

## Genotype × Environment Interaction for Fiber Quality and Yield Related Traits under Climatic Conditions of Dera Ghazi Khan Division

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### Recommended Citation

Aziz, I., Nazeer, W., Faheem, M., Basheer, M., Bukhsh, A., & Bilal, N. (2023). Genotype × Environment Interaction for Fiber Quality and Yield Related Traits under Climatic Conditions of Dera Ghazi Khan Division, *Journal of Bioresource Management*, 10 (3).

ISSN: 2309-3854 online

(Received: Nov 22, 2022; Accepted: Aug 25, 2023; Published: Sep 30, 2023)

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## GENOTYPE × ENVIRONMENT INTERACTION FOR FIBRE QUALITY AND YIELD RELATED TRAITS UNDER CLIMATIC CONDITIONS OF DERA GHAZI KHAN DIVISION

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### ABSTRACT

Cotton (*Gossypium hirsutum* L.) is a fibre and oilseed crop and offers raw materials to industries and livelihood for the rural poor. During the last decade, climate change has negatively affected crop production all over the world. Under such scenarios of climate change, plant breeders must explore the genetics of crops for better yield and fibre quality. Considering the Extent of Cotton in Pakistan's economy, the present research was planned to evaluate six cotton varieties in different locations for yield stability. Six varieties namely IUB-13, CIM-600, S-32, FH-Lalazar, CIM-616 and Z-33 were surveyed at farmer fields in Rajan Pur, D G Khan and Muzafargarh districts. Data was collected for plant height, fruiting branches per plant, days to flower opening, boll shedding percentage, bolls per plant, boll weight, locules per boll, G.O.T. % age, seed cotton yield, fibre fineness, fibre length, fibre strength, and fibre uniformity. The Collected data was subject to analysis of variance and all the under-examined traits showed significant results except for No. of locules per boll, GOT % age, seed cotton yield, fibre fineness, fibre strength, fibre length and fibre uniformity ratio. In case of overall mean value of seed cotton yield. Genotype G-3 (S-32) showed maximum seed cotton yield in all three locations and thus declared as the highly stable genotype compared with all other genotypes.

**Keywords:** Cotton, environmental effect, genotype × environment, ammi analysis, fibre quality traits.

### INTRODUCTION

Cotton is a profitable crop in Pakistan after wheat and also known as "White Gold ". It is an important crop that plays a pivotal part in social, political, and economic affairs globally (Kairon et al., 2004). Cotton is a commercial crop, and it produces significant fibre globally. It is an annual crop and is cultivated worldwide mainly for fibre, but cotton seeds are also used as feed for animals (Constable and Bange, 2015). Pakistan fulfils the 18.8 % demand for vegetable oil through cotton seeds. The protein contents in cotton seed ranges from 27-45 % and oil content from 9.7 to 12.89 % (Kumar et al., 2023).

*Gossypium hirsutum* L. (upland cotton) is a valuable spinnable fibre and oilseed entity that offers raw materials to the industry as well as a source of income for the rural poor. Globally, cotton has been growing in more than 70 countries (Voora et al., 2020). In Pakistan, it is mainly grown in Sindh and Punjab. Pakistan is a major cotton-growing country and exports cotton and cotton-based products. There is a huge demand for cotton at national and international markets, and to fulfil the demand, need to increase the yield of cotton with help of good agronomic methods and breeding approaches. To earn more foreign currency, better fibre quality and yield are important factors (Sajjad et al., 2015).

The contribution of cotton to the textile industry with respect to national earnings is about 55 % of foreign exchange (Fortucci, 2002). Pakistan's textile sector is the largest sector of the country which has about four hundred textile mills, three hundred oil expellers and one thousand ginneries. Cotton provided raw material to all these sectors (Govt. of Pakistan, 2009). Being a significant impact on GDP, it is rightly called as a major cash crop for Pakistan. Cotton contributes about 0.8 % to the GDP of Pakistan and adds its value to the agriculture sector and it contributes 4.1 per cent to agriculture. Cotton is cultivated over an area of 2373 thousand hectares and last year it increased by 6.5 % and 2527 thousand hectares (Economy survey of Pakistan, 2019-20). The production of cotton is projected at about 9.18 m bales, which is lower by 6.8 % over the previous year's production of 9.82 m bales (Economy survey of Pakistan, 2019-20).

Crop production is dependent on genotype and the provided environment where the crop has grown (Gul *et al.*, 2014). G x E interaction and its impact on genotypes helps in selection of multi-environment stable genotypes. That's the need of research to study G x E interaction which gives the profile of better parents for selection having novel trait of stable yield with regard to environment.

The present study was planned to evaluate cotton genotypes under three distinct locations for the determination of G × E interaction. Assessing genotype adaptability in a specific location and yield stability in terms of yield, yield components, fibre quality traits. To make the analysis better it is important to perceive the genotype response pattern to the environment, furthermore, the G x E interaction helps to measure the specific genotype productivity against the environment. G x E interaction (GEI) helps the breeder to develop the crop which is suitable for the specific environment which helps to achieve the

goal of high yield. The study focuses on measuring the G x E interaction, and its effect on the adaptability and stability of different genotypes. The study further leads to determining the components of yield and fibre quality traits in different cotton genotypes.

## MATERIALS AND METHODS

### *Study Site and Research Material*

G x E interaction study in cotton genotypes was carried out at three different locations i.e., Dera Ghazi Khan, Rajanpur, and Muzaffargarh districts in 2020. The experimental material consisted of six cotton varieties/genotypes viz., IUB-13, CIM-600, S-32, FH-Lalazar, CIM-616 and Z-33 (Table 1). The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. From each site, thirty plants of each genotype were selected.

**Table 1: List of genotypes under study**

| Sr.# | Genotype | Sr.# | Genotype   |
|------|----------|------|------------|
| 1    | IUB-13   | 4    | FH-LALAZAR |
| 2    | CIM-600  | 5    | CIM-616    |
| 3    | S-32     | 6    | Z-33       |

### *Data Collection*

Data were taken from randomly selected ten plants from each replication of different experimental sites. Data were collected for the various morphological traits (Plant height (cm), Days to first flowering, No. of fruiting branches per plant, No. of locules per boll, Seed cotton yield (gm), bolls per plant, boll weight (gm) No. of locules per boll and lint % and fibre quality traits i.e., fibre fineness ( $\mu\text{g}/\text{inch}$ ), fibre length (mm), fibre strength (g/tex) and fibre uniformity ratio ( % ). Fibre quality traits were calculated using HVI-900 at the Fibre Technology Department, University of Agriculture, Faisalabad. Mean values calculated from

each genotype were further subjected to statistical analysis.

Formula for Lint % calculation:

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

### **Statistical Analysis**

The collected data were treated to analysis of variance (ANOVA) defined by (Steel & Torrie, 1997) and the G × E interaction study done by the AMMI model (Gauch and Zobel, 1996).

## **RESULTS AND DISCUSSION**

### **Analysis of Variance**

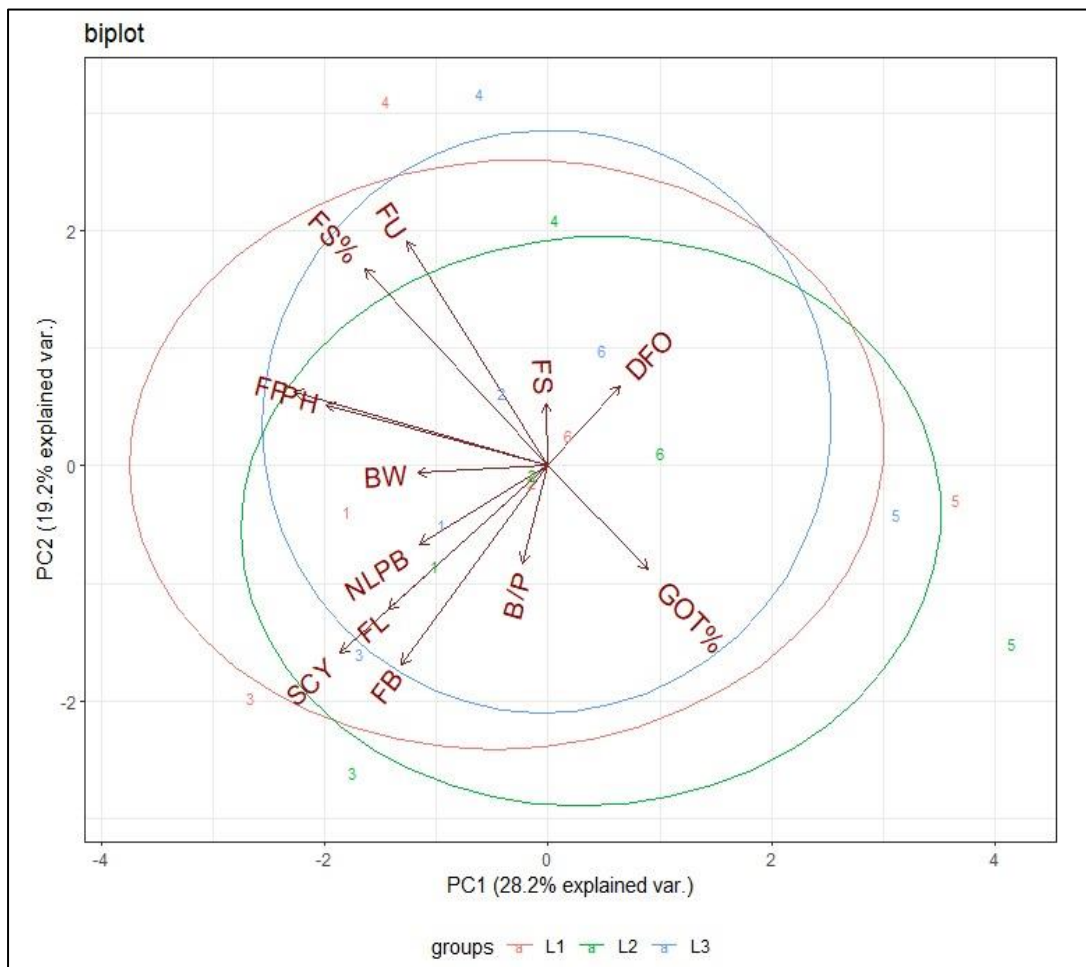
Table 2 showed the results of analysis of variance in different traits of cotton. Genotypes exhibited significant differences for plant height, whereas significant for environment and G × E interaction as described by, Dewdar, (2013), Gul et al., (2014). Days to first flowering had substantial differences for the genotypes, G × E interaction and significant for environment as reported by Esmail, (2007) Gul et al., (2014) & Maleia et al., (2017). Flower shedding percentage showed highly significant differences for genotypes, significant for environment and non-significant for G × E interaction as discussed by Rahman et al., (2017), Mukoyi et al., (2018) and Simasiku et al., (2020). Number of fruiting branches showed highly significant for genotypes and environment while non-significant for G × E interaction as reported by Zeng et al., (2014), Singh et al., (2014) and Zubair et al., (2018). Number of bolls per plant showed significant differences for genotypes and highly significant differences for environment and significant differences for G × E

interaction as described by Gul et al., (2014) and Lingaiah et al., (2020). Number of locules per plant also had substantial differences for environment while non-significant for genotypes and G × E interaction as published by Khan et al., (2015) and Ahmad et al., (2019). Boll weight (gm) enclosed highly significant differences for environment while significant for genotypes and G × E interaction as reported by Meredith *et al.* (2012), Abbas et al., (2013) and Singh et al., (2014). Ginning out turn percentage (GOT %) showed significant differences for environment, while non-significant differences for genotypes and G × E interaction as discussed by Mudada et al., (2017) and Balcha et al., (2019). Seed cotton yield showed highly significant differences for genotypes while non-significant for environment and G × E interaction as reported by Gul et al., (2014) Mudada et al., (2017). Fibre fineness showed significant differences for genotypes while non-significant for environment and G × E interaction as published by Singh et al., (2014), and Greveniotis et al., (2018). Fibre strength showed significant differences for genotypes while non-significant for environment and G × E interaction as discussed Singh et al., (2014) and Sadabadi et al., (2018). Fibre length showed significant differences for genotypes while non-significant for environment and G × E interaction. Smith et al., (2010) and Saidabad et al., (2018) found that fibre length varies due to environment. Fibre uniformity ratio showed significant differences for genotypes while non-significant for environment and G × E interaction as found by Kamran et al., (2018) and Maleia et al., (2019).

**Table 2: Analysis of variance for different traits of cotton under Genotypes × Environment**

| SOV                     | DF | PH            | DFE         | FSP               | NFB               | NB/P        | NL/P       | BW          | GOT %              | SCY               | FF                | FS                 | FL                     | FU R                  |
|-------------------------|----|---------------|-------------|-------------------|-------------------|-------------|------------|-------------|--------------------|-------------------|-------------------|--------------------|------------------------|-----------------------|
| Genotypes               | 5  | 1827.1<br>3** | 30.9<br>2** | 433.6<br>**       | 92.62<br>**       | 42.50<br>** | 0.29<br>NS | 1.40*       | 4.13 <sup>NS</sup> | 4715.<br>54**     | 1.16<br>*         | 8.18*              | 22.7*                  | 75.8<br>1*            |
| Environment             | 2  | 420.29<br>*   | 44.0<br>5*  | 45.37<br>*        | 38.51<br>**       | 300.1<br>** | 0.82<br>*  | 13.76<br>** | 7.71*              | 4.2 <sup>NS</sup> | 4.3 <sup>NS</sup> | 4.28 <sup>NS</sup> | 4.<br>28 <sup>NS</sup> | 1.6 <sup>N</sup><br>s |
| Genotypes × Environment | 10 | 190.09<br>*   | 68.3<br>1** | 7.3 <sup>NS</sup> | 9.7 <sup>NS</sup> | 43.10<br>*  | 0.39<br>NS | 0.58*       | 5.16 <sup>NS</sup> | 1.4 <sup>NS</sup> | 8.1 <sup>NS</sup> | 8.8 <sup>NS</sup>  | 1.6 <sup>NS</sup>      | 7.3 <sup>N</sup><br>s |
| Replications            | 6  | 45.87         | 26.8        | 13.46             | 0.54              | 0.09        | 0.01       | 0.038       | 0.58               | 0.37              | 0.09<br>2         | 3.5972             | 2.743                  | 4.61<br>6             |
| Error                   | 30 | 77.36         | 13.3<br>2   | 12.01             | 0.72              | 15.20       | 0.30       | 0.21        | 3.44               | 1.44              | 0.12<br>71        | 11.114             | 2.37                   | 13.7<br>34            |

\*,\*\* **Abbreviations:** *SOV*= Source of Variance, *PH*=Plant Height, *DFE*=Days to first flowering, *FSP*= Flower shedding percentage, *NFB*= No. of Fruiting branches, *NB/P*= No. of bolls per plant, *NL/P*= No. of locules per plant, *BW*= Boll weight, *GOT %*=Ginning out turn percentage, *SCY*=Seed cotton Yield, *FF*=Fibre Fineness, *FS*=Fibre Strength, *FL*=Fibre Length, *FUR or FU*= Fibre uniformity Ratio



**Figure 1: AMMI Biplot analysis of six cotton genotypes for plant height (PH), days to first flower open (DFO), fibre strength (FS), fruiting branches (FB), number of bolls per plant (B/P), number of locule per boll (NLPB), boll weight (BW), ginning out turn % (GOT % ), seed cotton yield (SCY), fibre fineness (FF), fibre strength (FS), fibre length (FL) and fibre uniformity (FU). The arrows showed the correlation among the traits.**

### ***Ammi Biplot Analysis among Different Yield Contributing Traits of Cotton***

The Ammi biplot analysis was performed to check the interaction of genotype and location (Fig.3.1). The biplot analysis revealed 28.2 % of total explained variability in the PC1 and 19.2 % of total explained variability in the PC2. It was clear from the biplot analysis that plant height, number of fibre strength, days to flowering, fibre strength and fibre uniformity positively correlated, while number of bolls per plants, number of locules per boll, boll weight, fruiting branches per plant, fibre length and seed cotton yield. It was observed that the genotype 4 (FH-LALAZAR) showed highest OP vector for fibre strength and fibre uniformity in all three locations suggesting that this genotype is highly stable and best for these traits in all three locations, while the genotype 5 (CIM-616) fall away from the OP vector in the negative side thus this genotype is poor performer for these traits in all three locations. The genotype 6 (Z-33) showed more OP vector for days to flower opening and fibre strength in all three location and recommended as best for these traits, while the genotype 3 (S-32) showed OP vector on the negative side thus declared as poor performer for these traits in all three locations. The genotype 3 (S-32) showed high OP vector for number of bolls per plants, fruiting branches per plant, fibre length and seed cotton yield and recommended as the best and highly stable genotype for these traits in all three locations, while the genotype G-6 (Z-33) showed negative OP vector thus recommended as poor genotype for these traits. The genotype G-1 (IUB-13) shared more OP vector for plant height, number of locule per boll and boll weight in all three locations thus recommended as best genotype for these traits, while the genotype G-5 (CIM-616) is the poor performer for these traits in all three locations. In case of overall mean

performance of seed cotton yield the genotype G-3 (S-32) showed maximum seed cotton yield in all three locations and thus declared as the highly stable genotype compared with all other genotypes.

### **CONCLUSION**

The biplot analysis revealed 28.2 % of total explained variability in the PC1 and 19.2 % of total explained variability in the PC2. It was clear from the biplot analysis that plant height, number of fibre strength, days to flowering, fibre strength and fibre uniformity was positively correlated, while number of bolls per plants, number of locules per boll, boll weight, fruiting branches per plant, fibre length and seed cotton yield. In case of overall mean performance of seed cotton yield the genotype G-3 (S-32) showed maximum seed cotton yield in all three locations and thus declared as the highly stable genotype compared with all other genotypes.

It was concluded that the traits showing the positive association with seed cotton yield may be vital and useful for future breeding approach and should take care while selection the traits having negative corelated to seed cotton yield. It was observed genotypes showing better performance in all three locations may be used to develop the new genotypes for the improved grain yield and wider adaptability.

### **AUTHORS COMTRIBUTION**

All authors contributed equally.

### **CONFLICT OF INTERESTS**

All concerned authors declare no conflict of interests either financial or personal relationships regarding this manuscript.

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