Research Article

Field Evaluation of Advanced Cotton Genotypes Against Insect Pest Complex in Agro-Climatic Conditions of Tandojam, Sindh

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Abstract | The resistance levels of eighteen cotton genotypes to sucking complex (thrips, jassids, and whiteflies) and bollworms (spotted and pink) were assessed in the experimental field of Nuclear Institute of Agriculture, Tandojam. The experiment was conducted under Randomized Complete Block Design (RCBD) with three replications. The result of overall mean revealed that NIA-M-20 had comparatively greater resistance to the attack of jassids (0.21/leaf) whitefly (0.29/leaf) and thrips (1.63/leaf). Similarly, NIA-M-16 also showed the lowest infestation of whitefly (0.29/leaf). Whereas, infestation of bollworms illustrated that NIA-M-20 was highly susceptible against spotted and pink bollworms with percent infestation of 5.52 and 2.79%, respectively. The genotype NIA-HM-27 proved to be most efficient by rendering the lowest (0.82%) infestation of spotted and pink bollworm but showed medium response and found susceptible against jassid (0.28/leaf), thrips (2.21/leaf) and whitefly (0.31/leaf). Best yield performance (2467.8 kg/ha) was of NIA-HM-6N that showed high tolerance against sucking pests as well as bollworms. Moreover, the perusal of data showed that the population trend of all insects remained below economic threshold level (ETL) during the period of study.

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Introduction

Cotton plays a pivotal role in agro-based economy of Pakistan and is a key source of foreign exchange earnings. It is multi-purpose crop as it provides edible oil as well as fiber. Cotton accounts for 1.9% in GDP and 8.6% of value addition in agriculture (Anonymous, 2006). In Pakistan, it is cultivated on an area of 2961 thousand hectares with 13.983 million bales and ranks 4th in overall world production after China, India and USA (GOP, 2015). The average cotton yield in Pakistan is about 752 kg/ha, which is substantially low as compared to other countries of the world (GOP, 2018). Many factors are responsible for this low productivity, but the most serious one is the intensity of insect pests attack (Arshad and Suhail, 2010).

Insect pests complex of cotton is divided into two categories; sucking pest and chewing pests or bollworms. The importat sucking insect pests are *Amrasca devastans* (Homopetra:Cicadellidae), *Thrips tabaci* (Thysanoptera:Thripidae) *and Bemesia tabaci* (Homoptera:Aleyrodidae). The bollworms complex includes *Helicoverpa armigera* (Lepidoptera:Noctuidae), *Pectinophora gossypiella* (Lepidoptera:Gelechiidae), *Earis insulana and E. vitella* (Lepidoptera:Noctuidae) (Mohyuddin *et al.*, 1997). It is estimated that sucking and bollworms pest complex causes approximately 30-40% yield loss in Pakistan (CCRI, 2005). In order to evade these losses, farmers mostly depend on the use of pesticides (Arif *et al*., 2007). Major recipient of the insecticides in Pakistan is the cotton crop which receives 61.92% of the total pesticides (Khan *et al*., 2010).

Use of synthetic insecticides not only poses ecological contamination and health hazards but also emerging insecticidal resistance and disturbs the natural balance between the beneficial agents (pathogens, parasitoids and predators) and pests population in agro-ecosystem (Ahmad and Khan, 1991; Hamburg and Guest, 1997; Sorejani, 1998). Chandani *et al*. (2015) documented that environment friendly insecticides should be preferred because, conventional insecticides are mostly used to control insect pests complex but, these cause many harms i.e. resistance, resurgence, pest outbreak, damage to eco-cycle, pollution and health hazards, etc.

Host plant resistance gives insect pests control without any added cost. Moreover, this method is environment friendly and economical (Pedigo, 1989; Khan and Saxena, 1998). Insecticidal use can be minimized easily by using resistant varieties (Hua and Hua, 2000). There are several physio-morphic characters of cotton genotypes that impose various resistance/tolerance levels against the insect pest attack. In Pakistan breeders continuously made efforts to evolve insect resistant varieties by using several breeding methods, however after few years these genotypes become susceptible. According to Li *et al*. (2008) proper utilization of existing germplasm through hybridization and induction of new germplasm are essential to create adequate genetic variability and developing superior genotypes. Germplasm variability not only enhances the probability of developing multiple resistance against abiotic and biotic stresses but also obtain required characteristics that can be exploited in future programs of breeding (van Esbroeck and Bowman, 1998).

Keeping in view, the present study was carried out on eighteen advanced genotypes of cotton with the aim to determine their comparative attraction for sucking and chewing complexes of cotton under agro-climatic condition of Tandojam (Sindh, Pakistan) under unsprayed condition.

Materials and Methods

Total of eighteen advanced genotypes i.e. NIA-HM-2, NIA-HM-7, NIA-HM-18, NIA-HM-5, NIA-HM-20R, NIA-HM-6R, NIA-HM-30, NIA-HM-26, NIA-HM-20N, NIA-HM-27, NIA-HM-19, NIA-HM-6N, NIA-M-23, NIA-M-16, NIA-M-20, NIA-M-10, NIA-M-5 and NIA-M-9 were sown at the experimental area of Nuclear Institute of Agriculture, Tandojam on 09-05-2017. The study was conducted under RCBD with three replications. Plot size was 5m x3m with plant to plant distance 30 cm and row to row was maintained at 75 cm. All standard agronomical practices were adopted and no synthetic insecticide application was done during the whole study period.

The population of jassid, whitefly and thrips per leaf was taken early morning at fortnightly interval starting from the start of June to end of September. Three plants were randomly selected in one plot. Three leaves i.e. upper, middle and lower from each plant were observed to record the population (Ahmed *et al*., 2011). Bollworms infestation was recorded by observing the buds, flowers and dissecting the bolls from three plants selected randomly per plot. Percent infestation of spotted (*Earis spp.*) and pink (*Pectinophora gossypiella*) bollworms was separately calculated by recording the total and damaged number of buds, flowers and bolls from three plants per plot using the formula:

$$\text{Infestation (\%)} = \frac{\text{No. of damaged fruiting parts}}{\text{Total no. of fruiting parts}}$$

The yield from each genotype in a replicated plot was weighed and then converted in kg/ha^{-1}. The data regarding the population of sucking insect pests, bollworms infestation and yield was analyzed by using one way ANOVA through statistix software 8.1. Means were compared through Tuckey's HSD test. Statgraphics Centurion XVI version 16.1.11 was used for cluster analysis. Squared Euclidean distance was used for the cluster matrix. Dendrogram was developed for visualizing the results and interrelation of the cotton genotypes.

Results

The seasonal mean of jassid infestation on different cotton genotypes presented in Table 1 shows that NIA-HM-26 indicated maximum susceptibility with population of 0.54/leaf that was at par with NIA-HM-20R bearing population 0.53/leaf. The minimum population of 0.21/leaf was recorded on NIA-M-20 followed by NIA-M-23 and NIA-HM-6N with population of 0.25 and 0.26/leaf, respectively. The next best genotypes were NIA-HM-27, NIA-M-19 and NIA-HM-19 with lowest population of 0.28, 0.32 and 0.33/leaf, respectively.

The data regarding mean population of thrips on different advanced cotton genotypes is displayed in Table 2. The seasonal mean population of thrips ranged between 1.63 to 4.23/leaf among the tested genotypes. NIA-HM-20R harbored the highest (4.23/leaf) population of thrips and found as the most susceptible genotype followed by NIA-HM-6R and NIA-M-19 with population of 3.82 and 3.35/leaf, respectively. The minimum population of thrips was observed on NIA-M-20 (1.63/leaf) and found statistically at par with NIA-HM-20N bearing population 1.68/leaf. NIA-M-5, NIA-M-10 and NIA-M-23 were also found tolerant genotypes with population mean of 1.85, 207 and 2.08/leaf, respectively.

The results revealed that population of whitefly remained very low throughout the season. However, analysis of variance showed that population of whitefly varied significantly among the tested genotypes (Table 3). The highest population of 0.51/leaf was observed on NIA-HM-5 followed 0.50/leaf on NIA-HM-20R and was non-significantly different from each other. The minimum whitefly was observed on NIA-M-20 and NIA-M-16 with population mean of 0.29/leaf.

Based on the percent infestation of spotted bollworm, the results showed significant variation among different cotton genotypes (Table 4). The highest percent infestation of 7.11% was found in NIA-M-19 that

Table 1: Comparison of means of jassid population on different cotton genotypes.

Genotypes	Jassid/Leaf	Genotypes	Jassid/Leaf	Genotypes	Jassid/Leaf
NIA-HM-2	0.34 a-e	NIA-HM-30	0.37 a-e	NIA-M-23	0.25 de
NIA-HM-7	0.47 a-c	NIA-HM-26	0.54 a	NIA-M-16	0.34 a-e
NIA-HM-18	0.44 a-d	NIA-HM-20N	0.46 a-d	NIA-M-20	0.21 e
NIA-HM-5	0.42 a-e	NIA-HM-27	0.28 b-e	NIA-M-10	0.40 a-e
NIA-HM-20R	0.53 a	NIA-HM-19	0.33 a-e	NIA-M-5	0.37 a-e
NIA-HM-6R	0.48 ab	NIA-HM-6N	0.26 c-e	NIA-M-19	0.32 a-e

Means sharing similar letter are not significantly different at $p<0.05$.

Table 2: Comparison of means of thrips population on different cotton genotypes.

Genotypes	Thrips/Leaf	Genotypes	Thrips/Leaf	Genotypes	Thrips/Leaf
NIA-HM-2	3.11 a-e	NIA-HM-30	2.87 b-f	NIA-M-23	2.08 c-f
NIA-HM-7	3.28 a-d	NIA-HM-26	2.90 b-f	NIA-M-16	2.42 c-f
NIA-HM-18	3.29 a-d	NIA-HM-20N	1.68 f	NIA-M-20	1.63 f
NIA-HM-5	3.15 a-d	NIA-HM-27	2.21 c-f	NIA-M-10	2.07 d-f
NIA-HM-20R	4.23 a	NIA-HM-19	2.40 c-f	NIA-M-5	1.85 ef
NIA-HM-6R	3.82 ab	NIA-HM-6N	2.17 c-f	NIA-M-19	3.35 a-c

Means sharing similar letter are not significantly different at $p<0.05$.

Table 3: Comparison of means of whitefly population on different cotton genotypes.

Genotypes	Whitefly/Leaf	Genotypes	Whitefly/Leaf	Genotypes	Whitelfy/Leaf
NIA-HM-2	0.32 b	NIA-HM-30	0.33 b	NIA-M-23	0.30 b
NIA-HM-7	0.42 ab	NIA-HM-26	0.38 ab	NIA-M-16	0.29 b
NIA-HM-18	0.34 ab	NIA-HM-20N	0.30 b	NIA-M-20	0.29 b
NIA-HM-5	0.51 a	NIA-HM-27	0.31 b	NIA-M-10	0.33 b
NIA-HM-20R	0.50 a	NIA-HM-19	0.44 ab	NIA-M-5	0.41 ab
NIA-HM-6R	0.38 ab	NIA-HM-6N	0.46 ab	NIA-M-19	0.42 ab

Means sharing similar letter are not significantly different at $p<0.05$.

Table 4: Comparison of mean percent infestation of spotted bollworm on different cotton genotypes.

Genotypes	Spotted % Infestation	Genotypes	Spotted % Infestation	Genotypes	Spotted % Infestation
NIA-HM-2	3.59 b-d	NIA-HM-30	2.11 cd	NIA-M-23	4.03 a-c
NIA-HM-7	3.51 b-d	NIA-HM-26	3.82 b-d	NIA-M-16	3.67 b-d
NIA-HM-18	2.52 b-d	NIA-HM-20N	2.23 cd	NIA-M-20	5.52 ab
NIA-HM-5	2.37 cd	NIA-HM-27	0.82 d	NIA-M-10	1.72 cd
NIA-HM-20R	2.55 b-d	NIA-HM-19	2.02 cd	NIA-M-5	3.30 b-d
NIA-HM-6R	1.79 cd	NIA-HM-6N	1.03 cd	NIA-M-19	7.11 a

Means sharing similar letter are not significantly different at $p<0.05$.

Table 5: Comparison of mean percent infestation of pink bollworm on different cotton genotypes.

Genotypes	Pink % Infestation	Genotypes	Pink % Infestation	Genotypes	Pink % Infestation
NIA-HM-2	2.18 a-f	NIA-HM-30	3.18 a-c	NIA-M-23	2.53 a-e
NIA-HM-7	2.38 a-f	NIA-HM-26	3.68 a	NIA-M-16	2.18 a-f
NIA-HM-18	1.72 b-f	NIA-HM-20N	1.61 c-f	NIA-M-20	2.79 a-d
NIA-HM-5	2.91 a-d	NIA-HM-27	0.82 f	NIA-M-10	1.25 d-f
NIA-HM-20R	1.02 ef	NIA-HM-19	0.85 f	NIA-M-5	2.69 a-d
NIA-HM-6R	2.88 a-d	NIA-HM-6N	1.48 d-f	NIA-M-19	3.38 ab

Means sharing similar letter are not significantly different at $p<0.05$.

Table 6: Comparison of yield (kg/ha) of different cotton genotypes.

Genotypes	Yield kg/ha	Genotypes	Yield kg/ha	Genotypes	Yield kg/ha
NIA-HM-2	1741.1 a-c	NIA-HM-30	1582.2 bc	NIA-M-23	1282.2 c
NIA-HM-7	1628.9 bc	NIA-HM-26	1503.3 bc	NIA-M-16	1216.7 c
NIA-HM-18	1429.8 bc	NIA-HM-20N	1708.9 a-c	NIA-M-20	1788.9 a-c
NIA-HM-5	1643.3 bc	NIA-HM-27	1723.3 a-c	NIA-M-10	1693.3 a-c
NIA-HM-20R	1390.0 bc	NIA-HM-19	1722.2 a-c	NIA-M-5	1764.4 a-c
NIA-HM-6R	2150.0 ab	NIA-HM-6N	2467.8 a	NIA-M-19	1525.6 bc

Means sharing similar letter are not significantly different at $p<0.05$.

was statistically at par with NIA-M-20 (5.52%) and NIA-M-23 (4.03%). The most tolerant genotypes among the selected 18 cotton genotypes were NIA-HM-27 with percent infestation of 0.82% followed by NIA-HM-6N (1.03%) and NIA-M-10 (1.72%). Regarding pink bollworm infestation, NIA-HM-27 followed by NIA-HM-19, NIA-HM-20R and NIA-M-10 showed high level of tolerance with percent infestation of 0.82, 0.85, 1.02 and 1.25%, respectively. The most susceptible genotypes were NIA-HM-26, NIA-M-19, NIA-HM-30 and NIA-HM-5 having percent infestation of 3.68, 3.38, 3.18 and 2.91%, respectively, as compared with other genotypes (Table 5).

In respect of average yield per hectare, the statistically maximum yield was obtained from the genotype NIA-HM-6N i.e. 2467.8 kg /ha followed by NIA-HM-6R, NIA-M-20, NIA-M-5 with 2150, 1788.9, 1764.4 kg per hectare whereas the lowest yield was obtained in the genotype NIA-M-16 i.e. 1216.7 kg/ha followed by NIA-M-23 with 1282.2 kg/ha under similar condition (Table 6).

Cluster analysis clearly separated the genotypes into different clusters on the basis of their performance against the insect pests infestation (Fig. 1). The main cluster A that includes five genotypes viz. NIA-HM-20N, NIA-M-10, NIA-HM-27, NIA-HM-19 and NIA-HM-6N. This cluster can be divided into two sub-clusters named as AI and AII. The sub-cluster AI consisted of NIA-HM-20N and NIA-M-10 that were closely related to each other. Both of these genotypes exhibited high tolerance level against the infestation of thrips, whitefly, spotted bollworm and pink bollworm. Similarly, NIA-HM-19 and NIA-HM-6N clustered in to AII and showed least infestation of insect pests except whitefly that was found in abundance on these genotypes. However, NIA-HM-27 was found somewhat different from the other four genotypes within the same cluster. This genotype was the most tolerant with the lowest percent infestation of spotted and pink bollworms. Two genotypes, NIA-HM-2 and NIA-M-16 found closely related to each other by showing almost similar infestation of jassid and pink bollworm. While NIA-M-23, NIA-M-20, NIA-HM-18, NIA-HM-7, NIA-HM-6R, NIA-HM-30, NIA-HM-5 and NIA-HM-26 were found somewhat similar to each other in their susceptibility against insect pests and present as a separate genotype in the dendrogram. Three genotypes i.e. NIA-M-5, NIA-HM-20R and NIA-M-19 appeared to be distinctly unique and the most distant from other genotypes of cotton. NIA-M-5 was among the genotypes that showed high tolerance against the attack of thrips. While the genotype NIA-HM-20R appeared to be highly susceptible against the attack of jassid, thrips whitefly but exhibited high tolerance in case of pink bollworm attack. NIA-M-19 harbored the highest infestation of spotted bollworm and pink bollworm and regarded as the most susceptible genotype among all the tested genotypes.

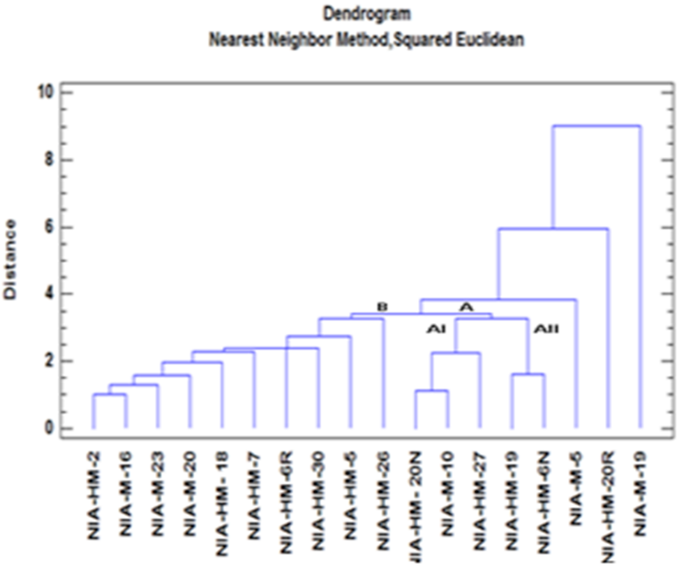

Figure 1: Comparison of genotypes for their susceptibility to sucking insects and bollworms.

Discussion

Cultivation of tolerant cotton genotypes is considered as one of the safest measures to avoid pest situation i.e., determining relative resistance in conventional genotypes, is an essential component for successful integrated pest management approach and sustainable cotton production. Eighteen advanced cotton genotypes were evaluated for their comparative resistance against insect pests complex of cotton under natural field conditions. The results revealed that tested genotypes varied significantly in their susceptibility against sucking insects of cotton. It is apparent from the results that the NIA-M-20 was the most tolerant genotype against jassid, thrips and whitefly. These findings are in conformity with Shad *et al.* (2001), Chu *et al.* (2002), Sial *et al.* (2003), Syed *et al.* (2003), Ahmad *et al.* (2004), Ali and Aheer (2007), Amjad *et al.* (2009), Khan (2011), Salman *et al.* (2011), Ghafoor *et al.* (2011), Javaid *et al.* (2012), Asif *et al.* (2017a) and Asif *et al.* (2017b) who also reported that different cotton genotypes varied in their relative resistance against the sucking pests. Likewise, Babar *et al.* (2013) conducted study on different cultivars of cotton and screened five genotypes i.e. Sitara-11M, IR5-NIBGE, Sitara-10M, Bt-121, IR4-NIBGE and Sitara-10M for resistance against jassid, thrips and whitefly. The lowest population of jassids was found on IR4-NIBGE and Sitara-11M whereas IR4-NIBGE also showed maximum tolerance against whitefly. The least susceptible variety to the infestation of thrips was Sitara-10M. Shahid *et al.* (2012) reported that minimum attack of thrips exhibited by FH-118, followed by GN-2085 while FH-177, FH-179 and FH-114 were most susceptible.

The present studies have indicated that attack of bollworms (spotted and pink) and yield varied substantially on the cotton genotypes. On the whole, it was observed that NIA-HM-27 exhibited least infestation of both spotted and pink bollworms. Many researchers found significant results of host plant resistance against bollworms i.e. Jin *et al.* (1999), Razaq *et al.* (2004), Nasreen *et al.* (2004), Pathan *et al.* (2007) and Lanjar *et al.* (2014). Solangi *et al.* (2016) monitored dynamics of spotted and pink bollworm on several cotton genotypes. They concluded that lowest infestation of bollworms was observed on Sattari-Bt. However, NIAB-78 also showed some tolerance against both pests.

Conclusion

The genotypes NIA-M-20 and NIA-HM-27 were found the most tolerant with respect to lowest infestation of sucking pests and bollworms, respectively. These genotypes can be included in future breeding programs for resistance enhancement and also in integrated pest management (IPM) programs for control of these pests to avoid yield losses.

Author's Contribution

Muhammad Usman Asif planned and conducted the experiment, recorded the data, performed statistical analysis of the data and wrote the manuscript. Raza Muhammad provide technical guidance and helped in data analysis and critical review of the manuscript. Waseem Akbar contributed in execution of the experiment and helped in data collection. Mubasshir Sohail helped in data analysis and interpretation of results. Muhammad Awais helped in the manuscript writing and review.

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