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Research Article

INFESTATION OF DIFFERENT INSECT PESTS ON NOVEL COTTON CULTIVARS AND THEIR IMPACTS ON COTTON FIBER QUALITY PARAMETERS

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Abstract

Pakistan is the 5th largest producer of cotton in the world. Exports of cotton and textile products have a share of around 60 percent in overall exports of the country. A field experiment was conducted to evaluate the different fiber quality parameters in relation to different insect pest populations. The introduction of this new types of cultivars may satisfy the needs of farmers for better quality and quantity, laborers who harvest crops, and other investors, including those in the cotton sector. A field research was carried out at the Cotton Research Station, Faisalabad, Pakistan, during the year 2023 cotton cultivars (VH-447, FH-1133, BH-228, SLH-94, MNH-S GOLD, BH-227, FH-1214, MNH-1095, VH-442, MNH-1090, RH-BAGHO BAHAR, MNH-1050, and MNH-TP) were evaluated for resistance to sucking pests such as whitefly (*Bemisia tabaci)*; jassid (*Amrasca biguttula biguttula)*; and thrips (*Thrips tabaci)* as well as bollworms such as pink bollworm (*Pectinophora gossypiella)*; spotted bollworm (*Earias insulana*; *E. vitelli)*; and American bollworm (*Helicoverpa armigera)*. There were notable variations across the genotypes in terms of the population of sucking and bollworm insect pest infestation, which lowers cotton production and negatively affects fiber quality. FH-1133 showed the lowest average populations of thrips (1.00/leaf), jassid (0.27/leaf), and whiteflies (2.00/leaf), indicating the highest resistance. The average population (9.84%) of pink bollworm larvae in residual boll. The virus percentage on different cotton genotypes recorded after 30, 60, 90, and 120 days was 0.00, 9.00, 14.00, and 19.00%, respectively. The cultivar FH-1133 was observed to be good for all other genotypes of cotton due to its yield (2372.50 kg/acre), and it had the following lint quality attributes: GOT (46.50%), staple length (28.50 mm), fiber fineness (4.70 µg/inch), and fiber strength (33.20 g/tex).

Keywords: Cotton variety; fiber characteristics; plant characteristics; Insect pest infestation

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1. INTRODUCTION

Cotton, *Gossypium hirsutum* (L.), well-known as “white gold” is an essential cash crop of Pakistan for upholding the economy and is conventionally grown in agricultural plains of Punjab and Sindh territories (Ali *et al.*, 2022). Pakistan ranks 13th in the world for yield per acre and is the fifth largest producer of cotton in the world. It is also the world's top exporter of yarn and the third-largest exporter of raw cotton (Shar *et al.*, 2021). However, a number of biotic and abiotic variables contribute to the loss in cotton output; among the biotic ones, insect pests are the main limiting factor that negatively impacts the cotton crop. Sucking and chewing bugs are two of the most destructive pests to cotton crops (Hussain *et al.*, 2023). A wide variety of sucking pests devastate cotton plants, and the state of the pest problem is ever-changing. The main hazard to the cotton crop is sucking pests like leafhoppers, aphids, thrips, and whiteflies, and the majority of these insects have become resistant to several conventional pesticides (Shera *et al.,* 2020). The morphological changes in the plant system also favors decreased reproduction of insect pests.

A significant fiber crop that is essential for the development of the textile industry is *Gossypium hirsutum* L. (Anwar *et al.,* 2022). In Pakistan, the industry's constant goal to boost a nation's economy is the need for extra-long, strong fiber with a shining colour. It sustains and adds roughly 0.6% of GDP and 3.1% of agricultural value to the textile industry (Dea, 2023). Due to a number of issues such as Resurgence, Resistance and Residue aspects, Pakistan, a major cotton producer (ranked fifth in the ICAC), is witnessing a marked reduction in the production of main kinds of cotton crops (Nazeer *et al.,* 2023). In Punjab, cotton cultivars are certified according to standards for fiber quality, which include a micronaire of 3.8 to 4.9, a length of 28 mm, and 25 g/tex (fiber strength) and above. Every year, a range of upland cotton types are made available to producers (Hussain *et al.,* 2022). Increases in cotton output per acre, boll size and weight, fiber length and strength, lint colour, drought resilience, decreased pest infestation, and temperature tolerance are all crucial for meeting export criteria for cotton quality and quantity (Ali *et al.,* 2019). Differentiating factors for these cultivars include fiber chattels, plant nature, maturity index, yield, and additional features including herbicide as well as insect opposition environmental adaptability and transgenes (Hussain *et al.,* 2022). Multilocation cotton varietal trials are conducted by public and commercial entities to evaluate yield and fiber quality characteristics and support producers. Modern textile makers are searching for cotton fibers that are longer, more-stronger, highest finer, and much more consistent. Compared to traditional ring spinning technologies, modern high-speed yarn manufacturing processes at the highest spinning speeds have distinct criteria for fiber quality (Tesema, 2024). Due to this factor, processors are forced to use cotton fiber with greater strength while making yarn. Spinning mills for textiles are always searching for ways to increase the ratio of quality to cost. They also have to figure out processing ratios, which are made by mixing fibers from many bales that have comparable qualities. Although cotton growers may notice variations in the fibers' characteristics, like colour fluctuation, no technology can forecast the quality metrics such as the boll develops (Tan *et al.,* 2013; Tang *et al.,* 2015). No database model, as well as an otherwise orientation source exists to predict how genetic and atmospheric alterations might be adjusted to the growing environment of cotton plants. It is essential to comprehend how soil and climate impact different cotton cultivars. The properties of the seed or fiber can influence the quality of cotton. Still, it is usually associated with fiber characteristics (Elmogahzy and Farag 2018). Because there is now more rivalry between countries for cotton production and consumption, the quality of the fiber has increased as well as technological advancements in the yarn-making process. The quality of cotton fiber can be enhanced by postharvest distribution, genetics, and crop management. To create options for improvement, it is essential to comprehend how fiber properties affect processing as well as how their relationships, inheritance, and environmental factors affect them. Enhancing dimensions of fibers or fiber length as well as strength has historically been the main focus of breeding to improve fiber quality for yarn production systems. The environment causes variability in fiber characteristics, making it difficult to improve them by breeding or biotechnological methods. Variability in fiber quality makes it difficult to process fiber, thus biotechnological future and breeding techniques should simultaneously improve fiber qualities and reduce varietal variation (Gudi *et al.*, 2024).

The goal of the current study project was to examine how variations in fiber quality characteristics, both geographically and varietally, affect yarn metrics in the finished product. Nowadays, cotton is produced by farmers using high-yielding cultivars without taking into account the fiber's qualities, forcing textile mills to import cotton in order to obtain cotton with superior fiber qualities. This study's primary goal is to investigate how newly produced cotton varieties behave differently depending on the surrounding environment.

2. Materials and Methods

Structural variants contribute to a large fraction of genomic variation and have long been implicated in phenotypic diversity and that replace the existing genotypers. Thirteen auspicious cotton genotypes, viz. VH-447, FH-1133, BH-228, SLH-94, MNH-S GOLD, BH-227, FH-1214, MNH-1095, VH-442, MNH-1090, RH-BAGHO BAHAR, MNH-1050, and MNH-TP (Table 1) were sown using a Randomized Complete Block Design with three replications on May 27, 2023, at the Cotton-Research-Station, (CRS) Faisalabad, Pakistan. The dimensions of the net plot were 20 by 10 feet, with a 75 cm row and 30 cm plant spacing (Munir *et al.*, 2015). The suggested field procedures were followed.

TABLE 1: DESCRIPTION OF VARIOUS COTTON GENOTYPES

S/No.	Genotypes	Description of Institutes	Locations/cities
1	VH-447	Cotton Research Station, Vehari	Vehari
2	FH-1133	Cotton Research Station, Faisalabad	Faisalabad
3	BH-228	Cotton Research Institute, Bahawalpur	Bahawalpur
4	SLH-94	Cotton Research Institute, Sahiwal	Sahiwal
5	MNH-S GOLD	Cotton Research Institute, Multan	Multan
6	BH-227	Cotton Research Institute, Bahawalpur	Bahawalpur
7	FH-1214	Cotton Research Station, Faisalabad	Faisalabad
8	MNH-1095	Multan Cotton Research Institute, Multan	Multan
9	VH-442	Vehari Cotton Research Station, Vehari	Vehari
10	MNH-1090	Cotton Research Institute, Multan	CRI, Multan
11	RH-BAGHO BAHAR	Cotton Research Station, Khanpur	Khanpur
12	MNH-1050	Cotton Research Institute, Multan	Multan
13	MNH-TP	Cotton Research Institute, Multan	Multan

2.1. Data on population of sucking pests:

Starting on July 18 and lasting until September 24, 2023, the number of adult and juvenile thrips, adult whiteflies, and jassid per leaf was counted early every week. Out of the fifteen plants in total, fifteen leaves were randomly selected for each plot. The leaves were seen in the following order: first leaf from upper third of first plant, second leaf from center of second plant, third leaf from lower half of third plant, and so on. Using basic mathematical techniques, the average population/leaf of sucking pests for each genotype was calculated using the following formula:

$$Y = \frac{Y1 + Y2 + \cdots Y15}{N}$$

Where: N = Leaves in Total numbers,

Y = Leaves (mean number), as well as

Y1+Y2+, ···· +Y15 = Leaves (counting observed)

2.2. Number of American and Spotted Bollworms:

Twelve randomly selected plants in each plot were used to count the larvae of spotted, American, and pink bollworms. There were fresh rosette flowers observed each week. Using the aforementioned formula, the simple arithmetic means were used to get the average population per plant.

2.3. Number of Pink Bollworms (PBW):

After removing every remaining boll from each plot and storing them in a lab for three to four days, the population of PBW larvae in the leftover or infested bolls was counted. Following that time, the bolls were cut apart with a knife to reveal the pink bollworm larvae. The formula was used to determine the percent larvae.

$$\% \text{ damage} = \frac{number\ of\ pink\ bollworms\ infested\ bolls}{total\ number\ of\ bolls}\ x\ 100$$

2.4. Pesticide application:

Table 2. Data regarding population of sucking pest per leaf during 2023

S/No.	Name of genotypes	Average of sucking pests per leaf		
		(Jassid)	(Whitefly)	(Thrips)
		Mean±SE	Mean±SE	Mean±SE
1-	VH-447	0.60± 0.01d	12.07± 0.03b	6.13± 0.05a
2-	FH-1133	0.27±0.02e	2.00±0.27f	1.00±0.06e
3-	BH-228	0.66± 0.01cd	9.73±0.47b	4.87± 0.09bc
4-	SLH-94	0.93± 0.02abc	2.20±0.15f	1.00±0.08e
5-	MNH-S GOLD	0.80± 0.04abc	2.53±0.15ef	0.13±0.01e
6-	BH-227	0.72± 0.01bcd	3.00± 0.03def	0.33±0.02e
7-	FH-1214	0.92±0.03a	2.67±0.05ef	0.40±0.00e
8-	MNH-1095	0.27±0.01e	15.20±0.55a	0.53±0.02e
9-	VH-442	0.86±0.01ab	6.80±0.15c	0.87±0.03e
10-	MNH-1090	0.40±0.03e	2.20±0.08f	2.27±0.25d
11-	RH-BAGHO BAHAR	0.39±0.01e	4.87±0.19cde	5.27±0.18ab
12-	MNH-1050	0.65±0.02cd	5.20±0.16cd	3.93±0.08c
13-	MNH-TP	0.61±0.02d	2.93±0.11def	2.40±0.09d
F-Value		40.12	84.0	135.01
Tukey's HSD Value at 0.05%		0.19	2.42	0.94

Tukey's HSD at P = 0.05 indicates that means with comparable letter distributions are not substantially different; HSD = Honestly Significant Difference * indicates significance at P < 0.05 and ** indicates significance at P < 0.01.

When the numbers of sucking insects rise beyond the ETL threshold, the crop was routinely treated with insecticides at the required amount.

2.5. Yield:

Each genotype's overall yield was measured, documented, and stored separately. After that, convert it to yield per acre by keeping the plant population constant.

2.6. Cotton leaf curl virus (CLCuV) prevalence:

Throughout the season, all healthy and afflicted plants/plots were counted to determine the incidence of CLCuV. Using the formula, the proportion of viruses was determined (Klap *et al.,* 2020).

$$\text{Virus percentage} = +\frac{Virus\ infestated\ plants}{Total\ number\ of\ plants}\ x\ 100$$

2.7. Fiber characteristics:

After the crop reached full maturity, the seed cotton was carefully selected and let dry in the sun. Following that, a sample was obtained from each genotyping repetition. A small experimental ginning machine was used to gin these samples. The formula used to determine the ginning out turn % was as follows:

$$\text{Ginning out turn (GOT)\%} = \frac{Lint\ weight}{weight\ of\ seed\ cotton}\ x\ 100$$

Each sample was given forty grams of lint, along with an envelope into the paper containing a respected genotype name and ginning number, to the CRS fiber testing laboratory in Faisalabad. From there, the samples were subjected to various fiber quality analyses, including GOT (%), staple length (mm), fiber fineness (micro g/inches), and fiber strength (g/tex), utilizing the HVI spectrum-1 device (USA-made, manufactured by an Uster firm).

2.8. Statistical analysis:

Statistix software (version 8.1; Lawes Agricultural Trust Rothamsted Experimental Station, Rothamsted, UK) subjected the data to analysis of variance (ANOVA). The means were split using Tukey's HSD (Honestly Significant Differences) (Karar *et al.,* 2016).

3. RESULTS

3.1. Number of sucking pests in the population

Evaluation of cotton genotypes for CLCuV prevalence and host-plant resistance to insect pest complex. According to the results, there were extremely significant differences (F=40.12; df=12, 24; P<0.00; Table 2) in the jassid population of various cotton types belonging to different research institutions. The most jassid were identified on SLH-94, with 0.93 leaf-1; this was statistically close to genotypes FH-1214, VH-442, and MNH-S GOLD, which had 0.92, 0.86, and 0.80 jassid per leaf, respectively, and BH-227, which had 0.72 jassid per leaf. Following MNH-TP and VH-447 with 0.61 and 0.60, the genotypes BH-228 and MNH-1050 had a statistically similar population of jassid leaf-1, with 0.66 and 0.65. MNH-1090 (0.40/leaf), RH-BAGHO BAHAR (0.39/leaf), MNH-1095 (0.27/leaf), and FH-1133 (0.27/leaf) had the lowest documented populations of jassid per leaf, and these populations are statistically equivalent to one another.

Table 3. Data regarding population of bollworms per plant on various genotypes of cotton during 2023

S/No.	Name of genotypes	Average population of bollworms per plant			Average percent population of pink bollworms larvae in leftover boll
		Earias spp. Larvae	*Heliothis* spp. Larvae	Rosette flowers	
		Mean±SE	**Mean±SE**	**Mean±SE**	**Mean±SE**
1-	VH-447	0.00±0.00b	0.00±0.00b	0.00	77.27±3.54a
2-	FH-1133	0.00±0.00b	0.00±0.00b	0.00	9.84±3.57c
3-	BH-228	0.00±0.00b	0.00±0.00b	0.00	58.33±1.11abc
4-	SLH-94	0.00±0.00b	0.00±0.00b	0.00	57.14±2.08abc
5-	MNH-S GOLD	0.00±0.00b	0.00±0.00b	0.00	56.00±1.14bc
6-	BH-227	0.00±0.00b	0.00±0.00b	0.00	68.00±1.39ab
7-	FH-1214	0.00±0.00b	0.00±0.00b	0.00	56.00±2.52bc
8-	MNH-1095	0.00±0.00b	0.00±0.00b	0.00	76.88±1.81a
9-	VH-442	0.00±0.00b	0.00±0.00b	0.00	63.64±1.34abc
10-	MNH-1090	0.00±0.00b	0.00±0.00b	0.00	59.00±1.43abc
11-	RH-BAGHO BAHAR	0.00±0.00b	0.00±0.00b	0.00	64.00±3.46abc
12-	MNH-1050	0.00±0.00b	0.00±0.00b	0.00	59.00±1.34abc
13-	MNH-TP	2.13±0.08a	0.13±0.04a	0.00	57.14±1.19abc
F-Value		161.97	2.14	**0.00**	5.22
Tukey's HSD Value at 0.05%		0.25	0.15		

Tukey's HSD at P = 0.05 indicates that means with comparable letter distributions are not substantially different; HSD = Honestly Significant Difference * indicates significance at P < 0.05 and ** indicates significance at P < 0.01.

3.2. Whitefly (*Bemisia tabaci*) population average per leaf:

The results show that there are substantial variations in the number of whiteflies amongst the various kinds of cotton (F=84.00; df=12, 24; P<0.00; Table 2). The highest reported number of whiteflies per leaf was 15.20 on MNH-1095, with VH-447 coming in second at 12.07/leaf and BH-228 third at 9.73 per leaf. With 6.80 whiteflies per leaf, genotype VH-442 is statistically similar to MNH-1050 and RH-BAGHO BAHAR, which have 5.20 and 4.87 individuals per leaf, respectively. BH-227 and MNH-TP, on the other hand, have 3.00 and 2.93 whiteflies per leaf. With 2.67 and 2.53 genotypes, respectively, FH-1214 and MNH-S GOLD exhibit statistically comparable populations with low numbers of whiteflies per leaf. The statistically equivalent minimal populations of whiteflies per leaf were found on MNH-1090 (2.20/leaf), SLH-94 (2.20/leaf), and FH-1133 (2.00/leaf).

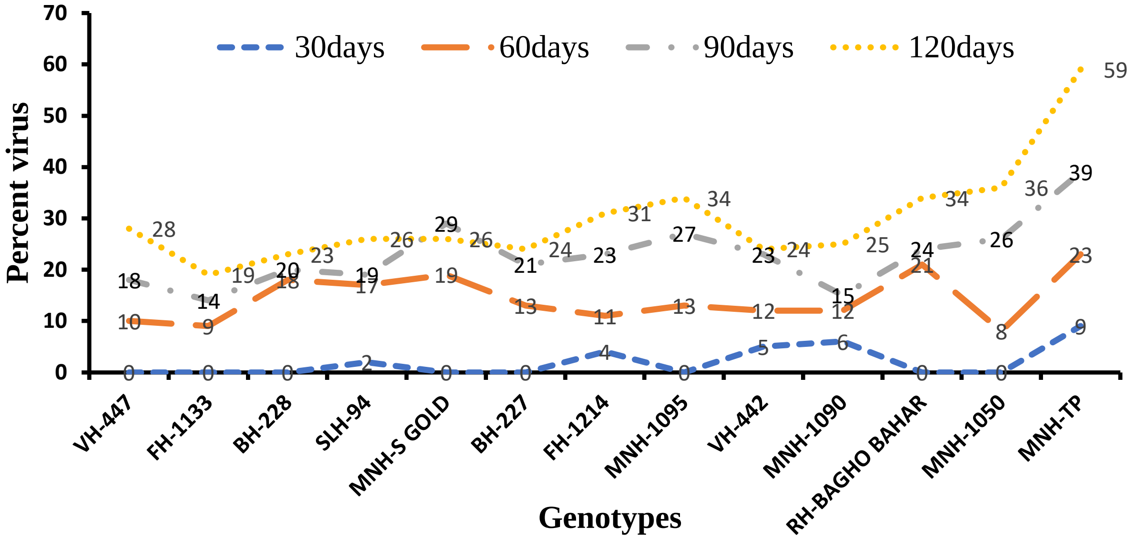


Figure 1. Data regarding virus percentage on various genotypes

3.3. Thrips (*Thrips tabaci*) on average have one colony per leaf:

The results show that there were notable variations in the number of thrips per leaf across the various genotypes of cotton (F=135.01; df=12, 24; P<0.00; Table 2). The highest number of thrips was found on VH-447 (6.13 individuals/leaf), which is comparable to RH-BAGHO BAHAR's 5.27 thrips per leaf (5.27) and BH-228's 4.87/leaf. MNH-TP and MNH-1090 have statistically comparable populations, with 2.40 and 2.27 thrips per leaf, respectively, but the genotype MNH-1050 had 3.93 thrips per leaf. With 1.0, 1.0, 0.87, 0.53, 0.40, 0.33, and 0.13 thrips per leaf, all other genotypes, including SLH-94, FH-1133, VH-442, MNH-1095, FH-1214, BH-227, and MNH-S GOLD, are statistically identical to one another.

3.4. The number of bollworms populations

3.4.1. The mean number of spotted bollworm larvae per plant:

The data indicates that there were extremely significant differences (F=161.97; df=12, 38; P<0.00; Table 3) in the number of spotted bollworms per plant across the various genotypes of cotton. The genotype MNH-TP had the highest reported number of spotted bollworms (2.13 live larvae/plant), whereas all other genotypes had 0.00 spotted bollworms per plant, which are statistically close to each other.

3.4.2. Average number of American bollworm larvae per plant:

The data shows that the population of American bollworms per plant does not significantly differ between cotton genotypes. The number of American bollworm larvae per plant varies from 0.00 to 0.13. The MNH-TP genotype had the highest reported number of spotted bollworms (0.13 live larvae/plant), whereas all other genotypes had 0.00 spotted bollworms per plant, which are statistically close to each other.

Rosette flowers per plant: No rosette flowers were found in any cotton genotype.

3.4.3. Average number of pink bollworm larvae:

The results indicate statistically significant variations (F=5.22; df=12, 38; P<0.00; Table 3) between the various genotypes of cotton with respect to the number of pink bollworms in the leftover bolls per plant. Bolls of VH-447 (77.27%) and MNH-1095 (76.88%) had the highest recorded number of pink bollworm larvae, which was statistically comparable to those of BH-227 (68.00%), RH-BAGHO BAHAR

(64.00%), VH-442 (63.64%), MNH-1050 (59.00%), MNH-1090 (59.00%), BH-228 (58.33%), MNH-TP (57.14%), SLH-94 (57.14%), MNH-S GOLD (56%), and FH-1214 (56.00%). The FH-1133 has a minimum of 43.59% of pink bollworms in cotton bolls that are left over.

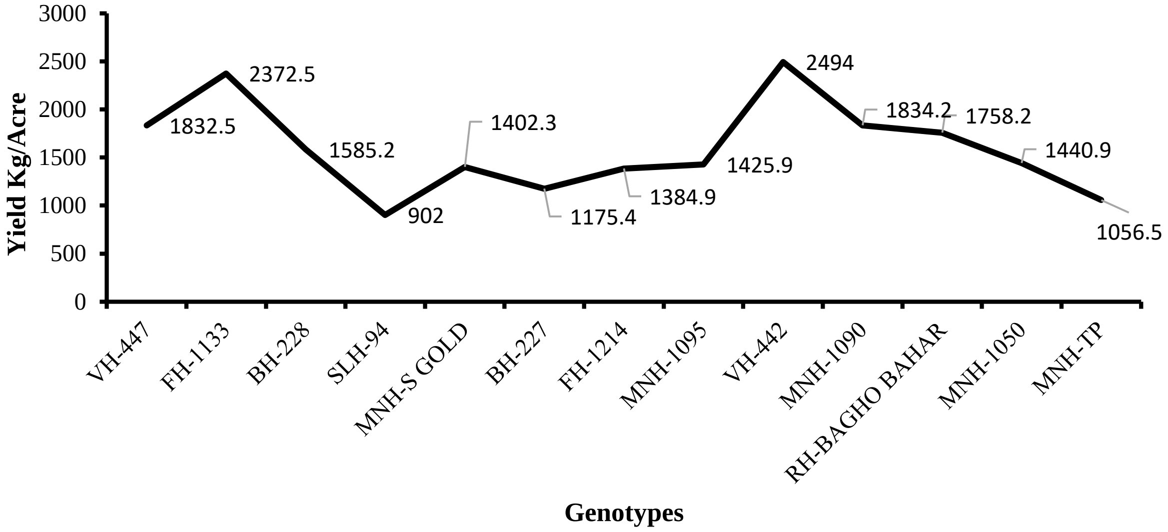


Figure 3. Average number of cotton bolls on per plant for different genotypes

3.5. Virus (CLCuV) among genotypes

3.5.1. Percentage of virus (CLCuV) after 30 days of seeding:

Data was collected on the virus percentage for various genotypes of cotton. It was discovered that, following genotype sowing, the genotypes in MNH-TP had the highest virus percentage (9.00%), while the genotypes in SLH-94 had the lowest virus percentage (2%), as illustrated in Figure 1.

3.5.2. Percentage of CLCuV (after 60 days of seeding):

The data (Figure 1) shows the percentage of virus (CLCuV) after 60 days after sowing and indicates that the highest percentage of virus was detected in genotypes in RH-BAGHO BAHAR and MNH-TP, which are 23% and 21.00%, respectively. After seeding genotypes, the lowest virus was found in genotype FH-1133, or 9%.

3.5.3. Percentage of CLCuV (after 90 days of seeding):

Figure 1's data shows the percentage of the virus (CLCuV) after 90 days. Following genotype planting, the highest percentage of virus was found in genotypes in MNH-TP, or 39%, while the lowest percentage was found in genotypes in FH-1133 (14%).

3.5.4. Percentage of CLCuV (after 120 days of seeding):

The information shows the percentage of the virus (CLCuV) after 120 days. It was discovered that, after seeding, genotypes MNH-TP had the highest percentage of virus, recorded at 59.00%, while genotypes FH-1133 had the lowest percentage of virus, reported at 19.00%.

3.6. Yield

3.6.1. Average yield per acre of various cotton genotypes:

The yield per acre across different genotypes of cotton demonstrates highly significant variances (F = 35.91; df = 12, 38; P 0.00; Figure 2). With a reported production of 2493.60 kg per acre, VH-442 had the highest yield. MNH-1090, VH-447, RH-BAGHO BAHARBH-228, and FH-1133 followed with yields of 1834.2, 1832.50, 1758.20, 1585.20, and 2372.50 kg per acre, respectively. MNH-S GOLD (1402.30) and FH-1214 (1384.90) demonstrated statistically similar yield per acre, followed by genotypes MNH-1050 (1440.90) and MNH-1095 (1425.90). MNH-TP produced 1056.50 kg/acre, but BH-227 produced 1175.40 kg/acre. The minimal production was expressed in SLH-

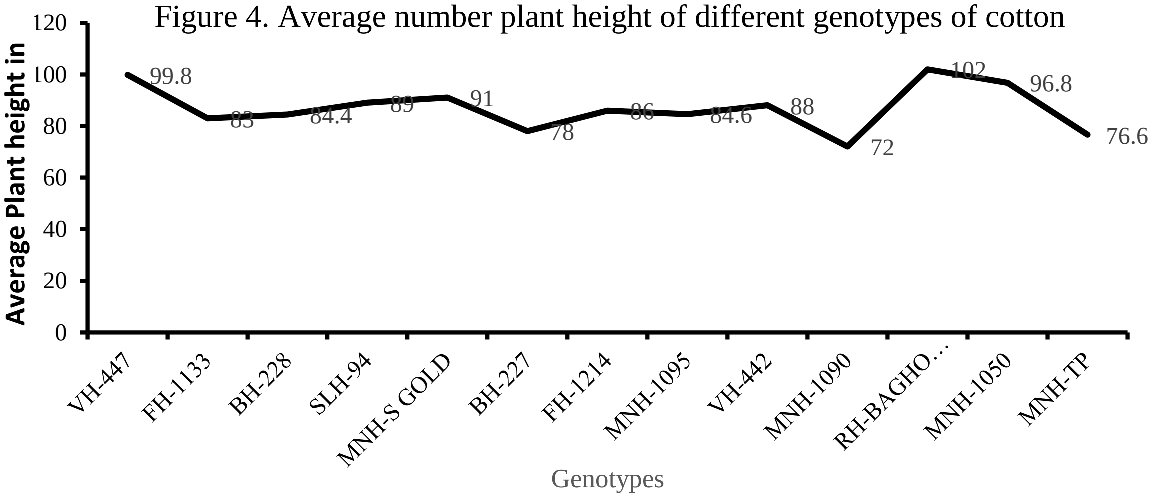
94, or 902.0 kg per acre, as can be shown in Figure 2.

3.6.2. Average *number of bolls per plant:*

Table 4. Data regarding Fiber characteristics of (*GOT%, Staple Length (mm), Fiber fineness (µg/inch),* Fiber strength (g/tex) various genotypes of cotton during 2023

Genotypes	**GOT%**	**Staple Length (mm)**	**Fiber fineness (µg/inch)**	**Fiber strength (g/tex)**
VH-447	41.20	24.00	5.10	30.10
FH-1133	46.50	28.50	4.70	33.20
BH-228	46.00	26.10	6.00	30.00
SLH-94	46.10	24.00	5.70	28.90
MNH-S GOLD	46.10	24.70	5.60	30.00
BH-227	46.10	23.80	5.20	28.90
FH-1214	44.10	24.60	6.00	30.20
MNH-1095	43.70	25.30	4.60	35.00
VH-442	43.80	28.10	4.80	30.20
MNH-1090	46.20	24.20	5.30	35.00
RH-BAGHO BAHAR	41.60	24.30	5.00	30.00
MNH-1050	44.60	27.00	3.50	29.90
MNH-TP	45.50	24.60	4.90	31.20

Figure 4. Average number plant height of different genotypes of cotton



The data shown in Figure 3 pertains to the average number of bolls per plant. It can be observed that the genotypes MNH-1050 and FH-1214, which correspond to 29.8 and 29.4, respectively, have the highest average numbers of bolls per plant recorded. On the other hand, as Figure 3 illustrates, BH-227 (15.6) had the lowest quantity of bolls per plant.

3.7. Average *amount of cotton bolls per plant on various genotypes*

3.7.1. Average *plant height (cm) per plant:*

The genotypes RH-BAGHO-BAHAR and MNH-1050 had the highest plant heights in cm, measuring 102 and 96.8 cm, whereas the genotypes MNH-1090 and BH-227 had the lowest, measuring 72 and 78 cm, as seen in Figure 4.

3.8. Fiber characteristics

3.8.1. Ginning *Out Turn Percentage (GOT%)*:

Table 4 presents information on ginning out turn percentage (GOT %). FH-1133 (46.5%), MNH-1090 (46.2%), SLH-94 (46.1%), MNH-SGOLD (46.1%), and BH-227 (46.1%) had the highest percentage of G.O.T. Conversely, VH-447 (41.2%) and RH-BAGHO BAHAR (41.6%) had the lowest G.O.T. %. Every genotype is still the greatest.

3.8.2. Staple *Length (mm):*

As in Figure 6, the maximum staple length for MNH-1050 was observed at 27.0 mm. This value is better than all other genotypes of cotton, but it is still below the norm at 27.5 mm. In BH-227, the minimum staple length of 23.8 mm was noted.

3.8.3. Fiber fineness (µg/inch):

Based on the results, genotype MNH-1050 had the highest reported fineness (3.5 µg/inch) when compared to other cotton genotypes. In FH-1133 and SLH-94, the minimum fineness was found to be 5.7 µg/inch, which is below the norm of 5.0 µg/inch, as indicated in Table 4.

3.8.4. Strength of fiber (g/tex):

The highest fiber strength was measured at 35.0 for genotypes MNH-1095 and MNH-1090 when compared to the standard fiber strength of 30±2, while the lowest fiber strength was measured at 28.9 g/tex for genotypes SLH-94 and BH-227, as indicated in Table 4.

4. DISCUSSION

Every year, insect pest damage to cotton crops causes a large loss in productivity worldwide (Naeem-Ullah *et al.,* 2020). It is crucial economically to eradicate these pests as effectively as possible to reduce crop loss. Sucking insects provide a serious risk to cotton during the different growth stages (such as vegetative, flowering, seedling, and fruiting) of the crop's development (Rajendran *et al.,* 2018). Significant infestations of whiteflies, jassid, thrips, and bollworms were discovered in the cotton leaves and bolls during this investigation. The physical traits, yield, and fiber quality of the assessed cultivars varied. Profound differences exist across cultivars in the levels of boll and leaf infection, as well as in how they respond to these pests (Amin *et al.,* 2016).

Significant variations in the degrees of boll and leaf infection among cultivars suggested variances in their susceptibility and reactions to these pests. Whitefly, jassid, and thrips infestation was observed among different cotton varieties and reported that two varieties were resistant, whereas two were susceptible (Abbas *et al.* 2018). The present study showed that FH-1133 sustained lower infestation levels of jassid, whitefly as well as thrips in comparison to the other cultivars. We monitored the jassid abundance from the vegetative to the harvest stages. Infested bolls and leaves became rusty crimson and pallid, twisted downward, dried out, and dropped to the ground. This might be because different cotton cultivars have different amounts of trichomes (Wang *et al.,* 2021), morphological traits (Shao *et al.,* 2016), and biochemical compositions (Egbuta *et al.,* 2017). These differences could have had an impact on the pests' ability to eat, oviposit, and build up their populations, leading to a range of infestation levels (Koul, 2016). Infestation of green bolls by pink bollworm, indicated that VH-447 and MNH-1095 were the most susceptibility cotton varieties while Fh-1133 was most resistant genotypes. The plant height (102–72 cm) and number of bolls per plant (29.8–15.6) of our examined cultivars varied.

Similar results were obtained by Amin *et al.,* (2016), who looked at nine different species of cotton that had been infested by sucking insects and discovered differences in the height of the plants (88.7 to 127.8 cm), the number of branches (10.0 to 16.0), and the number of bolls per plant (13.0 to 76.8). The cultivars we examined differed in terms of locules per boll, weight, size, and number of leaves and sympodial branches per plant. We noted that the cultivars varied in terms of GOT (46.50-41.60%), Staple Length (26.50-24.00 mm), Fiber fineness (6.00-3.50 µg/inch) and Fiber strength (35.00-28.90 g/tex), respectively.

The findings of Azad *et al.,* (2011), who grew the cotton cultivars CB9, CB10, and SR05 without using insecticides, and observed differences in yield (618-792 ka ha-1), GOT (36.2-37.3%), seed index (7.8-8.3g), and germination percentage (81.3-

82.3%) are in line with these. According to the Hossain *et al.,* (2012) study, CB3 and CB9 had micronaires of 3.96 and 3.93 and lint indices of 5.9 and 6.0 g per 100 seeds, respectively.

5. Conclusion and Suggestion

It was discovered that the genotype FH-1133 was resistant to the lowest level of chewing and sucking pest complex infestation and the good seed cotton production or yield. These genotypes can be used in integrated pest management (IPM) programmes to control these pests and prevent production losses, as well as in future breeding programmes aimed at enhancing resistance. In addition, in order to obtain the highest possible degree of fiber quality, the growth zones must be chosen to improve the qualities of the fiber. Environmental variations have an influence on the physical and chemical qualities of cotton fiber, hence ranking cultivars.

6. Conflict of interest

The authors declared absence of conflict of interest.

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