*Original Research Article*

# GENETIC STUDIES OF F2 POPULATION FOR FIBER AND YIELD RELATED ATTRIBUTES IN *GOSSYPIUM HIRSUTUM*

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**Abstract:** *Cotton (Gossypium hirsutum L.)is grown as a commercial crop throughout the world and it maintains the national economy of Pakistan. Genetic variation is ultimate necessity of plant breeder for the utilization of high yielding varieties to minimize the gap between production and demand. An experiment was conducted for the estimation of correlation, path coefficient analysis, principal component analysis and cluster analysis for yield components in cotton (Gossypium hirsutum L.). Four genotypes and twelve F2 hybrids planted in field by using the randomized complete block design with two replications. Collected Data was subjected to analysis of variance (ANOVA) to observed difference for all traits which showed significant differences among studied traits. Correlation studies revealed that boll weight and number of bolls per plant showed strong and positive correlation with seed cotton yield. Path coefficient analysis revealed that boll weight and number of bolls per plant had positive direct effects on seed cotton yield. Based on biplot analysis it was identified that FH-342 × FH-458 and AGC-501×VH-363 performed best for the boll weight, number of bolls per plant and seed cotton yield attributes. Dendrogram revealed genotypes under study were grouped in three clusters. Hence, selection for these characters will help in selecting genotypes with high yield and traits which contribute directly in cotton yield enhancement..*

**Keywords:** cotton, PCA, correlation, path coefficient, cluster

## Introduction

Cotton is the one of most important crops because it is largely cultivated on commercial area and popularly known as "white gold" (Kaleri *et al.*, 2021; Zafar et al. 2022; Abbas et al., 2015). More than 50 species of cotton have been found as cultivated species. Cotton is a large source of textile fiber.Climate change has a significant effect on cotton production. Numerous high-yielding cultivars lack the superior fibre quality required by the textile industry (Ali *et al.*, 2019). In the past decade, yield and quality have declined due to the current genotype's lack of genetic diversity (Nawaz *et al.*, 2019). Utilizing and enhancing the genetic variety of current germplasm is essential for producing the necessary genotypes (Shuli *et al.*, 2018). Breeding programmes should be used to expand the genetic diversity of cotton cultivars (Hafeez et al., 2021; Yehia and El-Hashash, 2022; Puspito et al., 2015). Utilizing genetic variety will facilitate the development of germplasm with desirable characteristics. Knowledge of the type and degree of genetic variety, genetic development, and heredity is essential for the selection of superior genotypes and the evaluation of the relationship between yield components and fibre quality (Latif *et al.*, 2015; Memon *et al.*, 2017).

Study of correlation plays a vital role for the development of cotton. It also shows the relationship between various characters and the yield contributing traits is the main focus for selection (Monicashree and Balu, 2018). Genetic development in seed cotton and lint yield can be improved with the help of correlation. To study the direct and indirect effect, path analysis plays the vital role which can't explain through correlation analysis (Baloch*et al.*, 2015). Yield is a very complex attribute. It is the total sum of all those characters which are controlled by poly-genes and have a complex type of gene interaction. Hence, it is necessary to know the traits that influence the seed cotton yield, directly or indirectly (Ali et al., 2013; Ali et al., 2014; Ali et al., 2016; Rehman *et al.*, 2020).

**Materials and Methods**

The present study was conducted to assess the genetic variability among 4 parents and their 12 $F_2$segregating populations that were obtained from Cotton Research Group, Department of Plant Breeding and Genetics, University of Agriculture Faisalabad (Table 1). This experiment is performed under RCBD with two replications. The climatic conditions during the crop period are represented in figure 1 and 2.

**Table 1: Experimental material**

| Code | Parents & $F_2$ Populations | Code | Parents & F2 Populations |
|------|------------------------------|------|---------------------------|
| **G1** | FH-458 | **G9** | AGC-501×VH-363 |
| **G2** | AGC-501 | **G10** | AGC-501×FH-342 |
| **G3** | VH-363 | **G11** | VH-363×FH-458 |
| **G4** | FH-342 | **G12** | VH-363×AGC-501 |
| **G5** | FH-458×AGC-501 | **G13** | VH-363×FH-342 |
| **G6** | FH-458×VH-363 | **G14** | FH-342 ×FH-458 |
| **G7** | FH-458 ×FH-342 | **G15** | FH-342×AGC-501 |
| **G8** | AGC-501×FH-458 | **G16** | FH-342×VH-363 |

At maturity data of the following attributes was taken. Plant height (PH), number of monopodial branches (MB), number of sympodial branches (SB), number of seeds per boll (SPB), number of bolls per plant (BPP), boll weight (BW), lint index (LI), seed index (SI), ginning out turn percentage (GOT), fiber uniformity (FU), fiber length (FL), fiber strength (FS), fiber fineness (FF), seed cotton yield (SCY)
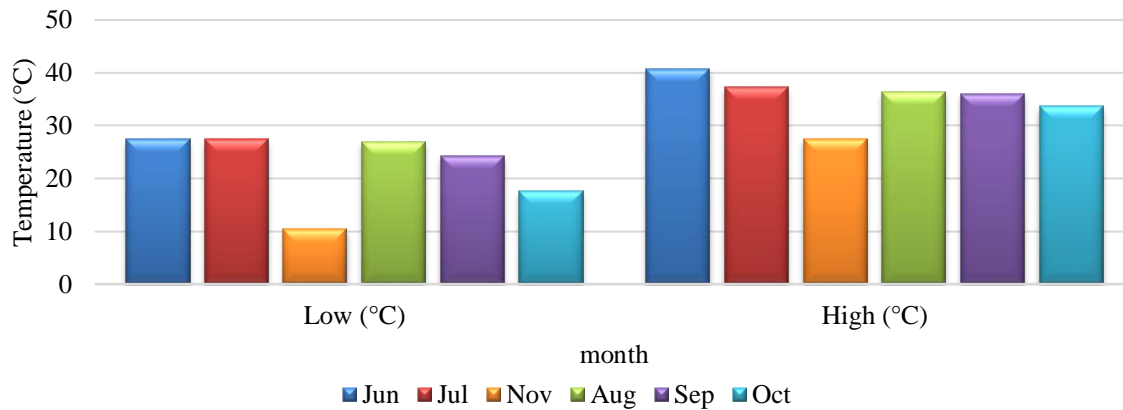


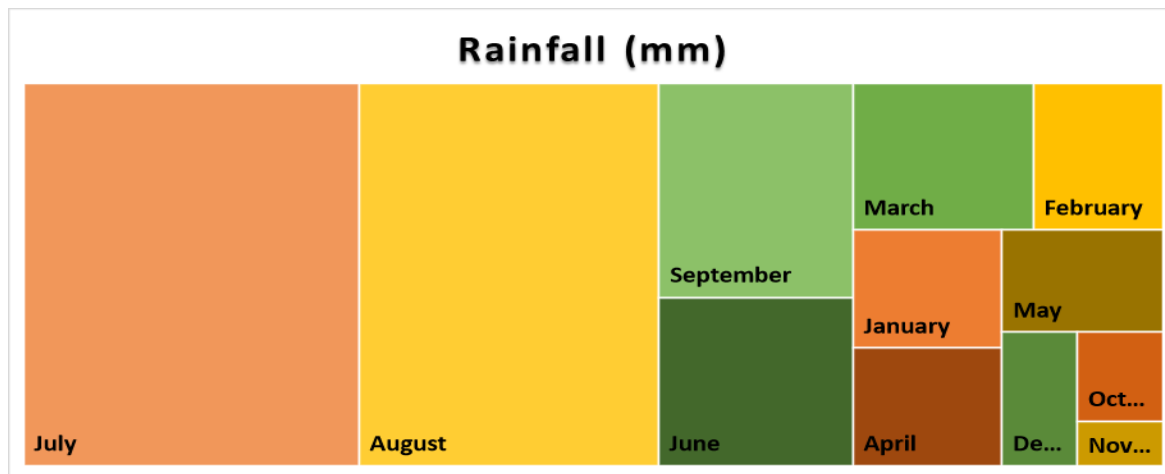**Figure 1: minimum and maximum temperature during crop period**



**Figure 2: Average rainfall during crop period**

**Result and Discussion**

Genetic diversity is of great importance as it offers a framework for utilizing genes to strengthen the desired traits (Begna, 2021; Govindaraj*et al.*, 2015). It helps in assessment of genotypes for devising breeding strategies, selection of diverse genotypes and prediction of genetic gain of the genotypes under study (Bhandari *et al.*, 2017; Mukhopadhyay and Bhattacharjee, 2016). Results of ANOVA manifested that all the genotypes were significantly different from each other as presented in Table 2.Percentage contribution of all the traits under study is presented in figure 3. A heat map is presenting the mean performance of all the genotypes under study for different attributes in figure 4. The correlation analysis (fig 5) revealed that BW and BPP were strongly positively correlated with SCY while SBP and FS strongly negatively correlated. LI and SI were strongly positively correlated with each other while FF is negatively correlated. Rehman *et al.* (2020) also noticed that SCY had a significant positive correlation with PH, BPP, SBP, and FS. The correlation study performed by Abdullah *et al.* (2016) revealed that PH, BPP, BW, FL, FS and FF had positive association with SCY. Rathinavel*et al.* (2017) also observed that SCY was significant and positively correlated with BPP followed by BW, PH, SI and FL. The results of current study are also in accordance with Memon *et al.* (2017) which observed that PH, BPP, BW and SI showed positive and significant associations with SCY. Kaleri *et al.* (2021) observed that SBP and BPP had a significant and positive association with SCY which are accordance with this study. Baloch *et al.* (2015) observed in correlation studies that SBP, BW with SCY. Thus, they suggested that selection for these traits will ultimately enhance the chances to increase SCY. Latif *et al.* (2015) and Monicashree and Balu (2018) revealed in their results that SCY had positive association with SBP, BPP and PHhence, selection for these characters will help in selecting genotypes with high yield.

Path matrix results in figure 6 depicted that BW and BPP had positive direct effects on SCY while PH, MB and SPB had negative direct effects. MB had positive direct effects on PH. FU positive direct effects on SB while it had negative direct effects on FL. Abdullah *et al.* (2016) also showed that BPP and

BW had direct positive effect on SCY and PH and GOT had direct negative effect on SCY. Memon *et al.* (2017) also observed that maximum positive direct effects to SCY were contributed by BPP, BW and SI. Latif *et al.* (2015) and Monicashree and Balu (2018) also observed the similar results of path analysis. Nawaz *et al.* (2019) also observed that FF, SI and BPP showed direct positive effects on SCY.

For breeding programs, understanding the genetic relationships between various types of germplasm is especially helpful. For precise plant genetic diversity studies, heterotic group assignment, and cross planning, this data can be used. For this purpose, the two most significant analyses which are commonly used are PCA and cluster analysis (Simasiku *et al.*, 2021). PCA results in figure 7 exhibited that G14 and G9 performed best for the BW, SCY and BPP attributes. Selection of these two genotypes will be led to better SCY with high BW and more BPP.G8, G7 and G4 depicted best for the FU and SB. G3 and G6 performed better for SI and LI. G1, G2, G11 and G12 performed worst so these genotypes will be neglected at the time of selection to boost up better performance for further breeding selection programs. Latif *et al.*(2015), Rathinavel (2019) and Yehia and El-Hashash (2022) also used PCA in their studies to classify and identify genotypes in diverse conditions.

Cluster analysis is a technique for categorizing and clarifying a sample of objects (or subjects) based on a number of distinct groups, while keeping objects within the same group similar (Jarwar *et al.*, 2019). Dendrogram results in figure 8revealed that under study genotypes mainly have three groups while G11 is separated from all these three groups. G1, G14, G9 and G12 fell in 1st group. G2, G5 and G10 fell in 2nd group. G3, G6, G4, G7, G15, G8, G13 and G16 fell in third group. These groups showed that the genotypes within group performed same behavior while one group performed different from the 2nd group. Rathinavel, (2019) also used cluster analysis and his results showed that 12 distinct clusters. Simasiku *et al.* (2021) observed 5 clusters of the genotypes under study while Jarwar *et al.* (2019) observe 3 clusters of 12 genotypes for different traits under study. On the basis of these characteristics, the members of a specific group or cluster can be chosen to maximize yield potential and fibre quality.

**Table 2: Analysis of variance for all the attributes**

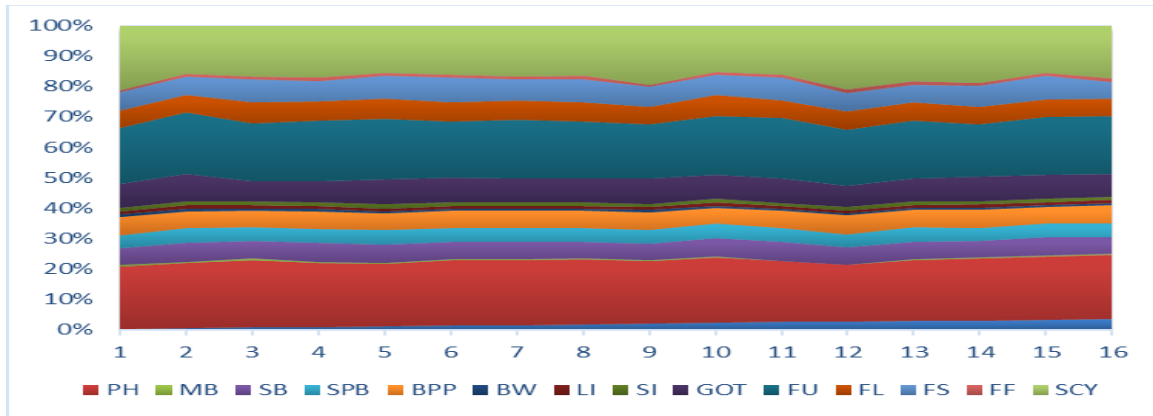| Source | DF | PH | MB | SB | SPB | BPP | BW | LI | SI | GOT | FU | FL | FS | FF | SCY |
|--------|-----|------|--------|--------|--------|--------|------------|------------|------------|-------------|------------|------------|-------------|------------|--------------|
| **Rep** | 1 | 0.66 | 0.05 | 0.53 | 1.13 | 1.05 | 0.10 | 0.30 | 0.30 | 5.80 | 5.20 | 7.03 | 5.45 | 0.01 | 129.75 |
| **Geno** | 15 | 33.12** | 0.20** | 1.14** | 0.74** | 6.62** | 0.09** | 0.18** | 0.18** | 13.67** | 7.60** | 5.07** | 24.00** | 0.73** | 223.85** |
| **Error** | 15 | 2.76 | 0.00 | 0.01 | 0.10 | 0.12 | 0.00 | 0.01 | 0.01 | 0.09 | 0.18 | 0.13 | 0.09 | 0.00 | 3.43 |

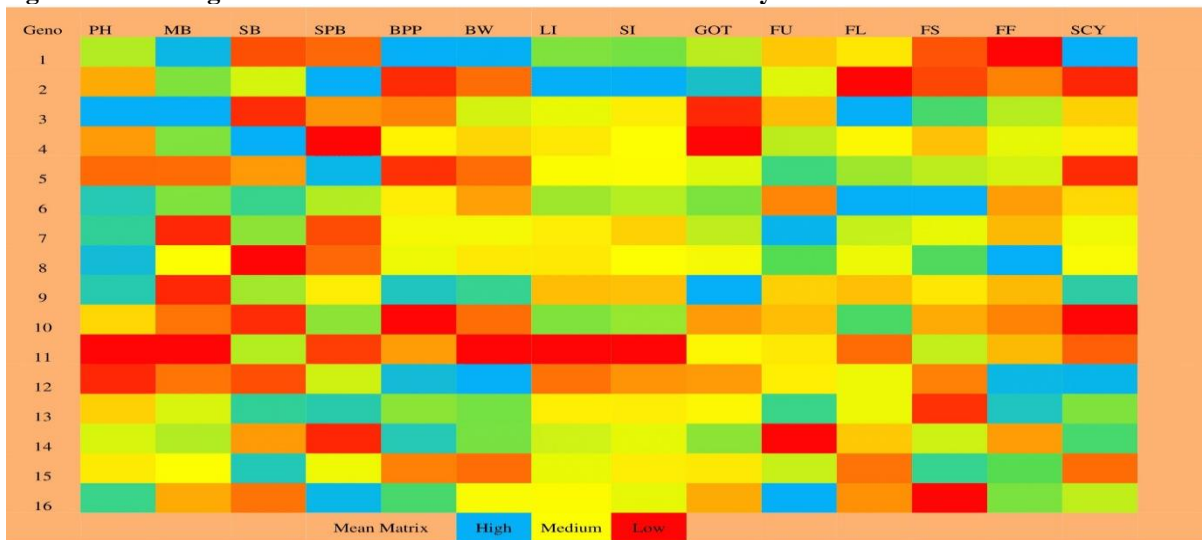**Figure3: Percentage contribution chart of all attributes under study**



**Figure4: Mean performance matrix of all the genotypes for various attributes under study**
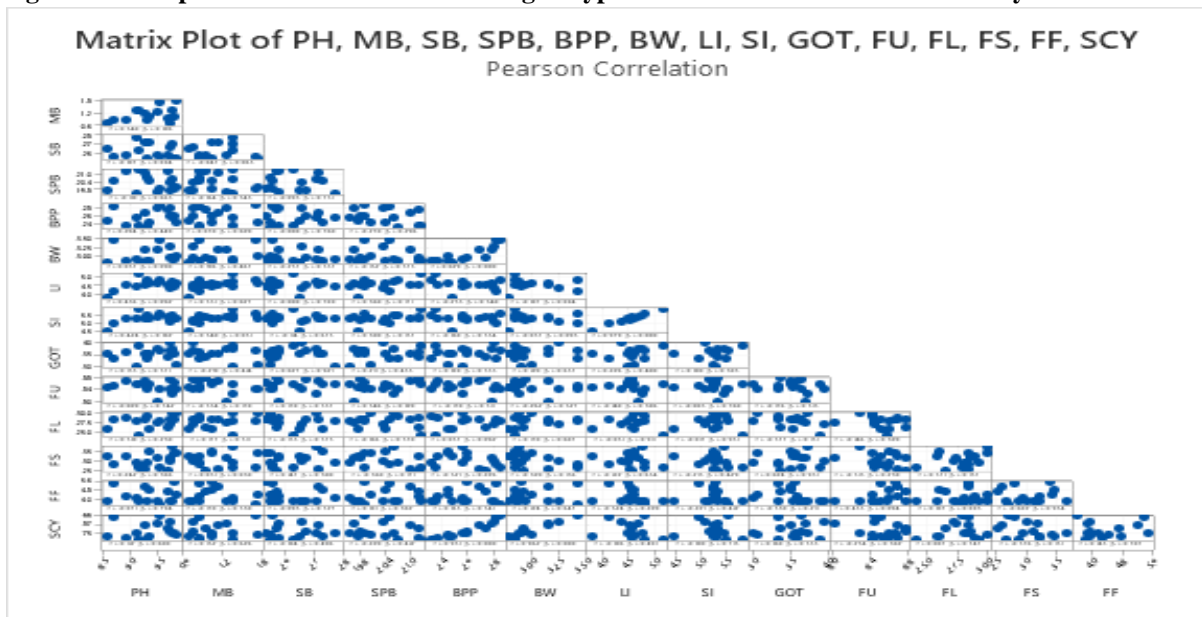


**Figure5: Correlation matrixof all attributes with SCY**

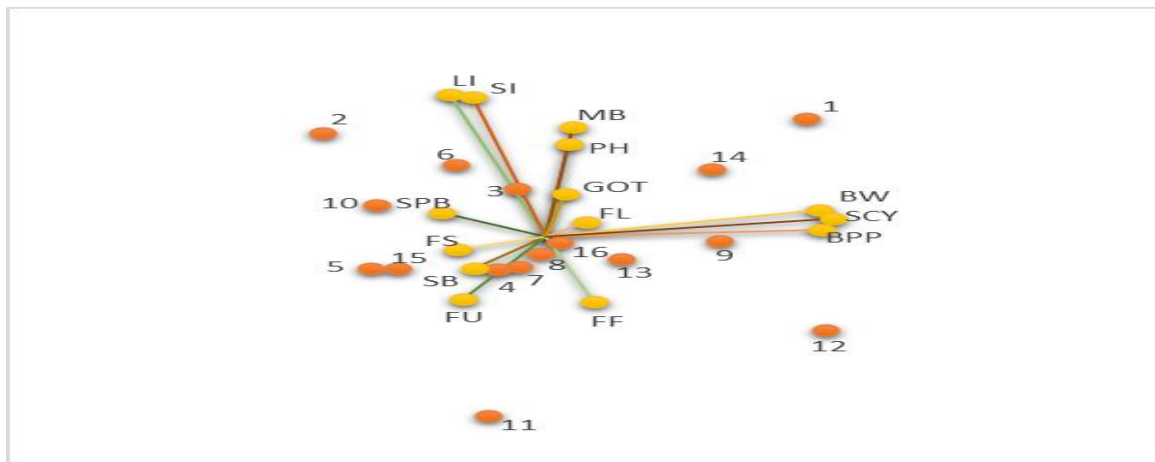**Figure6:Pathmatrix of all the attributes under study**



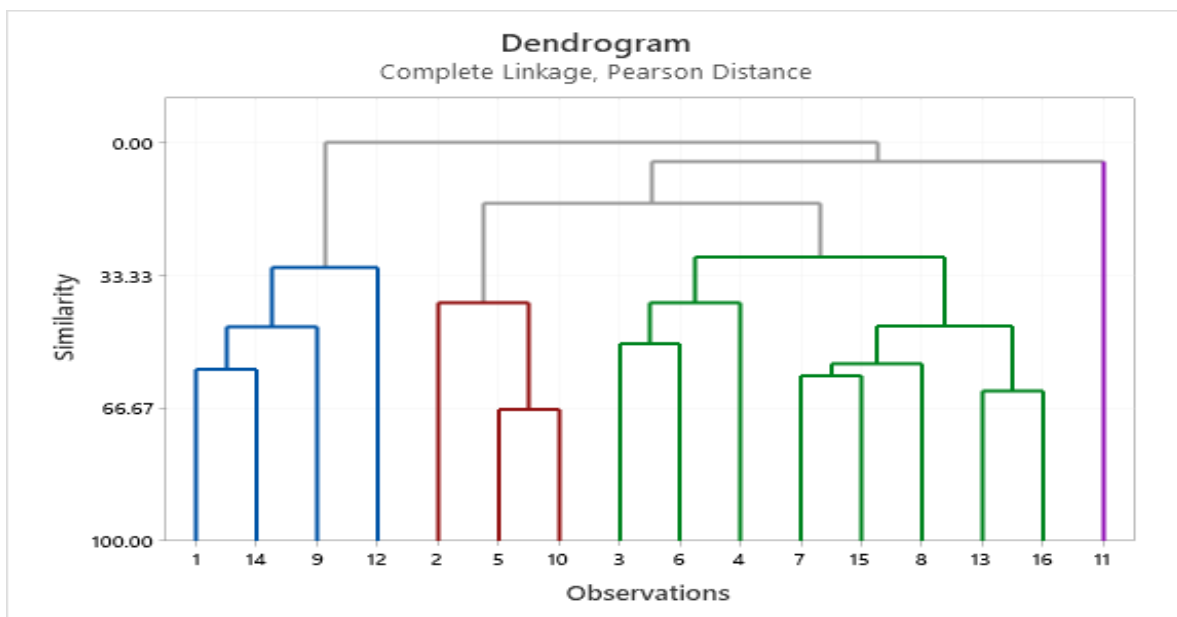**Figure 7:PCAgraphof all the genotypes & traits under study**



**Figure 8: Dendrogram for all genotypes**

**Conclusion**

From the above study it was concluded that BW and BPP showed positive association with SCY. Thus, the characters showing positive correlation with SCY may be further assessed through early generation selection. Based on biplot analysis it was conclude that FH-342 × FH-458 and AGC-501×VH-363 performed best for the BW, SCY and BPP attributes. Overall, characters including SCY, BPP, SBP and BW can be further used as selection criteria to increase the cottonseed yield in cotton.

**Conflict of interest**

The authors declared absence of conflict of interest.

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