

Research Article

Effect of Earliness on Whitefly Population, CLCuD and Yield in Cotton (*Gossypium hirsutum* L.)

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Abstract: Six Genotypes were tested to study the effect of earliness on population of whitefly, CLCuD and yield. Analysis of variance showed significant differences among genotypes for all the studied characters. Maximum CLCuD % was shown by CIM-496 along with highest value for whitefly population. Maximum yield and minimum CLCuD % was shown by FH-142. According to correlation studies, days to first boll open has negative association with whitefly population and cotton leaf curl disease. While whitefly population and cotton leaf curl disease showed significant positive association with each other. Yield has significant negative correlation with whitefly population and cotton leaf curl disease and positive correlation with days to first boll open. Principal component analysis showed the maximum contribution of PC 1 towards total variability. Whitefly population and cotton leaf curl disease showed maximum negative factor loadings while yield showed maximum positive factor loading on PC 1.

Keywords: Earliness, Whitefly, CLCuD, Yield, Correlation.

INTRODUCTION

Cotton is an important cash crop of Pakistan which directly contributes to Pakistan economy as it has 1.0 percent share in GDP and 5.2 percent contribution in agriculture value addition (Anonymous, 2017) so often termed as “White gold” (Janu & Dahiya, 2017). Cotton yarn, cotton oil, lint, cloth and garments are major source of earning and contribute 1.6% in GDP of Pakistan (Anonymous, 2012). The production of cotton is reduced by various factors among which diseases and insects pests are key factors. Therefore only cotton insect pest management has always been a challenging task for the entomologists in the whole world. On different growth stages cotton is attacked by 162 different species of insect pests (Kannan *et al.*, 2004). As Bt cotton does not interfere with the activity of sucking insects so the condition is being more favorable for the sucking insect pest development and multiplication. Among the sucking insects of cotton, whitefly and jassid are the most destructive insects (Ghafoor *et al.*, 2011). As whitefly and jassid attack the crop at vegetative stage causing 40-50 % damage (Naqvi, 1976). During last few years whitefly only has been considered as the most serious pest of cotton

regarding cotton leaf curl virus spread (Ali *et al.*, 1995). Furthermore, whitefly constantly sucks the cell sap, resulting in 50% reduction in boll production and also reduces plant vigor. It also secretes honeydews which causes sooty mold to develop (Ahmad *et al.*, 2002) which in turn deteriorates the quality of lint fibre.

Besides whitefly one other major problem in cotton is late maturing varieties. Late maturing varieties of cotton result in production of poor quality fiber as fiber length, fineness and strength is affected due to late picking. Late picking also affects ginning out turn, seed index and lint index. So breeding for early maturing varieties is the solution for this problem because early maturing varieties can reduce losses due to insect pest complex and diseases as early maturing genotypes increase the possibility that harvest can be completed before wheat crop. Early maturity is also preferred because of decreased inputs of fertilizer, irrigation, plant protection and providing proper time for rotation of other crops (Shakeel *et al.*, 2012). The objective of this study is to assess the cotton cultivars for earliness and yield and to find correlation among different characters, the findings of which could be utilized in

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further breeding programs to develop CLCuD resistant genotypes.

MATERIALS AND METHODS

The experiment was conducted at experimental area of Cotton Research Station, Faisalabad, Pakistan. In this experiment six cotton varieties two tolerant against CLCuD (FH-142 and MNH-886), two moderately tolerant against CLCuD (FH-118 and FH-4243) and two susceptible genotypes (NIAB-111 and CIM-496) were sown at sowing date of 20th April during 2017 in three replications in RCBD design with plot size of 10m x3m of each variety with R x R distance of 75 cm and P x P distance of 30 cm. The

recommended practices, except spraying of insecticides were followed for raising the crop.

The earliness characters i.e. days to First Square, days to first flower and days to first boll open were determined by simply counting number of days from germination upto that character. The data of CLCuD and whitefly population was taken on fortnightly basis. Adult population of *B. tabaci* was recorded from each variety by randomly selecting 10 plants and observing three leaves per plant (top, middle and bottom) before 10.00 am in the morning as (average number of adults/leaf) throughout the cropping season. Disease % was calculated by using the formula given below:

$$\text{Disease (\% age)} = \frac{\text{Sum of all disease ratings}}{\text{Total number of plants}} \times 100$$

Data was statistically analyzed for analysis of variance (ANOVA), LSD (0.05) for the comparison of means, correlation (Pearson) analysis and principal component analysis using software statistix 8.1.

RESULTS AND DISCUSSION:

Table 1. ANOVA

| SOV | DF | Mean squares | | | | | |
|-------------|----|--------------------------------|--------------------------------|-----------------------------------|---------------------|-----------|------------|
| | | Days to 1 st square | Days to 1 st flower | Days to 1 st Boll open | Whitefly Population | CLCuD | Yield |
| Replication | 2 | 9.72222 | 0.16667 | 2.1667 | 0.01722 | 3.3889 | 100105 |
| Varieties | 5 | 5.38889** | 4.40000* | 13.8667** | 3.85556** | 85.5556** | 13110955** |
| Error | 10 | 0.85556 | 1.16667 | 1.8333 | 0.08722 | 0.7222 | 9089 |
| Total | 17 | | | | | | |

* SOV= source of variation
* DF= Degree of freedom

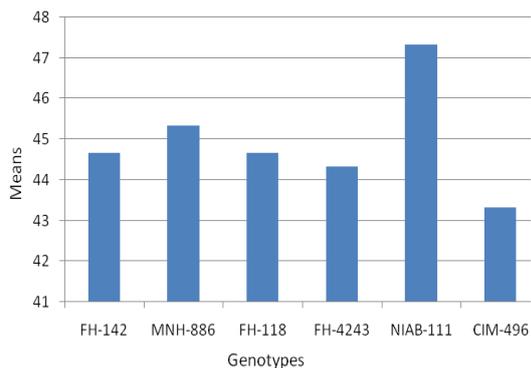
The analysis of variance (Table 1) showed significant differences among genotypes for all the characters i.e. days to first square, days to first flower, days to first boll open, whitefly population, cotton leaf curl disease and yield.

Table 2. Mean Performance regarding different traits of Genotypes

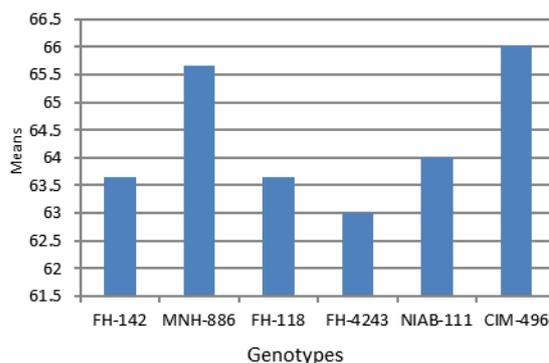
| Varieties | Mean values | | | | | |
|-------------------|--------------------------------|--------------------------------|-----------------------------------|---------------------|---------------|---------------|
| | Days to 1 st Square | Days to 1 st Flower | Days to 1 st Boll open | Whitefly population | CLCuD % | Yield Kg/Ha |
| FH-142 | 45 | 64 | 97 | 6.10 | 5.33 | 3032 |
| MNH-886 | 45 | 66 | 100 | 6.03 | 7.33 | 2749 |
| FH-118 | 45 | 64 | 99 | 6.30 | 11.33 | 2527 |
| FH-4243 | 44 | 63 | 101 | 6.53 | 11.33 | 2115 |
| NIAB-111 | 47 | 64 | 95 | 7.93 | 16.66 | 1499 |
| CIM-496 | 43 | 66 | 96 | 8.76 | 19.33 | 1432 |
| LSD (0.05) | 1.6828 | 1.9650 | 2.4633 | 0.5373 | 1.5461 | 173.45 |

According to mean values (Table 2), minimum days to First Square (43) were shown by genotype CIM-496 while maximum days to First Square (47) were shown by genotype NIAB-111. For days to first flower, minimum days (63) were shown by genotype FH-4243 while maximum days (66) were shown by genotype CIM-496. Similarly for days to first boll open lowest value was (95) and shown by NIAB-111 while highest value (101) was shown by genotype FH-4243.

For whitefly population minimum population was (6.03) and shown by MNH-886 and maximum population was (8.76) shown by CIM-496. CLCuD % values were in range of (5.33) to (19.33) and shown by genotypes FH-142 and CIM-496 respectively. Maximum yield (3032 kg/Ha) was shown by genotype FH-142 while minimum value was (1432 kg/Ha) was shown by CIM-496. The same information (Table 2) is presented graphically in Fig. 1-6.

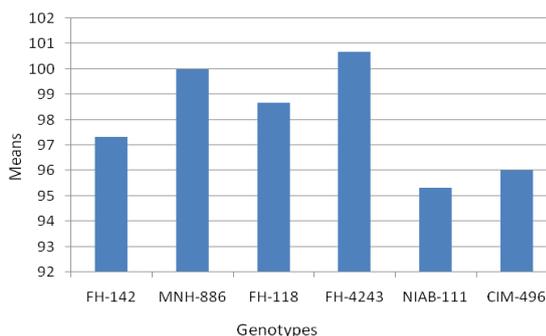


Days to 1st square (Fig.1)

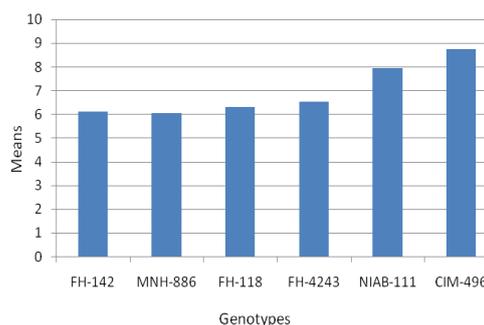


Days to 1st flower (Fig.2)

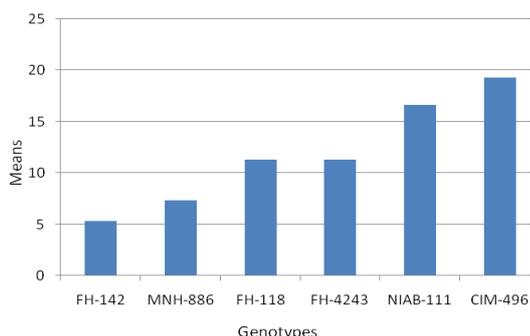
Da



Days to 1st boll open (Fig.3)

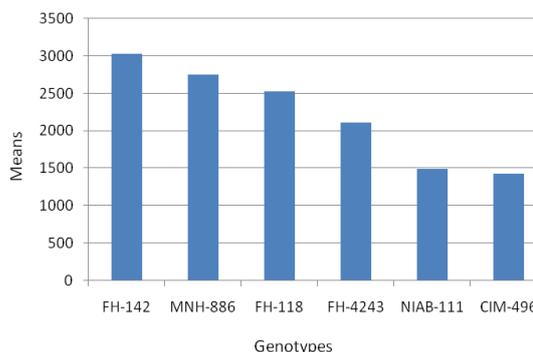


Whitefly population (Fig.4)



CLCuD % (Fig.5)

CLC



Yield (kg/ha)(Fig.6)

Yi

Mean Performance regarding different traits of Genotypes

Correlation Studies:

Table.3: Correlation Analysis (Pearson)

| | Days to 1 st Square | Days to 1 st flower | Days to 1 st boll open | Whitefly population | CLCuD |
|-----------------------------------|--------------------------------|--------------------------------|-----------------------------------|---------------------|----------|
| Days to 1 st flower | 0.0077 | | | | |
| Days to 1 st boll open | 0.0000 | -0.0536 | | | |
| Whitefly population | 0.0314 | 0.3906 | -0.5569* | | |
| CLCuD | 0.0571 | 0.2339 | -0.5010* | 0.9159** | |
| Yield | -0.1373 | -0.2112 | 0.4642* | -0.8830** | -0.9503* |

It is evident from (Table 3) that Days to first boll open also has negative significant correlation with whitefly population and CLCuD while it has positive correlation with yield. Amna *et al.*, 2013 found different results with the positive association of days to first boll opening and CLCuD %. Similarly whitefly

population has highly significant positive correlation with cotton leaf curl disease, Sharma *et al.*, 2006, Monga *et al.*, 2011 and Maharshi *et al.*, 2017 reported the same results while Akhtar *et al.*, 2004 reported non-significant association between whitefly levels and disease %. Whitefly has highly significant negative

correlation with yield. Likewise cotton leaf curl disease has significant negative correlation with yield, Javed *et al.*, 2017 also reported a significant genotypic and phenotypic negative correlation of CLCuD with yield contributing traits.

Principal Component Analysis

The preservation and utilization of genetic resources is possible by partitioning the total variance into its components. It also provides a chance for use of suitable germplasm in crop improvement for particular plant traits.

Table. 4: Principal Component Analysis of Different Traits of Cotton Genotypes

| Variable | PC I | PC II | PC III | PC IV |
|---------------------------------------|---------|---------|---------|---------|
| Eigen value | 3.28882 | 1.01004 | 0.96775 | 0.60864 |
| % of total variance | 54.8 | 16.8 | 16.1 | 10.1 |
| Cumulative variance % | 54.8 | 71.6 | 87.8 | 97.9 |
| Factors loading by various characters | | | | |
| Days to 1 st square | -0.0522 | -0.9722 | -0.1469 | 0.1577 |
| Days to 1 st flower | -0.2011 | 0.1859 | -0.8927 | 0.3092 |
| Days to 1 st boll open | 0.3549 | -0.0827 | -0.4098 | -0.8255 |
| Whitefly population | -0.5326 | 0.0664 | -0.0602 | -0.0746 |
| CLCuD % | -0.5278 | -0.0040 | 0.0731 | -0.2896 |
| Yield (Kg/Ha) | 0.5183 | 0.0950 | -0.0681 | 0.3296 |

In this study out of six Principle Components (PCs), two were extracted having Eigen value > 1. These two PCs contributed 71.6 % of the total variability while the remaining four PCs contributed only 28.4 % towards total variability. The PC I contributed (54.8 %) and PC II contributed (16.8 %) towards total variability. Saeed *et al.*, 2014 indicated the importance of PC I contribution towards variability while studying some other traits. The cotton leaf curl disease and whitefly population have maximum negative factor loadings on PC I while yield has maximum positive factor loading on PC I. The days to First Square showed maximum negative factor loading on PC II. PC III was negatively contributed by days to first flower while days to first boll open showed maximum negative factor loading on PC IV.

CONCLUSION:

These results suggested that early maturity is an important genetic trait showed by various phenotypic characters which could be combined through suitable breeding program to develop early maturing high yielding genotypes without loss of seed cotton yield. Furthermore, as whitefly population increases cotton leaf curl disease also increases and this disease has also negative association with yield so measures should be adopted to control whitefly population to improve yield.

REFERENCES:

- Ahmad, M., Arif, M.I., Ahmad, Z., & Denholm, I. (2002). Cotton whitefly *Bemisia tabaci* resistance to Organophosphate and pyrethroid insecticides in Pakistan. *Pest Manag. Sci.* 58(2), 203–208.
- Akhtar, K.P., Hussain, M., Khan, A.I., Haq, M.A., & Iqbal, M.M. (2004). Influence of plant age, whitefly population and cultivar resistance on infection of cotton plants by cotton leaf curl virus (CLCuV) in Pakistan. *Field.Crop. Res.* 86(1), 15-21.
- Ali, A., Khaliq, A., & Ashraf, M. (1995). Physical factors affecting resistance in cotton against jassid, *A. devastans* (Dist.) and thrips *T. tabaci* (Lind). *J.Agric.Res.* 33(2),173-178.
- Anonymous. (2012). Pak. Economic Survey, Ministry of Finance, Govt. of Pakistan.
- Anonymous. (2017). Pak. Economic Survey, Ministry of Finance, Govt. of Pakistan.
- Ghafoor, A., Hassan, M., Hussain, Z., & Kousar, S. (2011). Impact of Different Varieties of Stub Cotton on Population Dynamics of Whitefly at Faisalabad, Pakistan. *Pak. J. Zol.* 43 (1), 25-28.
- Janu, A., & Dahiya, K.K. (2017). Influence of weather parameters on population of whitefly, *Bemisia tabaci* in American cotton (*Gossypium hirsutum*). *J. Ent.& Zol. Std.* 5(4), 649-654.
- Javed, M., Hussain, S.B., & Baber, M. (2017). Assessment of genetic diversity of cotton genotypes for various economic traits against Cotton Leaf Curl Disease (ClcuD). *Genet. Mol. Res.* 16 (1), 1-12.
- Kannan, M., Uthamasamy, S., & Mohan, S. (2004). The impact of insecticides on sucking insect pest and natural enemy complex of transgenic cotton. *Curr. Sci.* 86(5), 726-729.
- Maharshi, A., Yadav, N.k., Swami, P., Singh, P., & Singh, J. (2017). Progression of cotton leaf curl disease and its vector whitefly under weather influences. *Int. J. Curr. Microbiol. App. Sci.* 6(5), 1-8.
- Monga, D., Chakrabarty, P.K., & Kranthi, R. (2011). Cotton leafcurl virusdisease in India-Recent status and management strategies Presented in 5th meeting of Asian Cotton Research and Development Network, Lahore.
- Naqvi, K.M. (1976). Crop protection to boost up the cotton production. Seminar organized by ESSO, Fert. Co. Ltd., Pakistan.
- Nazir, A., Farooq, J., Mahmood, A., Shahid, M., & Riaz, M. 2013. Estimation Of Genetic Diversity

- For ClCuV, Earliness And Fiber Quality Traits Using Various Statistical Procedures In Different Crosses of *Gossypium Hirsutum* L. Vestnik OrelGAU, 43(4), 2-9.
14. Saeed, F., Farooq, J., Mhmood, A., Hussain, T., Riaz, M., & Ahmad, S. 2014. Genetic diversity in upland cotton for cotton leaf curl virus diseases, earliness and fiber quality. Pak. J. Agric. Res. 27(3), 226-236.
 15. Shakeel, A., Farooq, J., Bibi, A., Khan, S., & Saleem, F. 2012. Genetic studies of earliness in *Gossypium hirsutum* L. IJAVMS. 6(3), 189-207.
 16. Sharma, J., Beniwal, J., & Kumar, A. (2006). Influence on weather variable on cotton leaf curl virus disease in cotton (*Gossypium hirsutum* L.). Journal of Cott. Res. Dev. 20 (2), 280-285.