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Genetic analysis of anatomical and trichome characters associated with jassid resistance in upland cotton

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Abstract

Resistance breeding for biotic and abiotic stresses is being considered as part of mainstream crop improvement to increase crop productivity under climate change era. Present study revealed that cotton anatomical features *viz*., distance between phloem and epidermis, palisade height and number of palisade cells shows significantly negative correlation with jassid susceptibility grade as resistant varieties had more number of palisade cells per unit area. The morphological features of trichome density and leaf thickness also exhibited highly significantly positive correlation with jassid resistance, indicating their importance in resistance breeding. The parent KC 2 showed the highest distance between phloem and epidermis, number of trichomes and leaf thickness. The hybrid KC 2 x MCU 12 recorded higher jassid resistance in related characters compared to other crosses. This resistance was reflected in artificial screening for KC 2. However, the parents MCU 5 and MCU 12 constituted moderately resistant group. The analysis of generation mean from cross KC 2 x MCU 12 revealed that predominance of dominance component for majority of the yield characters. The cross MCU 5 x MCU 12 showed predominance of dominance component for majority of the fiber quality traits. The duplicate epistasis was found to be more predominant when compared to complementary epistasis in both the crosses.

Keywords

Anatomic traits, jassid, resistance breeding, trichome, trait association

1. Introduction

Cotton (*Gossypium spp*.) is known as white gold, very important commercial fibre crop of global importance with a significant role in Indian agriculture, industrial development and improving the national economy. It provides employment to about 70 million people and contributes nearly 75 per cent of total

raw material to the textile industry in India. It is the back bone of the textile industry in India. *Gossypium* is the large, diverse and economically viable genus, which includes fourty six diploids and four tetraploids species indigenous to most of the tropical regions of the world (Fryxell *et al*., 1992). India cultivate about 120 lakhs hectares' and total production of 300 lakh bales at each bale 170 Kgs (Anonymous, 2014). India accounts for about a third of global cotton area and predominantly monsoon-season or Kharif crop. India is the only country in the world where all the four cultivated species of cotton *viz*., G.*hirsutum, G.herbaceum, G.arboreum* and *G.barbadense* are cultivated on commercial scale, besides hybrids. The southern cotton zone, comprising Karnataka, Andhra Pradesh and Tamil Nadu accounts for 19 per cent of total production of our nation (AICCIP, 2011). In Tamil Nadu, cotton is grown almost throughout the year in five ecological zones as winter irrigated, summer irrigated, winter rainfed black soil tract, winter rainfed red soil tract and as rice fallow crop (Kamalanathan et al, 1965). The pest scenario of Indian cotton cultivation is declined with adoption of Bt cotton. But declines happen to bollworms; the sap feeders, viz. aphids and jassids, are emerging as serious pests (Akoijam et al., 2014; Dhaliwal et al., 2010; Vennila., 2008). Cotton production in India still have production constrained due to many insect-pests, affecting right from germination stage to till harvesting and causes economic losses in cotton crop. This trend is simply because of Bt cotton cannot control sucking pests of cotton and there is no difference in sucking pests incidence in Bt and non Bt cotton hybrid.

The major share for the loss is due to the damage caused by sucking pests, the leaf hopper (Jassids) (*Amrasca devastans*) (Distant) (=*Amrasca biguttula biguttula* (Ishida)) is considered as a key pest in *G.hirsutum* L. lines in all cotton growing regions (Mathews, 1994). It causes severe yield losses (15 to 45 percentage) in Punjab, Maharastra and Tamil Nadu (Singh and Lakra, 1990). Nymphs and adults suck the sap from leaves, lowering the plant vitality, sustained feeding causes phytotoxemia known as 'hopper burn' resulting in complete drying and shedding of leaves (Nair, 1986). Without controlling the pests it is impossible to raise a good crop. Although about 60 per cent of the total insecticides manufactured in India are applied on the cotton crop complete pest control is not achieved. Besides, the indiscriminate use of pesticides by farmers has also resulted in increase in cost of production, development of resistance to major pest and resurgence of secondary pests and limitation of natural enemies of insect pests in cotton ecosystem. Therefore, there is a need for exploring alternative methods of managing this pest, particularly through the most sustainable method of genetic manipulation. In the past, studies on mechanism of resistance has indicated that due weightage had to be given to hair characters (length, density, angle) of leaf as well as plant height, sugar content and antibiotic and antixenotic principles may prove better in conferring resistance as the physical features are likely to be affected by several other factors. Keeping the above points in the mind, investigations were taken up to study the insect plant interaction, morphological and anatomical components of resistance, yield and related attributes and quality traits as related to resistance which are essential pre requisites for designing breeding methodology to evolve resistant genotypes combining higher yield and better fibre properties.

2. Materials and Methods

The experiment was carried out at Cotton Breeding Station (CBS), Centre for plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University (TNAU), Coimbatore. The genetic materials used for this study are KC 2 (Derivative from the cross MCU 10 × KC 1), MCU 12 (Multiple cross derivative) and MCU 5 (Derivative of cross between LRA 5166 × MCU 11) consisted of three *G.hirsutum* genotypes (tetraploid 2n = 4x = 52), three F_1 hybrids and their F_2's and backcrossed populations. F_1's were obtained

by crossing above three *G.hirsutum* genotypes. The selfed seeds of *G.hirsutum* lines were obtained from Cotton Breeding Station, TNAU, Coimbatore.

Hybridization and field trial: The parents and F_1's were raised during Kharif 2004. Each genotype was sown in six rows of 4.5m in crossing block with spacing of 75 cm x 30 cm. Two rows in each plot was selfed to obtain selfed seeds. Crosses were made between parents and F_1 plants to obtain backcross population. The conventional hand emasculation and pollination method developed by Doak's (1934) was followed. Emasculation of the flower buds was done in the ovule parent on the previous day evening. The entire staminal column with anthers was removed carefully along with corolla and bract with the help of nails without any damage to ovary. Pollination was done on the next day morning by dusting the pollen grains on the stigma of ovule parent.

Three hybrids with their segregating populations of F_2, F_3 and back cross generations along with their parents were raised in 6 m rows with spacing of 75 x 30 cm in a Randomized Block Design (RBD) with three replications during Kharif 2005. All recommended package of practices to raise a good crop was followed. One of the parents MCU 12 which is the ruling variety was taken as check. During Kharif 2004, F_1 seeds of the three crosses were raised along with their parents, F_1 plants were randomly chosen from each cross and back crossed to parent 1($F_1 \times P_1$) and to parent 2 ($F_1 \times P_2$) to produce BC_1 and BC_2 progenies respectively. Simultaneously, F_1 plants were selfed and F_2 seeds were harvested separately. Thus besides P_1 and P_2 seeds of four generation *viz*., F_1, F_2, BC_1 and BC_2 were generated under each cross. The F_1, F_2, BC_1 and BC_2 generations of all crosses were raised along with their parents in a compact family block design, with three replications. Each replication consisted of two rows in each of P_1, P_2, F_1, F_2, BC_1 and BC_2 in the entire cross combination. The spacing adopted was 75 cm between rows and 30 cm between plants. Each row was 4.5 m long to accommodate 15 plants. All the recommended cultural practices were carried out during crop season.

Data collection: To study the anatomical parameters, histological studies of leaves were carried out by the method described by Johanson (1940). With series of methods suggested by Johanson (1940), the slides were allowed to dry for at least 24 hours and examined for the various anatomical features of leaves. The anatomical features like thickness of phloem (µ), distance between phloem and epidermis (µ), number of palisade cells, palisade height (µ), parenchyma thickness (µ) were recorded by using the compound microscope with help of micrometry. Trichome density was estimated for six parents and thirty hybrids following the procedure of Maite *et al.* (1980). The third fully developed leaf from top was selected at random from the plants sampled for recording trichome density on 15, 30, 45 and 60 days after sowing. The number of trichomes per microscopic field was counted under compound microscope at 100x magnifications. The mean value was worked out and used for analysis.

Artificial screening for jassids: Artificial screening was conducted at the screen house, Department of Cotton. Screening was done for parents first and based on the resistant reaction of parents only three F_1's studied. Screening was done for F_1, F_2, BC_1 and BC_2 generations. Plants were sown in pots and for each entry five uniform plants were maintained, screening was done by releasing five pairs of leafhopper for each plant. The third instar nymphs of leafhopper from stock culture maintained were released. The leafhoppers were released on 25 days old plant and hopper burn injury was recorded upto 60 days of age.

Assessment of hopper burn damage: Hopper burn injury was assessed as per the Indian Central Cotton Committee (ICCC, 1960) methods and based on resultant symptoms of infestation. Visual ratings of hopper burn injury on each entry were recorded as 1 (free of symptoms) to 4 (extreme symptoms) on 45 and 60 days after sowing and mean injury index (grade index) was calculated. Jassid resistance index was calculated as proposed by Nageswara Rao (1973), which is

$$\frac{G_1 \times P_1 + G_2 \times P_2 + G_3 \times P_3 + G_4 \times P_4}{P_1 + P_2 + P_3 + P_4}$$

Where, G represented the number of the grade of ICCC and P the number of plant under the grade for each entry. Grouping of injury index into categories of resistance was as follows; 0.1-1.0 = resistant, 1.1-2.0 = moderately resistant, 2.1-3.0 = susceptible, 3.1-4.0 = highly susceptible. Based on the grade index hybrids and parents were categorized and they were discussed.

Statistical analysis: The analysis of variance and generation mean analysis was done using Genstat software. Generation mean analysis was done using the Mather and Jinks model (1982) as follows:

$Y = m + \alpha [d] + \beta [h] + \alpha^2 [i] + 2 \alpha\beta [j] + \beta^2 [l]$

where y, m, d, h, i, l and j represent mean of one generation, mean of all generation, sum of additive effects, sum of dominance effect, sum of additive × additive(complementary), sum of dominant×dominant (duplicate)and sum of additive × dominant interactions, respectively. α, β, α^2, $2\alpha\beta$ and β^2 are the coefficients of genetic parameters. A weighted least square analysis was performed on the generation means. Six parameters, viz., m, d, h, i, j and l were estimated after testing adequacy three parameter models through joint scaling test. Further models of increasing complexity were fitted if the chi square value was significant. The best fit model was the one which had significant estimates of all parameters along with non-significant chi square value. Broad-sense and narrow-sense heritability were estimated according to Warner (1952);

$h_b^2 = [V_{F2} – (V_{p1} + V_{p2} + 2V_{F1})/4]/V_{F2}$; $h_n^2 = [2 V_{F2} - (VB_1 + VB_{2)}]/ V_{F2}$

The components of variation for the six generations were calculated by the formulae of Mather and Jinks (1982) as:

$D = 4VF2 – 2(VB1 + VB2)$, $H = 4 (VB1 + VB2 – VF1 – VE)$, $Ew = (Vp1 + V_{p2} + 2V_{F1})/4$
And $F = VB1 - VB2$

Where, V_{F2}, V_{F1}, VB_1, VB_2, V_{p1} and V_{p2} are variance of F_2, F_1, BC_1,BC_2 , Parent 1 and parent 2,
D = additive variance effects, H = dominance variance. F = joint contribution (association) on all the loci.

3. Results

Gene effects for anatomical traits

The mean values of six generations *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2 in respect of three crosses were subjected to genetic analysis through generation mean analysis. The adequacy of the simple additive-dominance model without non-allelic interaction was tested by estimating the scales A, B and C. The parameters 'm', [d] and [h] were estimated when the data fitted well with the simple additive-dominance model and the goodness of fit between the observed means and those estimated from the three parameters was tested by chi-square test. Wherever the data failed to fit the simple additive-dominance model, the analysis was preceded further and a perfect fit estimate of the six genetic parameters 'm', [d], [h], [i], [j] and [l] was estimated on the assumption of additive-dominance model with digenic interaction. The scale A and B was significant in KC 2 × MCU 5. The scale C was significant in KC 2 × MCU 12 and MCU 5 x MCU 12. The results of joint scaling test for all the crosses indicated the inadequacy of the data to fit simple additive-dominance model for all crosses (Table 1). This is confirmed by chi-square values and its test of significant.

Hereafter we present results of all the crosses with respect to traits. The thickness of phloem (µ), the 'm' component was significant in all the crosses and the values ranged from 82.67 µ in KC 2 × MCU 5 to 108.67 µ in KC 2 × MCU 12. The [h] component was significant in KC 2 × MCU 12 and the values ranged between -87.00 µ in KC 2 × MCU 12 and 25.33 µ in KC 2 × MCU 5. The [i] component was significant in KC 2 × MCU 12 and the values ranged between -93.33 µ in KC 2 × MCU 12 and 34.67 µ in KC 2 × MCU 5. The [l] component was negatively significant in KC 2 × MCU 5 and the values ranged from -69.33 µ in KC 2 × MCU 5 to 78.00 µ in KC 2 × MCU 12 (Table 2). Scaling test for distance between phloem and epidermis (µ) showed that the scale A was significant in KC 2 × MCU 5 and MCU 5 × MCU 12. The scale B was significant in KC 2 × MCU 5, while the scale C was significant in KC 2 × MCU 5 and KC 2 × MCU 12. The results of joint scaling test presented in Table1 indicated the inadequacy of the data to fit simple additive-dominance model for all crosses. This is conformed by chi-square test values, which is significant in all the crosses. The 'm' component was significant in all the crosses and the values ranged between 130.22 µ (KC 2 × MCU 5) and 163.11 µ (MCU 5 × MCU 12). The [d] component was positively significant in KC 2 x MCU 5 and MCU 5 x MCU 12 and the values ranged from -6.67 µ in KC 2 x MCU 12 to 35.33 µ in MCU 5 x MCU 12. The [h], [i], [j] components were negatively significant in KC 2 x MCU 5. The [l] component was significant in KC 2 x MCU 5 and MCU 5 x MCU 12 and the values ranged between -109.78 µ in KC 2 x MCU 5 and 54.89 µ KC 2 x MCU 12 (Table 2). For number of palisade cells, the scale A was significant in KC 2 x MCU 12 and MCU 5 x MCU 12. The scale B and C were significant in MCU 5 x MCU 12. The results of joint scaling test presented in Table 1 indicated the inadequacy of the data to fit simple additive-dominance model for all the crosses. This is conformed by chi- square test value, which is significant in all the crosses. The 'm' component was significant in all the crosses and the values ranged from 14.09 in MCU 5 x MCU 12 to 14.62 in KC 2 x MCU 12. The [d] and [j] component was non-significant in all crosses. The [h], [i] and [l] component was significant in MCU 5 x MCU 12 (Table 2).

For palisade height (µ), the scales A and B were significant in KC 2 x MCU 5 and MCU 5 x MCU 12, but the scale C was significant only in MCU 5 x MCU 12. The results of joint scaling test presented in Table 1 indicated the inadequacy of the data to fit simple additive-dominance model except KC 2 X MCU 12. This is conformed by chi-square test values, which is significant. The 'm' component was significant in all the crosses and the values ranged from 71.78 µ in KC 2 x MCU 5 to 80.67 µ in MCU 5 x MCU 12.

The [d] and [h] components were significant in KC 2 x MCU 5. For the crosses KC 2 x MCU 5 and KC 2 x MCU 12 simple additive-dominance model was adequate due to absence of non-allelic interaction (Table 2). For parenchyma thickness (µ), scale A was significant in KC 2 x MCU 5 and KC 2 x MCU 12 and the scale B was significant in KC 2 x MCU 12 while scale C was non-significant in all the crosses. The results of joint scaling test presented in Table 1 indicated the inadequacy of the data to fit simple additive-dominance model for all crosses. This is also conformed by chi-square test values, which are significant. The 'm' component was significant in all the crosses. The values ranged from 61.78 µ in MCU 5 x MCU 12 to 71.11 µ in KC 2 x MCU 12. The [d] component was positively significant in KC 2 x MCU 5 and KC 2 x MCU 12. The values ranged between -8.67 µ in MCU 5 x MCU 12 and 23.33 µ in KC 2 x MCU 12. The [h] and [i] components were non-significant in all the crosses. The [j] component was positively significant in KC 2 x MCU 5 and KC 2 x MCU 12. The values ranged from 16.67 µ in KC 2 x MCU 5 to 31.00 µ in KC 2 x MCU 12. The simple additive-dominance model was adequate in cross MCU 5 x MCU 12 (Table 2).

Gene effects for trichome traits

The scale A was significant for trichome density / microscopic field in KC 2 x MCU 5 and KC 2 x MCU 12. The scale B was significant in KC 2 x MCU 12 where as scale C was significant in MCU 5 x MCU 12. The results of joint scaling test presented in Table 1 indicated the inadequacy of the data to fit simple additive-dominance model for all crosses. This is also conformed by chi-square test values that are significant in all the crosses. The 'm' component was significant in all the crosses and the values ranged from 17.33 in MCU 5 x MCU 12 to 19.80 in KC 2 x MCU 12. The [d] component was significant in KC 2 x MCU 12. The [h] component was significant in all the crosses and the values ranged from -10.73 in MCU 5 x MCU 12 to 8.87 in KC 2 x MCU 12. The [i] component was significant in all the crosses and the values ranged from -9.07 in MCU 5 x MCU 12 to 11.47 in KC 2 x MCU 12. The [j] component was significant in KC 2 x MCU 5. The [l] component was significant in KC 2 x MCU 5 and KC 2 x MCU 12 and the values ranged from -20.13 in KC 2 x MCU 12 to 17.51 in KC 2 x MCU 5 (Table 2).

Partitioning of genetic variance components

The variance estimated from the mean value of six generations viz.P_1, P_2, F_1, F_2, BC_1, and BC_2 for the three croses were partitioned in to non- heritable variance due to environment (EW), fixable variance due to additive genes (D) and non-fixable variance due to dominance derivation (H). Besides the co-variance of additive and dominance effect (F) and dominance ratio $(H/D)^{0.5}$ were also estimated and presented in Table 3. The D was positive in all the crosses for the distance between phloem and epidermis (µ). In dominance component (H) was positive for all the crosses except KC 2 x MCU 5. The covariance (F) was negative for all the crosses. The dominance ratio was not worked out for cross KC 2 x MCU 5, because the H value was negative, while KC 2 x MCU 12 recorded high dominance ratio of 1.31 followed by MCU 5 x MCU 12 (0.83) (Table 3). The additive component (D) was negative where as dominance component (H) was positive in all the three crosses for number of palisade cells. The covariance (F) was positive in cross KC 2 x MCU 5. The dominance ratio was not worked out any of the crosses, because D was negative in all the crosses (Table 3). For the Palisade height (µ), the dominance variance was more than additive and EW variances. The H values being 120.05 (KC 2 x MCU 12) to 718.09 (KC 2 x MCU 5). The co-variance was negative in all the crosses. The dominance ratio was not worked out any of the crosses, because the D component was negative in all the crosses. The dominance variance was more than additive and EW variances for Parenchyma thickness (µ). The H value range being 354.32 (KC 2 x MCU 12) to 676.48 (MCU 5 x MCU 12). The additive variance was negative in all the crosses. The dominance ratio was not worked out for any of the crosses, because the D component was negative in all the crosses.

Considering the trichome density / microscopic field, dominance variance was more than additive and environmental variances. The additive variance was negative in all the crosses and therefore dominant ratio was not worked out.

4. Discussion

In the recent past, cotton production is stagnant in many countries and more so in agriculture oriented countries like India. Biotic constraints particularly insect pests are known to affect the stability in production and cause considerable damage to the crop in terms of yield and fibre quality. Jassids pests are regularly serious and most important pest next to bollworms, causing damage and symptoms such as reddening, stunting, delayed maturity, lowered productivity and indirect loss in yield and fibre quality (Parnel *et al*., 1949). Technical advancements to contain the pest complex through integrated pest management have been successfully evolved. But still there is a gap in understanding the changing pest complex and timely adoption of technologies. Therefore, there is a need for continuous development of new strategies to meet the emerging challenges. One of the approaches is to develop cultivars that possess built in resistance to insect pests. Insect resistant cultivars are compatible with other tactics of integrated pest management practices, besides being sustainable and eco-friendly. The most important technique is to exploit the resistant genes already available in the cultivated species. Usually, such genotypes may not compare well with the high yielding varieties in respect of seed cotton yield. The other technology is to develop resistant cultivars by use of wild species and races of cotton. During outbreaks, crop failure due to this insect pest has been observed throughout the cotton growing areas in India. The pest has developed resistance to most of the insecticides and the chemical control measures besides being costly, fail to provide complete protection against the pest. This warrants exploitation of host plant resistance for management of jassids in cotton. It is important to examine the mechanism of resistance in any breeding programme focused to exploit host plant resistance. The study of gene action for various characters provides us information for further use of the materials in breeding programme. Fisher (1918) divided the genotypic variance into additive, dominance and interaction or epistatic components. Additive components arise from the differences between the two homozygote for a gene, AA and aa while dominance component is due to the deviation of the heterozygote (Aa) from the averages of the two or more genes. Later, Hayman and Mather (1955) partitioned the epistatic component into three types of interactions namely, additive x additive, additive x dominance and dominance x dominance. For selecting the appropriate breeding programme for the improvement of economic characters, it is essential to draw precise information on the various types of gene effects, so that the crop improvement will be very efficient and required results could be achieved in shorter duration.

Various anatomical parameters like distance to phloem elements from lower abaxial surface and structure of parenchyma tissues were reported to be associated with resistance to sucking pests (Ansingkar, 2002). In the present study, resistant parents recorded higher distance of phloem from lower epidermis and significant negative correlation between phloem distance and jassid susceptibility grade was also observed and supported the results that this character can be considered as a dependable character for screening even during the earlier stage of the crop. The parent KC 2 displayed higher distance of phloem from epidermis and can constitute the base materiel for further breeding programme. The cross MCU 5 x MCU 12 registered higher distance between phloem and epidermis. It is interesting to note that the two moderately resistant parents when combined together in hybrids, showed this favorable feature, which may be due to recombination nature of both the parents as compared to other. Hence it can be concluded that the hardness of the tissue may also pose considerable resistance for feeding by the sucking pest. Par-

titioning of variance reveals that the dominance ratio was observed more than one due to over dominance. Thickness of phloem elements were found to be positively correlated with jassid resistance, but it did not give any significant contribution towards resistance. Duplicate epitasis was observed for both the characters and it is also conferred by significant of scale 'C' in KC 2 x MCU 12. There fore in order to exploit the presence of interaction effects mainly dominance x dominance, recurrent selection techniques may be useful. The resistance varieties had more number of palisade cells per unit area and this character negatively correlated to jassid susceptibility and this may be due to compactness as it restricts any material to enter the cells. The parent KC 2 recorded higher number of palisade cells per unit area. Preponderance of both additive and dominance gene action indicated that, it may be exploited through reciprocal recurrent selection. Study reported that the character's thickness of phloem, distance between phloem and epidermis, number of palisade cells and palisade height were showed negative correlation with jassid injury index, where as parenchyma thickness indicated positive correlation (Shimna Bhaskaran, 2004; Shimna Bhaskaran et al 2006). Significant negative correlation between palisade cells height and jassid susceptibility grade was also observed. The resistant genotypes KC 2 and the cross KC 2 x MCU 12 (BC_1F_1) had higher palisade height compared to susceptible ones. The parenchyma thickness was positively correlated to jassid susceptibility. In both the cases dominance gene action were observed. Hence, Heterosis breeding may be rewarded in exploiting this character. In general, predominance of duplicate epistasis was observed for anatomical characters and therefore heterosis breeding may be effected for further exploitation of the material.

In present study, resistant genotypes KC 2 and the cross KC 2 x MCU 12 (BC) recorded higher number of trichomes on the lower surface pointing to the relationship between density of hairiness and resistant to jassid in cotton. Significant positive correlation between trichome density and jassid resistant was also observed. These materials can be utilized further in breeding programmes. Partioning of genetic variances indicated that duplicate epistasis was observed for cross KC 2 x MCU 12 indicating that it may be due to dominance x dominance and also confirmed by the significance of scale B in KC 2 x MCU 12. Therefore, recurrent selection can be rewarding for improving such traits. The stomatal number did not confer any significant contribution to jassid resistance. While leaf thickness recorded highly significant and negative correlation with jassid susceptibility. Leaf thickness was more in resistant parent KC 2 and KC 2 x MCU 12 (BC_1F_1). This result confirming the earlier latest finding (Atul et al. 2015). Abdallah *et al*. (2001) reported the relation of morphological observations and chemical composition in evidence for leafhopper resistance. For leaf thickness, duplicate epistasis was observed in resistance crosses indicating the need to resort recurrent selection for improving the trait. In general, by comparing both anatomical and morphological features indicated that predominance of duplicate epitasis was observed followed by dominance gene action. Hence, recurrent selection may be resorted for improving such traits in the crosses. In order to exploit the dominant gene action, recombination breeding methodologies can be adopted to transfer such trait to the high yielding genotypes. In general, anatomical and trichome characters indicated the predominance of duplicate gene action followed by dominance gene action observed predominant. There fore for further development can be made through recurrent selection for selecting the best segregants for most of the important characters. Artificial screening of jassid resistance revealed that the genotypes KC 2 was comes under resistant group and MCU 5 and MCU 12 were under moderately resistance group. Among the crosses KC 2 x MCU 12 showed moderately resistance. Hence, segregants can be exploited from these crosses for high yield with high resistant to jassids in the varietal improvement programme. It has widely been believed that, other than cotton several crops such as potato, lucerne, clover etc., the degree of jassid infestation is determined largely by the hairiness on the leaf surface. This supported the findings that the hairiness on the undersurface of the leaves was found to be the most important

morphological character closely associated with jassid resistance (Sankeshwar and Patil, 2016) The various ancillary characters *viz*., leaf area, hairiness, thickness of leaf veins, toughness of cuticle and number of stomata present on the lower surface of the leaf were found correlated with jassid damage by number of workers like Verma and Afzal (1940) and Batra and Gupta (1970). Several workers in India and abroad have reported that a hair of sufficient length and density on the ventral surface of the cotton leaves confer resistance to jassids. The toughness of the leaf veins, osmotic pressure of the cell sap and pH value of cell sap are also closely associated with the resistance to jassid infestation. It is possible that jassid resistant characters in the cotton plants may be linked with hairiness, but hairiness itself may not be the only important character. However, not all hairy varieties are necessarily to be a resistant cultivar to jassid infestation. Wild species, which are glabrous such as *G. armourianum* and others, are reported to be resistant to jassids (Mehetre et al. 2003), thus these genotypes also can be used for deriving parents and hybrids for resistance to jassid in future.

In conclusion, among the breeding materials used in the present study, parent KC 2 and the hybrid KC 2 × MCU 12 recorded lowest jassid injury index and other anatomical and trichome characters in the desirable direction followed by the parents MCU 5 and MCU 12. Therefore, these parent materials can be exploited for developing jassid resistant parents or hybrids in near future. Inter-crossing of resistant line in early generation and further selections may permit recombination of desirable resistance genes and maximize breeding progress in developing jassid resistant lines. Considering present study, both yield and quality characters (based on the same study and data was not presented), the genotypes MCU 5, MCU 12 and the hybrid MCU 5 × MCU 12 could be exploited for improving the economic traits with moderate resistance to jassid at farmer's field for large scale cultivations.

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References

Abdallah, Y.E.Y., S.I. Ibrahim, E.M. Abd-Elmoniem and L.A. Youssef. 2001. Incidence of some piercing - sucking insects in relation to morphological leaf characters, some chemical and nutritional component of some cotton cultivars. Ann. Agric. Sci., 46(2): 807-827.

AICCIP report. 2011. Annual Group Meeting of All india coordinated cotton improvement project held on 06-08 April, 2011, HAU, Hisar, Haryana, India.

Akoijam, R.,Telam,R.,Marangmai,L. 2014. Insect pest problems and its changing trends on crop losses. Environment and ecology

Anonymous, 2014. "Annual Report" All India Coordinated Cotton Improvement Project (2014-2015). Pp 2-4

Ansingkar, 2002. A new strategy for sucking pest resistance in cotton through introgression breeding. In: Proceedings of second meeting of Asian Cotton Research and Development Network-Taskent,Uzbekistan.

Atul,G., Chandele A.G., Gurve S.S., and Wargantiwar R.K. 2015. Study of Bio-physical characters of Bt hybrids for correlation with Cotton jassid. Annals of Plant Protection Sciences. 23 (2): 241-245

Batra, G.R and D.S. Gupta. 1970. Screening of varieties of cotton for resistance to jassid. Cott Grow. Rev., 47(4): 285-91.

Dhaliwal, G.S. and Koul, O. 2010. Quest for Pest Management: From Green Revolution to Gene Revolution. Kalyani Publishers, New Delhi

Doak, C.C. 1934. A new technique in hybridizing suggested changes in existing methods of emasculation and bagging of cotton flowers. J. Hered., 25: 201-204

Fisher R. A., 1918. The correlation between relatives on the supposition of Mendelian inheritance.Trans. R. Soc. 52: 399–433.

Fryxell, P.A., L.A. Craven and J.M.C.D. Stewart. 1992. A revision of *Gossypium* sect. Grandi calyx (Malvaceae), including the description of six new species. Syst. Bot. 17: 91-114.

Hayman, B.I. and Mather. 1955. The description of genetic interaction in continuous variation. Biometrics, 11: 69-82.

Indian Central Cotton Committee (ICCC). 1960. Cotton in India – a monograph Vol. II. ICCC, Bombay. 217-300 pp.

J.P. Singh, R.K. Lakra. 1990. Effect of Insecticides on the Growth of Plant and Incidence of Bollworms in Cotton. Indian Journal of Plant Protection, 18(1): 21-26

Johanson DA (1940). Plant Microtechnique, McGrew-Hill Publications, New Delhi. P. 523

Kamalanathan S, SS Narayamin, PV Marappan. 1965. The effect of micronutrients on yield and quality of MCU 3 cotton. Madras Agri J.255-258.

Maite, R.K., F.R. Bidinger, K.V.S. Reddy and J.C. Davies. 1980. Nature of occurrence of richomes in sorghum lines with resistance to sorghum shootfly. Joint Progress report, Sorghum Physiology-3, Sorghum Entomology-3, ICRISAT, Patancheru, A.P., India, pp: 20-23.

Mather, K and J.L. Jinks. 1982. Biometrical Genetics - The study of continuous variation. Chapman and Hall Ltd., London. p: 403.

Mathews, G.A. 1994. Jassids (Hemiptera : Cicadellidae) pp: 343-357, In: Insect Pests of Cotton (Ed. G.A. Mathews and J.P. Tunstall) CAB International, Walling ford. p: 593.

Mehetre SS., Gawande V.L., Aher A.R., and Saitwal V.M. 2003. Variability for Leaf Hairiness Pattern in *Gossypium L. Species.* Indian J Plant Genetic Res. 16 (3): 178-181.

Nageswara Rao, P. 1973. An index for jassid resistance in cotton. Madias Agri. J. 60 : 264- 266

Nair, M.R.G.K. 1986. Insects and mites of crops in India. Indian Council of Agricultural Research publications. New Delhi. p: 408.

Parnell, F.R., H.E. King and D.F. Ruston. 1949. Jassid resistance and hairiness of the cotton plant. Bull. Ent. Res., 39: 539-575.

Sankeshwar, M and R.S. Patil. 2016 Effect of trichome density on the resistance to the jassids in inter-specific G. hirsutum x G. barbadense cotton recombinant inbred lines (RIL) population. J. Farm Sci., 29(4): 479-481

Shimna Bhaskaran, R. Ravikesavan and T.S. Raveendran. 2006. Leaf anatomy associated jassid resistance in cotton (*Gossypium spp*) – A new approach for Resistance Breeding. National Conference on Plant Sciences Research and Development,
(II-4) held at PSG college of Arts and Science, Coimbatore.

Shimna Bhaskaran. 2004. Genetic and anatomical studies on jassid resistance in cotton (*Gossypium* spp.). M.Sc., (Ag.) Thesis, TNAU, Coimbatore.

Vennila, S. 2008. Pest management for cotton ecosystems or ecosystem management for cotton production? Curr. Sci. 94 : 1351-52.

Verma, P.M. and M. Afzal, M. 1940. Studies on cotton jassid, *Empoasca devastans* (Dist.) in Punjab. varietal susceptibility of development of the pest on different varieties of cotton. Indian.J. Agric. Sci 10(6): 911-926.

Warner, J.N. 1952. A method for estimating heritability. Agron. J. 44:427–443.

Table 1. Scaling and Joint scaling test for various anatomical characters in in three crosses of upland cotton

Crosses	Scaling test for elongation percentage			
	A	B	C	Joint scaling test γ^2 value
Thickness of phloem (µ)				
KC 2 x MCU 5	17.33** ± 7.02	17.33* ± 5.93	0.00 ± 12.88	13.81**
KC 2 x MCU 12	6.67 ± 7.91	8.67 ± 5.43	108.67** ± 14.92	53.29**
MCU 5 x MCU 12	7.33 ± 9.08	2.67 ± 8.78	42.44* ± 17.10	8.26*
Distance between phloem and epidermis (µ)				
KC 2 x MCU 5	-5.33** ± 8.79	-52.00** ± 8.57	-120.44** ± 19.73	45.12**
KC 2 x MCU 12	-37.33 ± 8.84	15.33 ± 7.69	10.89** ± 15.84	26.87**
MCU 5 x MCU 12	96.00** ± 7.88	12.67 ± 7.63	82.44 ± 6.36	153.06**
Number of palisade cells				
KC 2 x MCU 5	-1.40 ± 0.84	1.93 ± 0.97	0.22 ± 1.46	9.20*
KC 2 x MCU 12	-3.87** ± 1.00	1.00 ± 0.96	-0.91 ± 1.28	17.58**
MCU 5 x MCU 12	8.40** ± 1.41	7.40** ± 1.02	2.82* ± 1.32	83.40**
Palisade height (µ)				
KC 2 x MCU 5	49.47** ± 7.04	20.00** ± 6.82	15.24 ± 9.24	54.05**
KC 2 x MCU 12	-0.53 ± 5.77	10.67 ± 6.54	0.36 ± 10.13	3.24
MCU 5 x MCU 12	23.33** ± 6.39	10.67* ± 7.98	44.67** ± 9.02	29.55**
Parenchyma thickness (µ)				
KC 2 x MCU 5	34.00** ± 5.18	0.67 ± 8.86	16.89 ± 9.75	43.93**
KC 2 x MCU 12	23.33** ± 5.36	-38.67** ± 5.66	-6.89 ± 8.71	79.35**
MCU 5 x MCU 12	12.00 ± 8.15	20.67** ± 6.36	1.11 ± 8.89	13.89**
Trichome density / microscopic field				
KC 2 x MCU 5	-8.80** ± 1.24	-1.73 ± 1.53	-3.56 ± 1.99	51.07**
KC 2 x MCU 12	4.53** ± 1.42	4.13* ± 1.69	-2.80 ± 1.94	25.13**
MCU 5 x MCU 12	1.33 ± 1.38	-2.00 ± 1.34	8.40** ± 1.91	30.13**

** Significant at 1 % level

Table 2. Genetic effects for various anatomical and trichome characters in three crosses of upland cotton

Crosses	m	[d]	[h]	[i]	[j]	[l]
Thickness of phloem (µ)						
KC 2 x MCU 5	82.67** ± 2.89	1.33 ± 3.98	25.33 ± 14.31	34.67 ± 14.02	0.00 ± 4.26	-69.33* ± 20.49
KC 2 x MCU 12	108.67** ± 3.36	9.33 ± 4.08	-87.00** ± 16.05	-93.33** ± 15.71	-1.00 ± 4.33	78.00 ± 22.11
MCU 5 x MCU 12	101.78** ± 2.70	11.33 ± 4.10	-4.11 ± 15.10	-32.44 ± 13.57	2.33 ± 4.36	22.44 ± 23.70
Distance between phloem and epidermis (µ)						
KC 2 x MCU 5	130.22** ± 4.06	23.33** ± 3.90	121.11 ** ± 18.87	115.11** ± 18.03	-2.67** ± 4.79	-109.78* ± 25.14
KC 2 x MCU 12	154.22** ± 3.42	-6.67 ± 4.77	-57.22 ± 17.42	-32.89 ± 16.67	-26.33 ± 5.46	54.89 ± 2.21
MCU 5 x MCU 12	163.11** ± 4.49	35.33** ± 4.65	35.89 ± 20.55	26.22 ± 20.23	41.67 ± 25.56	-134.89* ± 26.84
Number of palisade cells						
KC 2 x MCU 5	14.16** ± 0.25	-0.07 ± 0.49	-2.96 ± 1.51	0.31 ± 1.42	-1.67 ± 0.55	-0.84 ± 2.46
KC 2 x MCU 12	14.62** ± 0.23	-0.27 ± 0.58	-2.59 ± 1.54	-1.96 ± 1.47	-2.43 ± 0.64	4.82 ± 2.65
MCU 5 x MCU 12	14.09** ± 0.25	1.07 ± 0.79	12.61** ± 1.91	12.98** ± 1.86	0.50 ± 0.84	-28.78** ± 3.41
Palisade height (µ)						
KC 2 x MCU 5	71.78** ± 1.69	18.67* ± 4.22	50.29* ± 11.26	A	A	A
KC 2 x MCU 12	73.56** ± 1.88	-2.67 ± 3.29	14.84 ± 10.56	A	A	A
MCU 5 x MCU 12	80.67** ± 1.44	5.33 ± 4.18	-5.67 ± 10.72	-10.67 ± 10.14	6.33 ± 4.76	-23.33 ± 18.99
Parenchyma thickness (µ)						
KC 2 x MCU 5	65.56** ± 1.69	13.33* ± 4.18	15.11 ± 11.32	17.78 ± 10.77	16.67* ± 4.80	-52.44 ± 19.35
KC 2 x MCU 12	71.11** ± 1.69	23.33** ± 3.22	3.22 ± 9.74	-8.44 ± 9.44	31.00** ± 3.52	23.78 ± 15.58
MCU 5 x MCU 12	61.78** ± 1.43	-8.67 ± 4.22	13.89 ± 10.75	A	A	A
Trichome density / microscopic field						
KC 2 x MCU 5	19.04** ± 0.35	2.20 ± 0.79	-7.91* ± 2.22	-6.98*± 2.11	-3.53* ± 0.90	17.51** ± 3.73
KC 2 x MCU 12	19.80** ± 0.35	4.53* ± 0.97	8.87* ± 2.49	11.47* ± 2.39	0.20 ± 1.02	-20.13* ± 4.35
MCU 5 x MCU 12	17.33** ± 0.31	0.27 ± 0.77	-10.73** ± 2.11	-9.07* ± 1.99	1.67 ± 0.86	9.73 ± 3.63

* Significant at 5 % level
** Significant at 1 % level
A – Adequacy of additive – dominance model
Parent with larger phenotypic value was used as P_1 in each cross

Table 3. Portioning of genetic components of variance for various anatomical and trichome characters in three crosses of upland cotton

Cross combination	EW	D	H	F	$[H/D]^{0.5}$
Thickness of phloem (µ)					
KC 2 x MCU 5	75.55	272.92	650.15	-53.33	1.54
KC 2 x MCU 12	85.39	515.50	656.49	-121.90	1.13
MCU 5 x MCU 12	251.75	152.42	2.53	-18.10	0.13
Distance between phloem and epidermis (µ)					
KC 2 x MCU 5	272.38	1031.02	-179.04	-14.28	-
KC 2 x MCU 12	185.40	366.08	626.05	-14.29	1.31
MCU 5 x MCU 12	124.44	1168.94	797.46	-3.81	0.83
Palisade height (µ)					
KC 2 x MCU 5	87.14	-276.14	718.09	-15.24	-
KC 2 x MCU 12	131.90	-4.22	120.05	-5.71	-
MCU 5 x MCU 12	153.02	-348.90	454.61	-43.81	-
Number of palisade cells					
KC 2 x MCU 5	2.26	-1.62	5.65	0.75	-
KC 2 x MCU 12	2.17	-5.56	11.61	-0.65	-
MCU 5 x MCU 12	2.19	-13.06	28.39	-3.81	-
Parenchyma thickness (µ)					
KC 2 x MCU 5	144.13	-264.22	471.13	128.57	-
KC 2 x MCU 12	67.62	-55.84	354.32	0.00	-
MCU 5 x MCU 12	97.14	-348.9	676.48	-43.81	-
Trichome density / microscopic field					
KC 2 x MCU 5	5.40	-7.56	15.51	2.20	-
KC 2 x MCU 12	3.62	-17.48	42.25	4.04	-
MCU 5 x MCU 12	4.68	-9.20	17.11	1.18	-