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Screening of different advanced genotypes of transgenic cotton (*Gossypium hirsutum* L.) against thrips (*Thrips tabaci* Lindemann.) under Faisalabad Agro-ecosystem

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Abstract
The present study aimed at screening fifteen genotypes of cotton (*Gossypium hirsutum* L.) for population dynamics of thrips, *Thrips tabaci* Lindemann. This study was carried out at the Cotton Research Station, Faisalabad, Pakistan during the two cropping seasons 2016 and 2017. The experiment was conducted under Randomized Complete Block Design (RCBD) with three replications. The results showed that FH-142 proved to be least attractive cultivar with 0.67 *T. tabaci*/leaf in September and October-2016 while in 2017 *T. tabaci* population observed was 1.33/leaf in May, 1.67/leaf in September and 2.67 /leaf in October. The maximum population of *T. tabaci* was recorded on FH-451 (15.50/leaf) followed by FH-455 (14.67/leaf during 2017. On cumulative basis, highest peak of *T. tabaci* population was observed on FH-455 (12.92/leaf). In conclusion, advanced genotypes of transgenic cotton was proved to resist the population buildup of *T. tabaci* throughout the period of study.

Keywords: Cotton, genotypes, *Thrips tabaci*, sucking pest, population dynamics

1. Introduction

Cotton (*Gossypium hirsutum* L.: Genus: Hirsutum; Family: Malvaecae) is a cash crop of Pakistan after wheat and it is cultivated at the largest scale in Pakistan compared to other crops. Cotton crop generates largest export revenues for the country and in addition to the lint, the seed of cotton for oil and meal contribute 80 percent of the national production of oilseed. Cotton and cotton related products accounts for 10 percent of gross domestic product (GDP) and 55 percent of the foreign exchange earnings of the country. The area under the cultivation of cotton crop amplified expressively in the last 30 years, around 7.86 million acres in 2015–2016 [1]. After China, USA and India, Pakistan rank fourth largest cotton producer in the world [2]. Cotton crop provides livelihood to the millions of people from field to factories apart from earning a substantial foreign exchange [3].

Introduction and successful employment of transgenic *Bt* cotton under climatic conditions of Indo-Pak region, not merely solved bollworm complex incidence but also checked the number of insecticidal spray which probably leads sever incidence of sucking pest and it caused considerable damage in both traditional and *Bt* cotton and attained the status of major pest status at present [4]. Among sucking insect/mite pest complex of cotton, whitefly (*Bemisia tabaci* (Genn), Homoptera: Aleyrodidae), jassid (*Amrasca devastans* (Dist.), Homoptera: Cicadellidae), thrip (*Thrips tabaci* (Lind.), Thysanoptera: Thripidae) and red-spider mite (*Tetranychus urticae* (Koch.), Acari: Tetranychidae) are the most destructive ones [3, 5, 6]. *Thrips tabaci* Lindemann is considered as a key factor in limiting profitable cultivation of cotton. Due to severe thrips infestation, leaves become distorted and are turned in a brownish color around the edges and cup upward. Thrips also found on underside of the leaves damaging them by piercing the epidermis of the tissues and sucking the sap oozing out of wounds [7]. As a result, leaves became slivery due to the formation of white patches or streaks which finally caused scarring and distortion of leaves [8].

Chemical pesticides are highly relied upon to control sucking pests on cotton crop which not only causes non-negotiable threats to public but also a huge source of environmental pollution

[9, 10]. Unchecked use of chemical pesticides has been responsible for development of insect pest resistance to pesticides and emergence of new pests. Therefore, risks regarding public and increasing ecological pollution posed by these pesticides have increased continuous and increasing difficulty against its usage [11, 12].

Plant resistance provides control of insect pests without any additional cost. It is economical and also safe for the environment [13]. Variations

of resistance levels among the different cotton varieties against sucking pests have been reported by earlier workers [14, 15].

The knowledge about incidence of *T. tabaci* during cropping season and its possible dynamics helps in designing pest management strategies hence present study was undertaken in fifteen advanced genotypes of transgenic cotton with the objective to assess the relative attraction of these genotypes for *T. tabaci*.

2. Materials and methods

2.1 Cotton Genotypes

The selected advanced genotypes of cotton (FH-488, FH-342, FH-313, FH-404, FH-490, FH-152, FH-450, FH-451, FH-452, FH-453, FH-455, FH-456, FH-457, FH-168 and FH-142) were taken from Cotton Research Station, Faisalabad, Pakistan and were cultivated at research farm of the Cotton Research Station, Faisalabad, Pakistan under Randomized Complete Block Design (RCBD) with three replicates of each genotype during two cropping seasons (2016 and 2017). The Row-to-Row distance was maintained at 75 cm and Plant-to-Plant distance of 30 cm. All standard cultural practices were applied throughout the two cropping seasons.

2.2 Incidence of *T. tabaci*

The cotton crop was kept under observation from the start of germination till final picking. *T. tabaci* population started to develop in two-leaf stage of the crop. Adults as well as immature of *T. tabaci* were counted from ten randomly selected plants from each treatment. Data was recorded from upper, middle and lower parts of each plant. Data was recorded on a weekly basis until the end of the cotton crop. All plots were kept unsprayed throughout the study period.

2.3 Statistical Analysis

The data recorded from upper, middle and lower parts of ten randomly selected plants were averaged to get a replicated value and then subjected to One-way ANOVA to know the significant differences among different genotypes with respect to population incidence of *T. tabaci*. Means were compared by running Tukey's HSD post-hoc test using SPSS v.10 statistical software.

3. Results

3.1 Response of cotton genotypes during 2016

The ANOVA showed highly significant differences with respect to the performance of different advanced genotypes of cotton against *T. tabaci* during 2016 for all months except October were statistically non-significant differences were observed (Table 1). The results revealed that the first highest population peak of *T. tabaci* was recorded during June-2016 on FH-456 (12.67 per leaf) followed by FH-451 (12.33 per leaf) whereas the second highest population peak was observed in August-2016 on FH-457, FH-456 and FH-453 (7.67, 7.33 and 7.00 per leaf, respectively) (Table 2). The population of *T. tabaci* remained at the lowest level of 0.67 per leaf in October-2016 on FH-488, FH-313, FH-490 and FH-142. The population of *T. tabaci* in other months was at moderately acceptable level. Overall, FH-142 performed better than other tested genotypes against *T. tabaci* during first year of study.

Table 1: Analysis of Variance of data regarding population counts of *T. tabaci* during 2016 and 2017 on different advanced genotypes of cotton

Year	Month	MS
2016	May	4.13651**
	June	13.0917**
	July	5.4032**
	August	5.23175**
	September	2.50794**
	October	0.69841^{NS}
2017	May	3.80317**
	June	13.7556**
	July	20.3746**
	August	9.4667**
	September	3.14286^{NS}
	October	1.18413^{NS}
Pooled	May	3.85714**
	June	9.51928**
	July	8.46667**
	August	6.14841**
	September	2.22222**
	October	0.60952^{NS}

^{NS} Non-significant at the 5% level of significance

** Highly significant at the 5% level of significance

Table 2: Population counts of *T. tabaci* during 2016 on different advanced genotypes of cotton

Genotype	Month					
	May	June	July	August	September	October
FH-488	1.33±0.33^{c}	9.17±0.44^{a-d}	2.67±0.33^{c}	4.33±0.67^{ab}	1.00±0.00^{b}	0.67±0.33^{a}
FH-342	3.00±0.58^{abc}	10.50±0.50^{abc}	3.33±0.88^{bc}	4.00±1.00^{ab}	2.00±0.58^{ab}	1.00±0.58^{a}
FH-313	2.00±0.58^{bc}	10.17±0.93^{a-d}	3.00±0.58^{bc}	5.33±0.67^{ab}	1.00±0.00^{b}	0.67±0.33^{a}
FH-404	1.67±0.33^{c}	7.50±0.29^{bcd}	3.00±0.58^{bc}	5.67±1.33^{ab}	1.33±0.67^{ab}	1.33±0.67^{a}
FH-490	1.67±0.67^{c}	8.12±0.48^{bcd}	3.00±1.15^{bc}	5.33±0.33^{ab}	1.00±0.00^{b}	0.67±0.33^{a}
FH-152	3.00±1.00^{abc}	6.50±0.29^{d}	3.67±1.67^{abc}	5.33±1.20^{ab}	1.67±0.33^{ab}	1.33±0.67^{a}
FH-450	3.00±0.58^{abc}	7.98±0.59^{bcd}	4.00±1.00^{abc}	6.33±0.67^{ab}	1.67±0.33^{ab}	1.00±0.58^{a}
FH-451	2.67±0.67^{abc}	12.33±0.33^{a}	3.33±0.88^{bc}	5.00±0.00^{ab}	2.67±0.67^{ab}	1.67±0.33^{a}
FH-452	4.00±1.00^{abc}	12.00±0.58^{a}	5.33±1.45^{abc}	6.67±0.67^{ab}	2.33±0.67^{ab}	1.33±0.33^{a}
FH-453	3.33±0.88^{abc}	7.50±0.29^{bcd}	4.00±1.15^{abc}	7.00±0.58^{a}	3.00±1.15^{ab}	1.33±0.88^{a}
FH-455	2.67±0.67^{abc}	11.17±0.60^{ab}	4.33±1.20^{abc}	6.67±0.67^{ab}	2.00±0.00^{ab}	1.67±0.33^{a}
FH-456	4.67±0.33^{ab}	12.67±1.45^{a}	6.33±1.20^{ab}	7.33±0.33^{a}	4.00±0.58^{a}	2.33±0.33^{a}
FH-457	5.33±0.88^{a}	11.17±1.17^{ab}	7.00±1.15^{a}	7.67±0.88^{a}	2.67±0.67^{ab}	1.67±0.33^{a}
FH-168	2.67±0.67^{abc}	7.00±0.58^{cd}	3.33±0.88^{ab}	4.67±0.33^{ab}	1.33±0.33^{ab}	1.00±0.58^{a}
FH-142	1.33±0.33^{c}	8.00±0.58^{bcd}	2.33±0.33^{c}	3.00±0.00^{b}	0.67±0.33^{b}	0.67±0.33^{a}
HSD	2.6786	3.6933	3.4341	3.7611	2.7189	2.6043

Values sharing similar letters are non-significant at the 5% level of significance

3.2 Response of cotton genotypes during 2017

The ANOVA showed highly significant differences with respect to the performance of different advanced genotypes of cotton against *T. tabaci* during 2017 for all months except September and October were statistically non-significant differences were observed (Table 1). The results revealed that the first highest population peak of *T. tabaci* was recorded during June-2017 on FH-451 (15.50 per leaf) followed by FH-455 (14.67 per leaf) whereas the second highest population peak was observed in August-2017 on FH-457, FH-488 and FH-453 (10.67, 10.00 and 9.33 per leaf, respectively) (Table 3). The population of *T. tabaci* remained at the lowest level of 1.67 per leaf in October-2017 on FH-490 followed by 2.33 per leaf on FH-342 and FH-313. The population of *T. tabaci* in other months was at moderately acceptable level. Overall, FH-142 performed better than other tested genotypes against *T. tabaci* during second year of study.

Table 3: Population counts of *T. tabaci* during 2017 on different advanced genotypes of cotton

Genotype	Month					
	May	June	July	August	September	October
FH-488	2.67±0.33^{ab}	14.33±0.88^{a}	4.00±0.58^{d}	10.00±0.58^{ab}	5.33±0.33^{a}	4.00±0.58^{a}
FH-342	3.67±0.33^{ab}	10.50±0.87^{ab}	5.00±0.58^{d}	6.00±0.58^{efg}	3.33±0.33^{a}	2.33±0.33^{a}
FH-313	3.00±0.00^{ab}	8.33±0.67^{b}	5.67±0.33^{cd}	6.67±0.67^{c-g}	2.33±0.67^{a}	2.33±0.88^{a}
FH-404	2.33±0.88^{ab}	10.33±0.88^{ab}	7.00±0.58^{bcd}	7.67±0.67^{b-f}	2.67±0.33^{a}	2.33±0.33^{a}
FH-490	2.33±0.67^{ab}	9.83±1.09^{ab}	9.00±1.15^{abc}	7.33±0.67^{b-g}	2.33±0.88^{a}	1.67±0.33^{a}
FH-152	4.33±1.20^{ab}	10.83±1.09^{ab}	9.00±0.58^{abc}	6.00±1.53^{efg}	3.33±0.33^{a}	2.67±0.33^{a}
FH-450	3.67±1.20^{ab}	11.50±1.32^{ab}	10.33±0.67^{ab}	7.33±0.88^{b-g}	2.67±0.67^{a}	3.00±0.58^{a}
FH-451	3.33±0.88^{ab}	15.50±0.87^{a}	10.67±0.67^{a}	6.33±0.88^{d-g}	3.33±0.88^{a}	3.33±0.33^{a}
FH-452	4.67±0.88^{a}	13.33±1.20^{ab}	6.33±0.33^{cd}	8.67±1.45^{a-e}	3.67±0.67^{a}	2.67±0.88^{a}
FH-453	4.00±0.58^{ab}	13.67±1.20^{ab}	7.00±0.58^{bcd}	9.00±1.00^{a-d}	4.33±0.88^{a}	4.00±0.58^{a}
FH-455	3.67±0.88^{ab}	14.67±2.03^{a}	11.00±1.15^{a}	7.33±0.88^{b-g}	4.33±1.45^{a}	3.00±1.00^{a}
FH-456	5.33±0.33^{a}	13.83±0.93^{ab}	11.67±1.45^{a}	9.33±0.88^{abc}	4.67±0.67^{a}	3.33±0.88^{a}
FH-457	5.33±0.88^{a}	12.33±0.88^{ab}	6.67±0.88^{cd}	10.67±1.45^{a}	3.67±0.88^{a}	2.67±0.33^{a}
FH-168	3.00±0.58^{ab}	13.50±1.04^{ab}	5.00±0.58^{d}	5.00±0.00^{fg}	2.33±0.88^{a}	2.67±0.67^{a}
FH-142	1.33±0.33^{b}	9.83±0.93^{ab}	4.00±0.58^{d}	4.67±0.88^{g}	1.67±0.67^{a}	2.67±0.88^{a}
HSD	3.2382	5.8991	3.4214	2.7849	4.0744	3.0583

Values sharing similar letters are non-significant at the 5% level of significance

3.3 Pooled response of cotton genotypes

The ANOVA showed highly significant differences with respect to the performance of different advanced genotypes of cotton against *T. tabaci* during 2016 and 2017 for all months except October where statistically non-significant differences were observed (Table 1). The results revealed that the first highest population peak of *T. tabaci* was recorded during June on FH-455 (12.92 per leaf) followed by FH-452 (12.67 per leaf) whereas the second highest population peak was observed in August on FH-457, FH-142 and FH-168 (9.17, 8.83 and 8.83 per leaf, respectively) (Table 4). The population of *T. tabaci* remained at the lowest level of 1.17 per leaf in October on FH-488, FH-313, FH-490 and FH-142. The population of *T. tabaci* in other months was at moderately acceptable level. Overall, FH-142 performed better than other tested genotypes against *T. tabaci* during both year of study.

Table 4: Cumulative population counts of *T. tabaci* on different advanced genotypes of cotton

Genotype	Month					
	May	June	July	August	September	October
FH-488	2.00±0.00^{cd}	11.75±0.38^{a-e}	3.33±0.33^{fg}	7.17±0.60^{a-d}	3.17±0.17^{ab}	2.33±0.17^{a}
FH-342	3.33±0.33^{a-d}	10.50±0.50^{a-e}	4.17±0.73^{efg}	5.00±0.58^{cde}	2.67±0.17^{ab}	1.67±0.33^{a}
FH-313	2.50±0.29^{cd}	9.25±0.14^{cde}	4.33±0.17^{d-g}	6.00±0.58^{b-e}	1.67±0.33^{b}	1.50±0.29^{a}
FH-404	2.00±0.58^{cd}	8.92±0.55^{e}	5.00±0.50^{c-g}	6.67±0.88^{a-d}	2.00±0.29^{ab}	1.83±0.44^{a}
FH-490	2.00±0.58^{cd}	8.98±0.78^{de}	6.00±0.58^{b-e}	6.33±0.17^{b-e}	1.67±0.44^{b}	1.17±0.17^{a}
FH-152	3.67±1.01^{a-d}	8.67±0.44^{e}	6.33±0.60^{b-e}	5.67±1.33^{b-e}	2.50±0.29^{ab}	2.00±0.29^{a}
FH-450	3.33±0.88^{a-d}	9.74±0.95^{b-e}	7.17±0.44^{abc}	6.83±0.73^{a-d}	2.17±0.17^{ab}	2.00±0.00^{a}
FH-451	3.00±0.76^{a-d}	13.92±0.58^{a}	7.00±0.50^{abc}	5.67±0.44^{b-e}	3.00±0.76^{ab}	2.50±0.29^{a}
FH-452	4.33±0.88^{abc}	12.67±0.73^{a-d}	5.83±0.88^{b-f}	7.67±0.83^{abc}	3.00±0.58^{ab}	2.00±0.50^{a}
FH-453	3.67±0.67^{a-d}	10.58±0.51^{a-e}	5.50±0.76^{b-g}	8.00±0.58^{ab}	3.67±0.93^{ab}	2.67±0.17^{a}
FH-455	3.17±0.60^{a-d}	12.92±1.31^{abc}	7.67±0.73^{ab}	7.00±0.76^{a-d}	3.17±0.73^{ab}	2.33±033^{a}
FH-456	5.00±0.00^{ab}	13.25±1.18^{ab}	9.00±1.00^{a}	8.33±0.33^{ab}	4.33±0.60^{a}	2.83±0.60^{a}
FH-457	5.33±0.88^{a}	11.75±0.14^{a-e}	6.83±0.93^{a-d}	9.17±0.60^{a}	3.17±0.60^{ab}	2.17±0.17^{a}
FH-168	2.83±0.60^{bcd}	10.25±0.38^{a-e}	4.17±0.33^{efg}	4.83±0.17^{de}	1.83±0.44^{ab}	1.83±0.44^{a}
FH-142	1.33±0.33^{d}	8.92±0.71^{e}	3.17±0.33^{g}	3.83±0.44^{e}	1.17±0.17^{b}	1.67±0.33^{a}
HSD	2.4432	3.7252	2.5650	2.8192	2.6417	1.7370

Values sharing similar letters are non-significant at the 5% level of significance

4. Discussion

According to results, maximum population of *T. tabaci* was recorded on transgenic cultivars, i.e., FH-451 (15.50 /leaf) followed by FH-452 and FH-457 (14.67 and 12.76/leaf, respectively) during 2017 whereas minimum population of *T. tabaci* on transgenic cotton genotypes was observed in the following order: FH-142 followed by FH-313, FH-490 and FH-488. Our findings are well supported by Naveen, *et al*. [16] and Men, *et al*. [17] who reported that higher population of *T. tabaci* was recorded on different genotypes of Bt cotton. However, these results are in contradiction to Whitehouse, *et al*. [18] who observed that population of *T. tabaci* was low on

Bt cotton as compared to conventional cotton cultivars, this difference in behavior of *T. tabaci* may be attributed to difference in morphological characters of genotypes under study. Some of the studies showed that sucking pest were found equal abundance in Bt and non-Bt varieties [19]. Our results are also in conformity with Din, *et al*. [20] who checked natural resistance in Bt cotton and reported that FH-170 had a minimum population of *T. tabaci* (3.1/leaf), as compared to normal leaf cotton S-12 (3.61/leaf). The present findings were also confirmed by Majeed, *et al*. [21] who tested different transgenic cotton genotype viz. NIBGE-I, IR-443, IR-448, NK, FH-901, FH-925, NIAB-999 and NIAB-98 and reported that NK genotype was the least attractive (2.5/leaf) and was statistically at par from all other genotypes and NIAB-98 was the most attractive (5.8/leaf) to *T. tabaci* infestation. The present findings were also confirmed by Karar, *et al*. [22] who evaluated innovative cotton genotypes against insect pest prevalence and found that the genotypes FH-142 (0.67/leaf) and FH-326 (0.61/leaf) demonstrated statistically similar population, followed by NIAB -2 (0.29/leaf) against *T. tabaci* whereas. AA-926 had a minimum population (0.20/leaf).
The results of our study are also comparable with those of [23-27] who checked resistance levels of different transgenic cotton genotypes to sucking pest complex and observed that some Bt varieties recoded minimum *T. tabaci* incidence while some bt varieties were moderate to higher level of pest attack. The findings of the present study are contradictory to Raza, *et al*. [28] who observed population buildup of *T. tabaci* on cotton and concluded that Bt varieties had maximum mean population of *T. tabaci i.e.* FH-901 (10.44/leaf) followed by FH-113 and FH-114 (9.50 and 8.90 /leaf, respectively). Our results does not match with the findings of Rehman, *et al*. [29] who observed population dynamics of *T. tabaci* on transgenic and non-transgenic cultivars of cotton and results showed that transgenic cotton cultivars were more susceptible to *T. tabaci* infestation compared to conventional cotton genotypes and the highest population was observed on IR 901 and FH 113 (3.11 and 3.14 thrips per leaf, respectively). Akram, *et al*. [30] also reported that non-Bt varieties showed a somewhat greater degree of resistance to *T. tabaci* as compared to Bt varities.

5. Conclusion
In summary, it is generally assumed that transgenic cotton genotypes are more susceptible to the attack of sucking insect pests but in recent studies, tested advanced genotypes of transgenic cotton showed a greater degree of resistance against *T. tabaci* and these genotypes could prove as a good alternative to previous available varieties in the near future under persisting climatic conditions.

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