writing were done by SR and MAh under the supervision of KK and AS. KK and GS designed and supervised throughout the experiment and theoretical work. AS and MAs contributed to statistics and literature search. KK, MAs, AS and GS reviewed the manuscript.

## REFERENCES

Ali MA, Awan SI (2009). Inheritance pattern of seed and lint traits in cotton (*Gossypium hirsutum*). *International Journal of Agriculture and Biology,*11(1): 44-48.

Atwal A, Dhaliwal G (2002). Agricultural Pest of South–East Asia and Their Management. Kalyani Publisher, New Delhi, India, pp 321.

Baloch M, Baloch A, Baloch M, Mallano I, Baloch A, Abro S (2015). Association and heritability analysis for yield and fiber traits in promising genotypes of cotton (*Gossypium hirsutum* L.). *Sindh University Research Journal-SURJ* (Science Series), 47(2):303-306.

Costa DB, Souza B, Carvalho GA, Carvalho CF (2003). Residual action of insecticides to larvae of Chrysoperla externa (Neuroptera: Chrysopidae) under greenhouse conditions. *Ciência e Agrotecnologia*, 27: 835-839.

da Silva FP, Bezerra AP, da Silva AF (2008). Boll weevil (Anthonomus grandis Boheman) oviposition and feed in ratoon cotton of mutants lines of upland cotton. *Revista Ciencia Agronomica*, 39(1): 85.

Desalegn Z, Ratanadilok N, Kaveeta R (2009). Correlation and heritability for yield and fiber quality parameters of Ethiopian cotton (*Gossypium hirsutum* L.) estimated from 15 (diallel) crosses. *Agriculture and Natural Resources*, 43(1): 1-11.

Dewey R, Lu K (1959). A correlation and phenotypic correlation analysis of some quality characters and yield of seed cotton in upland cotton (*Gossypium hirsutum* L.). *Journal of Biological Sciences,* 1: 235-236.

Din Z, Malik T, Azhar F, Ashraf M (2016). Natural resistance against insect pests in cotton. *Journal of Animal & Plant Sciences*, 26(5:

Falconer D, Mackay T (1996). Introduction to quantitative genetics. Longmans Green, Harlow, Essex, UK.

Farooq J, Anwar M, Riaz M, Farooq A, Mahmood A, Shahid MT, Rafiq M, Ilahi F (2014). Correlation and path coefficient analysis of earliness, fiber quality and yield contributing traits in cotton (*Gossypium hirsutum* L.). *JAPS: Journal of Animal & Plant Sciences*, 24(3): 111-124.

Gopinath M, Rajamani S, Naik R, Rao C (2009). Genetic divergence for lint characters for upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*, 23(1): 46-48.

Jatt T, Abro H, Larik A, Soomro Z (2007). Performance of different cotton varieties under the climatic conditions of Jamshoro. *Pakistan Journal of Botany,* 39(7): 2427-2430.

Javed S, Javaid M, Hassan A, Awais M, Gulzar S, Rasool S, Nadeem M, Shahid MR (2016). Genetic diversity and morphological traits association in upland cotton imparting resistance against insect pests. *American-Eurasian Journal of Agricultural & Environmental Sciences,*16(5): 924-927.

Kanher FM, Syed TS, Abro GH, Jahangir TM, Tunio SA (2016). Some physio morphological leaf characters of gamma irradiated cotton lines to resistance against Jassid (*Amrasca Devastans* Dist.) *Journal of Entomology and Zoology Studies,* 4: 480-85.

Khan NU, Hassan G, Kumbhar MB, Marwat KB, Khan MA, Parveen A, Saeed M (2009). Combining ability analysis to identify suitable parents for heterosis in seed cotton yield, its components and lint% in upland cotton. *Industrial crops and products*, 29(1): 108-115.

Kumar CPS, Prasad V, Rajan REB, Joshi J, Thirugnanakumar S (2019). Studies on correlation and path-coefficient analysis for seed cotton yield and its contributing traits in cotton (*Gossypium hirsutum* L.). Plant Archives, 19(1): 683-686.

Magadum S, Banerjee U, Ravikesavan R, Thiyagu K, Boopathi NM, Rajarathinam S (2012). Association analysis of yield and fibre quality characters in interspecific population of cotton (Gossypium spp.). *Journal of Crop Science and Biotechnology*, 15(3): 239-243.

MajeedanoMS, Ahsaan MZ, Somroo AW, Channa AR (2014). Heritability and correlation estimate for some yield traits of *Gossypium hirsutum*. American Research Thoughts. 1: 781-90.

Miyazaki J, Stiller WN, Wilson LJ (2017). Sources of plant resistance to thrips: a potential core component in cotton IPM. *Entomologia Experimentalis et Applicata,* 162(1): 30-40.

Neyman J, Pearson ES (1928). On the use and interpretation of certain test criteria for purposes of statistical inference: Part I. *Biometrika*, 175-240.

PujerSK, Siwach SS, Sangwan RS, Sangwan O, Deshmukh JA (2014). Correlation and path coefficient analysis for yield and fibre quality traits in upland cotton (*Gossypium hirsutum* L). *Journal Cotton Research Development*, 28(2): 214-216.

Rahman SA, Iqbal MS, Riaz M, Mahmood A, Shahid MR, Abbas G, Farooq J (2013). Cause and effect estimate for yield contributing and morphological traits in upland cotton (*Gossypium hirsutum* L.). *Journal of Agricultural Research*, 51(4): 393-398.

Rathinavel K, Kavitha H, Priyadharshini C (2017). Assessment of genetic variability and correlation analysis of seed and seed cotton yield attributing traits of tetraploid cotton genotypes (*G. hirsutum* L.). *Electronic Journal of Plant Breeding*, 8(4): 1275-1283.

Rauf S, Shehzad M, Al-Khayri JM, Imran HM, Noorka IR (2019). Cotton (*Gossypium hirsutum* L.) breeding strategies. Advances in plant breeding strategies: Industrial and food crops: *Springer*. pp. 29-59.

Razaq M, Suhail A, Aslam M, Arif MJ, Saleem MA (2013). Patterns of insecticides used on cotton before introduction of genetically modified cotton in Southern Punjab, Pakistan. *Pakistan Journal of Zoology*, 45(2): 574-577.

Rehman A, Mustafa N, DU X, Azhar MT (2020). Heritability and correlation analysis of morphological and yield traits in genetically modified cotton. *Journal of cotton research*, 3(1): 1-9.

Sarwar G, Baber M, Hussain N, Khan IA, Naeem M, Ullah MA, Khan AA (2011). Genetic dissection of yield and its components in upland cotton (*Gossypium hirsutum* L.). *African Journal of Agricultural Research*, 6(11): 2527-2531.

Shaheen M, Abdul Rauf H, Taj MA, Yousaf Ali M, Bashir MA, Atta S, Farooq H, Alajmi RA, Hashem M, Alamri S (2021). Path analysis based on genetic association of yield components and insects pest in upland cotton varieties. *PloS one*, 16(12): e0260971.

Shahid MR, Farooq J, Mahmood A, Ilahi F, Riaz M, Shakeel A, Petrescu-Mag IV, Farooq A (2012). Seasonal occurrence of sucking insect pest in cotton ecosystem of Punjab, Pakistan. *Advances in Agriculture & Botanics*, 4(1): 26-30.

Steel RGD, Torrie JH Principles and procedures of statistics, a biometrical approach. Chapter: Book Name. 1980 of publication; *McGraw-Hill Kogakusha*, Ltd.

Thiyagu K, Nadarajan N, Rajarathinam S, Sudhakar D, Rajendran K (2010). Association and path analysis for seed cotton yield improvement in interspecific crosses of cotton (Gossypium spp). *Electronic Journal of Plant Breeding*, 1(4): 1001-1005.

Ud Din ZM (2015). Genetic architecture of some insect resistant traits in upland cotton. MSc thesis.*University of Agriculture*, Faisalabad, Pakistan.

Yan W, Du M, Zhao W, Li F, Wang X, Eneji AE, Yang F, Huang J, Meng L, Qi H, Xue G (2019). Relationships between plant architecture traits and cotton yield within the plant height range of 80–120 cm desired for mechanical harvesting in the Yellow River Valley of China. *Agronomy*, 9(10): 587-594.

Yaqoob M, Fiaz S, Ijaz B (2016). Correlation analysis for yield and fiber quality traits in upland cotton. *Communications in Plant Sciences*, 6(3/4): 55-60.

Zafar Y, Asif M, Kausar A, Riaz S, Niaz M, Wahid A, Abbas SQ (2009). Development of genetic linkage map of leaf red colour in cotton (*Gossypium hirsutum*) using DNA markers. *Pakistan Journal of Botany*, 41(3): 1127-1136.