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## Response of different advanced genotypes of transgenic cotton (*Gossypium hirsutum* L.) against *Amrasca biguttula biguttula* (Ishida) (Homoptera: Cicadellidae)

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### Abstract

The present study aimed at screening fifteen genotypes of cotton (*Gossypium hirsutum* L.) for population dynamics of *Amrasca biguttula biguttula* (Ishida). 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 0.33 jassid /leaf in October-2016 and 0.67 in September while in 2017 *A. biguttula biguttula* population observed was 0.67/leaf in October and May, 1.67/leaf in September and 2.67 /leaf in June. The maximum population of *A. biguttula biguttula* was recorded on FH-490 (7.33/leaf) followed by FH-152 and FH-453 (7.00/leaf) during 2017. On a cumulative basis, highest peak of *A. biguttula biguttula* population was observed on FH-450 (6.00/leaf). In conclusion, advanced genotypes of transgenic cotton proved to resist the population buildup of *A. biguttula biguttula* throughout the period of study.

**Keywords:** Cotton, genotypes, *Amrasca biguttula biguttula*, sucking pest, population dynamics

### 1. Introduction

Cotton (*Gossypium hirsutum* L.: Genus: *Hirsutum*; Family: Malvaceae) is widely considered as one of the most important fiber and non-food cash crop in Pakistan<sup>[1]</sup>. It is important for the national economy as it provides substantial foreign exchange earnings<sup>[2, 3]</sup>. Cotton crop provides bread and butter to the millions of people apart from earning foreign revenues<sup>[4]</sup>. Among the factors contributing to the low yield, insect pests are the major ones<sup>[5]</sup>. Cotton crop is attacked by a total of 162 insect pest species worldwide, which feed on cotton during different growth stages<sup>[6]</sup>. Pakistan ranks 4<sup>th</sup> as a grower and 3<sup>rd</sup> as an exporter of raw cotton in the World, but still lint yield is not upto the mark as compared to other countries. In Pakistan 20-40% losses in cotton crop are reported due to insect pest attack<sup>[7]</sup>. American cotton, *G. hirsutum* (L.), is more vulnerable to the outbreak of sucking insect/mite pests as well as bollworm complex than indigenous cotton, *Gossypium arborium*, under prevailing climatic conditions of Indo-Pak region<sup>[8]</sup>.

Cotton pests primarily are divided into sucking pests and bollworms. The pests of major significance in cotton are sucking pests like jassids (*Amrasca biguttula biguttula*, Ishida), aphids (*Aphis gossypii*, Glover), whiteflies (*Bemisia tabaci*, Gennadius) and thrips (*Thrips tabaci* Lindeman). Jassid is the pest of economically important crops including agricultural and non-agricultural plants<sup>[9]</sup>. Both adults and nymphs of jassid suck the sap from leaves and inject toxic saliva resulting in 'hopper burn' symptoms by feeding on the underside of the leaves. The attacked leaves turn pale and then rust-red. With a change in appearance, the leaves also turn downwards, dry up and fall to the ground. Owing to the loss of plant vitality, the cotton bolls also drop off resulting in yield reduction<sup>[10]</sup>. *A. biguttula biguttula* found on cotton was known to be a pest of vegetative stage but in recent years it has been occurring throughout the crop growth phase, causing significant yield losses. The incidence of cotton leaf hoppers on Bt cotton<sup>[11-13]</sup> and yield reduction has been reported up to 50% alone due to this pest<sup>[14]</sup>.

The plant protection management tactics generally include the application of pesticides to overcome the pest problem. In Pakistan, it is estimated approximately 70-90% insecticides of multinational and national insecticide companies were sprayed on cotton crop [15-17]. Chemical control not only induces the resistance in insects but also creates health hazards and ecological contamination and disturbing the balance between the forces of creation and forces of destruction in agro-ecosystem [18]. With the development of transgenic cotton, use of broad-spectrum insecticides has been reduced to a great extent. As a result, non-target sucking insect pests of cotton which includes jassid, whitefly, thrips, aphids, leaf bugs and spider mites survive better [19] and feed on their host more comfortably.

For the sustainable and effective management of this pest, the classification of resistant cotton varieties against *A. biguttula biguttula* will provide a baseline to get the highest yield. There is need to develop alternative means of control that are safe, local in production, low in cost and also environment friendly. Therefore, the present study was conducted to compare transgenic cotton cultivars for *A. biguttula biguttula* incidence, study the population dynamics and seasonal abundance of *A. biguttula biguttula* on cotton to identify the peak abundance period.

## 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 *A. biguttula biguttula*

The cotton crop was kept under observation from the start of germination till final picking. *A. biguttula biguttula* population started to develop in two-leaf stage of the crop. Adults as well as immature of *A. biguttula biguttula* 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 *A. biguttula biguttula*. Means were compared by running Tukey's HSD post-hoc test using Statistix 9.0 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 *A. biguttula biguttula* during 2016 for the month of July while in rest of the months statistically non-significant differences were observed (Table 1). The results revealed that the first highest population peak of *A. biguttula biguttula* was recorded during July-2016 on FH-456 (6.33 per leaf) followed by FH-457 (6.00 per leaf) whereas the second highest population peak was observed in August-2016 on FH-490, FH-152 and FH-450 (3.33, 3.00 and 3.00 per leaf, respectively). The population of *A. biguttula biguttula* remained at the lowest level of 0.33 per leaf in October-2016 on FH-488, FH-168 and FH-142. The population of *A. biguttula biguttula* in other months was at moderately acceptable level. Overall, FH-142 performed better than other tested genotypes against *A. biguttula biguttula* during first year of study (Table 2).

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

Year	Month	MS
2016	May	0.41270 <sup>NS</sup>
	June	0.50794 <sup>NS</sup>
	July	4.55556 <sup>**</sup>
	August	0.97381 <sup>NS</sup>
	September	0.64127 <sup>NS</sup>
	October	0.78413 <sup>NS</sup>
2017	May	0.73651 <sup>NS</sup>
	June	2.29127 <sup>NS</sup>
	July	4.39048 <sup>**</sup>
	August	0.92698 <sup>NS</sup>
	September	0.83175 <sup>NS</sup>
	October	1.37460 <sup>**</sup>
Pooled	May	0.36667 <sup>NS</sup>
	June	1.01925 <sup>NS</sup>
	July	3.03413 <sup>**</sup>
	August	0.45496 <sup>NS</sup>
	September	0.32937 <sup>NS</sup>
	October	0.65714 <sup>**</sup>

NS Non-significant at the 5% level of significance

\*\* Highly significant at the 5% level of significance

**Table 2:** Population counts of *A. biguttula biguttula* during 2016 on different advanced genotypes of cotton

Genotype	Month					
	May	June	July	August	September	October
FH-488	0.67±0.33 <sup>a</sup>	2.33±0.33 <sup>a</sup>	2.67±0.33 <sup>a</sup>	2.67±0.33 <sup>a</sup>	1.00±0.00 <sup>a</sup>	0.33±0.33 <sup>a</sup>
FH-342	1.33±0.88 <sup>a</sup>	2.33±0.88 <sup>a</sup>	3.33±0.88 <sup>a</sup>	1.67±0.33 <sup>a</sup>	2.00±0.58 <sup>a</sup>	1.00±0.58 <sup>a</sup>
FH-313	0.33±0.33 <sup>a</sup>	2.00±0.57 <sup>a</sup>	4.67±0.88 <sup>a</sup>	2.33±0.33 <sup>a</sup>	1.00±0.00 <sup>a</sup>	0.67±0.33 <sup>a</sup>
FH-404	0.67±0.33 <sup>a</sup>	3.00±1.52 <sup>a</sup>	3.00±0.58 <sup>a</sup>	2.67±1.20 <sup>a</sup>	1.33±0.67 <sup>a</sup>	1.33±0.67 <sup>a</sup>
FH-490	0.67±0.33 <sup>a</sup>	2.33±0.33 <sup>a</sup>	4.67±0.88 <sup>a</sup>	3.33±0.88 <sup>a</sup>	1.00±0.33 <sup>a</sup>	0.67±0.33 <sup>a</sup>
FH-152	0.33±0.33 <sup>a</sup>	3.00±0.57 <sup>a</sup>	3.67±1.67 <sup>a</sup>	3.00±0.58 <sup>a</sup>	1.67±0.33 <sup>a</sup>	1.33±0.67 <sup>a</sup>
FH-450	0.00±0.00 <sup>a</sup>	2.67±0.66 <sup>a</sup>	5.33±0.33 <sup>a</sup>	3.00±0.58 <sup>a</sup>	1.67±0.33 <sup>a</sup>	1.00±0.58 <sup>a</sup>
FH-451	0.33±0.33 <sup>a</sup>	2.00±0.57 <sup>a</sup>	3.33±0.88 <sup>a</sup>	2.00±0.58 <sup>a</sup>	0.67±0.33 <sup>a</sup>	1.67±0.33 <sup>a</sup>
FH-452	0.33±0.33 <sup>a</sup>	2.67±0.58 <sup>a</sup>	5.33±1.45 <sup>a</sup>	2.33±0.88 <sup>a</sup>	1.67±0.58 <sup>a</sup>	1.33±0.33 <sup>a</sup>
FH-453	0.67±0.33 <sup>a</sup>	2.67±1.20 <sup>a</sup>	5.00±0.58 <sup>a</sup>	2.50±0.50 <sup>a</sup>	2.00±0.67 <sup>a</sup>	1.33±0.88 <sup>a</sup>
FH-455	0.33±0.33 <sup>a</sup>	2.33±1.33 <sup>a</sup>	4.33±1.20 <sup>a</sup>	1.67±0.67 <sup>a</sup>	1.33±0.33 <sup>a</sup>	0.67±0.33 <sup>a</sup>
FH-456	1.00±0.00 <sup>a</sup>	3.00±1.15 <sup>a</sup>	6.33±1.20 <sup>a</sup>	3.00±0.58 <sup>a</sup>	1.67±0.33 <sup>a</sup>	2.00±0.58 <sup>a</sup>
FH-457	0.67±0.33 <sup>a</sup>	2.00±0.57 <sup>a</sup>	6.00±0.58 <sup>a</sup>	2.67±0.33 <sup>a</sup>	0.67±0.33 <sup>a</sup>	0.67±0.33 <sup>a</sup>
FH-168	1.00±0.58 <sup>a</sup>	2.67±0.88 <sup>a</sup>	3.33±0.88 <sup>a</sup>	2.33±1.20 <sup>a</sup>	1.33±0.33 <sup>a</sup>	0.33±0.33 <sup>a</sup>
FH-142	0.00±0.00 <sup>a</sup>	1.67±0.66 <sup>a</sup>	2.33±0.33 <sup>a</sup>	1.33±0.33 <sup>a</sup>	0.67±0.33 <sup>a</sup>	0.33±0.33 <sup>a</sup>
HSD	2.0629	4.6846	4.3769	3.5177	2.1457	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 *A. biguttula biguttula* during 2017 for the month of July and October while in the rest of the months statistically non-significant differences were observed (Table 1). The results revealed that the first highest population peak of *A. biguttula biguttula* was recorded during June-2017 on FH-488 and FH-404 (5.00 per leaf) followed by FH-451 and FH-455 (4.83 per leaf) whereas the second highest population

peak was observed in July-2017 on FH-490, FH-152, FH-404 and FH-450 (7.33, 7.00, 7.00 and 6.67 per leaf, respectively). The population of *A. biguttula biguttula* remained at the lowest level of 0.67 per leaf in October-2017 on FH-142 followed by 1.00 per leaf on FH-456 and 1.33 per leaf on FH-457. The population of *A. biguttula biguttula* in other months was at moderately acceptable level. Overall, FH-142 performed better than other tested genotypes against *A. biguttula biguttula* during the second year of study (Table 3).

**Table 3:** Population counts of *A. biguttula biguttula* during 2017 on different advanced genotypes of cotton

Genotype	Months					
	May	June	July	August	September	October
FH-488	1.33±0.33 <sup>a</sup>	5.00±2.08 <sup>a</sup>	4.00±0.58 <sup>bc</sup>	3.33±0.33 <sup>a</sup>	2.67±1.20 <sup>a</sup>	2.00±0.58 <sup>abc</sup>
FH-342	1.67±0.67 <sup>a</sup>	3.67±1.76 <sup>a</sup>	5.00±0.58 <sup>abc</sup>	4.00±0.00 <sup>a</sup>	3.00±0.58 <sup>a</sup>	2.33±0.33 <sup>abc</sup>
FH-313	2.00±0.58 <sup>a</sup>	4.67±0.88 <sup>a</sup>	5.67±0.33 <sup>abc</sup>	2.33±0.33 <sup>a</sup>	2.67±0.88 <sup>a</sup>	1.67±0.33 <sup>abc</sup>
FH-404	1.33±0.33 <sup>a</sup>	5.00±0.57 <sup>a</sup>	7.00±0.58 <sup>ab</sup>	2.67±0.33 <sup>a</sup>	2.00±0.58 <sup>a</sup>	2.33±0.33 <sup>abc</sup>
FH-490	1.00±0.58 <sup>a</sup>	4.17±0.44 <sup>a</sup>	7.33±0.88 <sup>a</sup>	3.00±0.58 <sup>a</sup>	2.33±0.88 <sup>a</sup>	1.67±0.33 <sup>abc</sup>
FH-152	1.67±0.88 <sup>a</sup>	5.17±0.73 <sup>a</sup>	7.00±0.58 <sup>ab</sup>	2.33±0.88 <sup>a</sup>	2.00±0.58 <sup>a</sup>	2.67±0.33 <sup>ab</sup>
FH-450	1.00±0.58 <sup>a</sup>	4.00±0.58 <sup>a</sup>	6.67±1.20 <sup>abc</sup>	3.33±0.88 <sup>a</sup>	2.67±0.67 <sup>a</sup>	3.00±0.58 <sup>a</sup>
FH-451	1.33±0.88 <sup>a</sup>	4.83±1.37 <sup>a</sup>	6.00±0.58 <sup>abc</sup>	3.00±0.58 <sup>a</sup>	3.33±0.33 <sup>a</sup>	2.67±0.33 <sup>ab</sup>
FH-452	1.67±0.88 <sup>a</sup>	4.33±0.88 <sup>a</sup>	6.33±0.33 <sup>abc</sup>	2.67±0.88 <sup>a</sup>	2.33±0.67 <sup>a</sup>	2.67±0.88 <sup>ab</sup>
FH-453	0.33±0.33 <sup>a</sup>	5.33±1.20 <sup>a</sup>	7.00±0.58 <sup>ab</sup>	4.00±1.15 <sup>a</sup>	3.00±0.00 <sup>a</sup>	1.33±0.33 <sup>abc</sup>
FH-455	1.33±0.33 <sup>a</sup>	4.83±0.73 <sup>a</sup>	4.67±0.67 <sup>abc</sup>	3.33±0.33 <sup>a</sup>	2.67±0.33 <sup>a</sup>	2.00±0.00 <sup>abc</sup>
FH-456	2.00±0.58 <sup>a</sup>	4.67±1.20 <sup>a</sup>	6.33±0.33 <sup>abc</sup>	3.00±0.58 <sup>a</sup>	2.33±0.67 <sup>a</sup>	1.00±0.58 <sup>bc</sup>
FH-457	0.67±0.33 <sup>a</sup>	2.33±0.33 <sup>a</sup>	4.33±0.33 <sup>abc</sup>	3.67±0.67 <sup>a</sup>	3.67±0.88 <sup>a</sup>	1.33±0.33 <sup>abc</sup>
FH-168	1.67±0.33 <sup>a</sup>	4.50±1.04 <sup>a</sup>	5.00±0.58 <sup>abc</sup>	3.33±0.88 <sup>a</sup>	2.33±0.88 <sup>a</sup>	2.00±0.58 <sup>abc</sup>
FH-142	0.67±0.33 <sup>a</sup>	2.67±0.88 <sup>a</sup>	3.67±0.33 <sup>c</sup>	2.33±0.33 <sup>a</sup>	1.67±0.67 <sup>a</sup>	0.67±0.33 <sup>c</sup>
HSD	2.9049	5.5744	3.2938	3.2382	3.5032	1.9876

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 *A. biguttula biguttula* during 2016 and 2017 for the month of July and October while in the rest of the months statistically non-significant differences were observed (Table 1). The results revealed that the first highest population peak of *A. biguttula biguttula* was recorded during June on FH-152 (4.08 per leaf) followed by FH-453 (4.00 per leaf) whereas the second highest population peak was observed in

July on FH-456, FH-453 and FH-490 (6.33, 6.00 and 6.00 per leaf, respectively). The population of *A. biguttula biguttula* remained at the lowest level of 0.50 per leaf in October on FH-142, 1.00 per leaf on FH-457 and 1.17 per leaf on FH-490, FH-488 and FH-313. The population of *A. biguttula biguttula* in other months was at moderately acceptable level. Overall, FH-142 performed better than other tested genotypes against *A. biguttula biguttula* during both year of study (Table 4).

**Table 4:** Cumulative population counts of *A. biguttulla biguttulla* on different advanced genotypes of cotton

Genotype	Months					
	May	June	July	August	September	October
FH-488	1.00±0.00 <sup>a</sup>	3.67±1.20 <sup>a</sup>	3.33±0.33 <sup>bc</sup>	3.00±0.00 <sup>a</sup>	1.83±0.60 <sup>a</sup>	1.17±0.17 <sup>ab</sup>
FH-342	1.50±0.76 <sup>a</sup>	3.00±1.26 <sup>a</sup>	4.17±0.73 <sup>abc</sup>	2.83±0.17 <sup>a</sup>	2.50±0.00 <sup>a</sup>	1.67±0.33 <sup>ab</sup>
FH-313	1.17±0.44 <sup>a</sup>	3.33±0.73 <sup>a</sup>	5.17±0.44 <sup>abc</sup>	2.33±0.17 <sup>a</sup>	1.83±0.44 <sup>a</sup>	1.17±0.17 <sup>ab</sup>
FH-404	1.00±0.29 <sup>a</sup>	4.00±0.87 <sup>a</sup>	5.00±0.50 <sup>abc</sup>	2.67±0.73 <sup>a</sup>	1.67±0.17 <sup>a</sup>	1.83±0.44 <sup>ab</sup>
FH-490	0.83±0.44 <sup>a</sup>	3.25±0.25 <sup>a</sup>	6.00±0.84 <sup>ab</sup>	3.17±0.44 <sup>a</sup>	1.67±0.44 <sup>a</sup>	1.17±0.17 <sup>ab</sup>
FH-152	1.00±0.29 <sup>a</sup>	4.08±0.58 <sup>a</sup>	5.33±0.60 <sup>abc</sup>	2.67±0.17 <sup>a</sup>	1.83±0.17 <sup>a</sup>	2.00±0.29 <sup>ab</sup>
FH-450	0.50±0.29 <sup>a</sup>	3.33±0.60 <sup>a</sup>	6.00±0.50 <sup>ab</sup>	3.17±0.73 <sup>a</sup>	2.17±0.17 <sup>a</sup>	2.00±0.00 <sup>ab</sup>
FH-451	0.83±0.44 <sup>a</sup>	3.42±0.42 <sup>a</sup>	4.67±0.73 <sup>abc</sup>	2.50±0.50 <sup>a</sup>	2.00±0.00 <sup>a</sup>	2.17±0.17 <sup>a</sup>
FH-452	1.00±0.50 <sup>a</sup>	3.50±0.87 <sup>a</sup>	5.83±0.88 <sup>abc</sup>	2.50±0.76 <sup>a</sup>	2.00±0.29 <sup>a</sup>	2.00±0.50 <sup>ab</sup>
FH-453	0.50±0.29 <sup>a</sup>	4.00±0.87 <sup>a</sup>	6.00±0.58 <sup>ab</sup>	3.25±0.38 <sup>a</sup>	2.50±0.29 <sup>a</sup>	1.33±0.33 <sup>ab</sup>
FH-455	0.83±0.33 <sup>a</sup>	3.58±0.36 <sup>a</sup>	4.50±0.76 <sup>abc</sup>	2.50±0.50 <sup>a</sup>	2.00±0.50 <sup>a</sup>	1.33±0.29 <sup>ab</sup>
FH-456	1.50±0.29 <sup>a</sup>	3.83±0.44 <sup>a</sup>	6.33±0.44 <sup>a</sup>	3.00±0.50 <sup>a</sup>	2.00±0.29 <sup>a</sup>	1.50±0.50 <sup>ab</sup>
FH-457	0.67±0.17 <sup>a</sup>	2.17±0.44 <sup>a</sup>	5.17±0.44 <sup>abc</sup>	3.17±0.44 <sup>a</sup>	2.17±0.33 <sup>a</sup>	1.00±0.00 <sup>ab</sup>
FH-168	1.33±0.44 <sup>a</sup>	3.58±0.93 <sup>a</sup>	4.17±0.33 <sup>abc</sup>	2.83±1.01 <sup>a</sup>	1.83±0.44 <sup>a</sup>	1.17±0.33 <sup>ab</sup>
FH-142	0.33±0.17 <sup>a</sup>	2.17±0.73 <sup>a</sup>	3.00±0.29 <sup>c</sup>	1.83±0.33 <sup>a</sup>	1.17±0.17 <sup>a</sup>	0.50±0.29 <sup>b</sup>
HSD	1.9581	3.9504	2.9310	2.5515	1.7011	1.5196

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

#### 4. Discussion

According to results, maximum population of *A. biguttulla biguttulla* was recorded on transgenic cultivars, i.e., FH-490 (7.33/leaf) followed by FH-152 and FH-404 which are statistically at par with each other (7.00/leaf) during 2017 whereas minimum population of *A. biguttulla biguttulla* on transgenic cotton cultivar was observed in the following order: FH-142 followed by FH-488, and FH-168. In an experiment regarding to our outputs nine cotton genotypes were tested for jassid incidence and DNH-105 was found relatively resistant to jassids among the varieties tested, as it showed least number of jassids per leaf (0.67) followed by CIM-506 with 0.99 leaf<sup>-1</sup> jassids. While BH-167 was found to be the most susceptible as it showed maximum jassids per leaf (1.41), however it was statistically at par with CIM-554 and DNH-57 having 1.36 leaf<sup>-1</sup> jassids each. [20]. Our results are contradictory to the [21] who tested nine cotton promising genotypes and reported that the genotype AGC-Nazeer, IBU-63, FH-Noor and FH-142 has maximum attack of jassid per leaf i.e., 0.93, 0.91, 0.87 and 0.87 and are statistically at par with each other and shows susceptible response towards jassid. The genotype FH-326 having 0.60 jassid per leaf and are statistically similar to MNH-988 (0.47), AA-926 (0.40). The genotype NIAB-Bt-2 has minimum attack of jassid per leaf i.e., 0.32 per leaf and is considered resistant. Difference in the results may be due to difference in climatic conditions. Our results are found partially similar to another study in which 350 cotton genotypes were tested for relative susceptibility against leafhopper, *A. biguttulla biguttulla*. Among the genotypes screened, no genotypes were found to be resistant, 50 genotypes were categorized as tolerant, 158 genotypes moderately tolerant, 91 genotypes susceptible and 51 genotypes highly susceptible against leafhopper with a population ranged from 0.10 to 0.78, 0.79 to 1.57, 1.58 to 2.36 and 2.37 to 6.25 leafhopper/3 leaves/plant respectively based on the standard deviation value [22]. In another investigation similar results were reported by relative resistance of ten different okra genotypes against major sucking pests and it was revealed that IIVR-10 showed the lowest mean population jassid (1.82) and the highest population was recorded in genotype 317-10-1 [23]. Our results are also in conformity with [24] who tested the relative resistance of thirty genotypes of okra against jassid and it was observed that the genotype Pusa sawani showed maximum

jassid population i.e. 3.32 per leaf followed by 3.24, 2.98 and 2.87 per leaf on Dera local, Okra-3 and Okra Sindh, respectively and differed significantly from one another. Minimum jassid population was recorded (1.22 per leaf) on Green wonder with non-significant difference from Punjab selection having 1.29 jassid per leaf. Our findings were also found similar to a study on the field screening of jassids preference as a host plant on nine varieties of eggplant, when different varieties were compared, it was found that highly preferred variety by jassid was Bemissal (3.36 jassids per leaf) whereas the least preferred variety recorded was Rubi (1.42 jassids per leaf) [25]. Results of present experiment match with those of [4] who tested six cotton genotypes and the results revealed that the maximum jassid population was observed on NIAB-86 (0.968 /Leaf) followed by SLH-257 (0.876 /Leaf) and MNH-635 (0.876 /Leaf) and were statistically similar to each other. Whereas the minimum jassid population was observed on CIM-446 (0.548/Leaf) which was statistically at par with CIM-482 (0.670 /leaf) and NIAB Karishma (0.6911/Leaf) and statistically at par with each other.

#### 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 *A. biguttulla biguttulla* 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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