International Journal of Botany Studies
ISSN: 2455-541X; Impact Factor: RJIF 5.12
Received: 06-01-2019; Accepted: 07-02-2019
www.botanyjournals.com
Volume 4; Issue 2; March 2019; Page No. 81-83

Association among seed yield traits and CLCuV in cotton

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Abstract

Cotton is an important cash fibre crop throughout the world. The production and quality of cotton is highly affected by biotic and abiotic stress which caused unbearable losses. The present study was conducted to evaluate cotton genotypes for cotton yield potential with effects of CLCuV. Two cotton genotypes FH-142 and FH-942 were grown in the research fields of Cotton Research Station, Ayub Agricultural Research Institute, Faisalabad, Pakistan. Statistical analysis was performed to evaluate the yield and it attributed traits to access the potential of FH-142 and FH-942 cotton genotypes. The genotype FH-142 was found with higher and better performance as compared to FH-942 through using breeder seed and bulk seeds. The traits including bolls per plant, yield, plant height and CLCuV% per plant were found as most contributing traits towards cotton yield and production. It was also found that the breeder seed has more plant population (32167 plants/ha) than the bulk seed (31075 plants/ha) which revealed higher potential and resistance against CLCuV.

Keywords: cotton, CLCuV, breeder seed, basic seed, seed yield, biotic stress

Introduction

Cotton is the most important fiber crop worldwide as well as high value cash crop in Pakistan. It occupies central position in world in general and especially in Pakistan. It is grown on large scale because of the adequate fiber quality, high lint yield and high adaptability to environmental calamities. Pakistan grows around 3 million hectares of cotton each year, accounts for approximately 10.5% of value added in agriculture and share 2.5% of gross domestic product (Anon., 2009) [1]. The environmental factors including biotic and abiotic are the major threats to agriculture. Biotic stresses including viruses cause many important plant diseases and are responsible for huge losses in quality and quantity of crop in all parts of the world as well as in Pakistan. Cotton leaf curl virus disease is caused by Gemini group of viruses and is vectored by whitefly. This disease was first reported in Nigeria in *Gossypium vitifolia* and *G. peruvianum* (Farquharson, 1912) [5] and second outbreak was recorded by Jones & Mason (1926) [10] in 1924. In Pakistan, it was first observed on stray plant in 1967 (Hussain and Ali, 1975) [9] and became in epidemic form in 1989. CLCuV cause huge losses to cotton production in Pakistan during 1991-92 and reduce the yield from 1.938 million metric ton to 1.445 million metric ton (Zafar *et al.*, 1997) [15]. CLCuV disease cause average reduction in plant height (40.6%), number of bolls per plant (72.5%), boll weight (33.8%), ginning outturn (3.9%), fiber strength (0.7%), fiber length (3.4%) and fineness (Mahmood *et al.*, 1996) [12]. The ample production of cotton to meet the needs of increasing world's population is now being realized. Introduction of genetically modified varieties that enhancing performances could have equally important for textile industry and farmer. Low seed quality sometime leads to low plant populations, poor field emergence and low cotton yield (Hopper and McDaniel 1999) [8]. To manage CLCuV% and enhancing the yield, control of whitefly is not the best strategy because of their high reproduction rate and developing resistance to insecticides (Holt *et al.*, 1999; Ahmad *et al.*, 2003) [7, 4]. Resistance in varieties and seed quality are the attributes to manage the disease because of easy to use, cost effective and environmentally friendly. Therefore, it is essential to use good quality seeds to produce high-quality lint and fiber yield (Hopper and McDaniel 1999; Welch 1999) [8, 2]. This study was initiated to illustrate the effect of seed quality of different varieties against CLCuV% and cotton yield.

Material and methods

Plant material

This experiment was conducted at Cotton Research Station, Faisalabad on 29-05-2017 to evaluate the performance of Bulk Seed and breeder Seed of two genotypes of cotton i.e. FH-142 (virus tolerant Bt variety) and FH-942 (virus susceptible non-Bt variety) with respect to ClcuV % and Seed Cotton Yield (Kg/ ha). The experiment was laid out according to split plot design having four replications.

Experimental Design

For each entry, plot size measured 5.30 m × 4.54 m comprising seven rows set 75 cm apart. Distance between plants within rows was 30 cm.

Measurement of Traits

For measuring the traits, the 10 representative and undamaged plants were selected in each line and marked for identification. Data were collected for No. of bolls per plant, plant height (cm), Seed Cotton Yield (Kg/ ha) and CLcuV %.

Results

Result from the analysis disclosed that significant differences were present among the variety and quality of seed. Seed cotton yield and CLCuV% parameters were significantly affected by the seed source. It was found from the mean comparison test that FH-142 breeder seed Performed well against CLCuV% and give high yield. Stepwise regression analysis was performed to find out the traits that were highly contributing towards cotton yield per plant. It was revealed from results (Table 1) that the higher contributing traits were Number of bolls, plant height and CLCuV. The predicted equation for cotton yield per plant as follows:

$$Y= 27.7608 + (-0.00108X1) + (-0.05338X2) + (0.09329X3)$$

Table 1: Stepwise Regression analysis for cotton yield

Variable	Coefficients	Std Error	T value
BPP (X1)	-0.00108	0.00174	-0.62
PH (X2)	-0.05338	0.06267	-0.85
CLCuV (X3)	-0.09329	0.06202	-1.50

R^2 = 0.1824 (18.24%), Adjusted R^2= 0.0220, Standard Deviation= 3.18614, Intercept= 27.7608

Genotypic and phenotypic correlation was computed to access the strength of association of traits with respect to genetic and environmental factors. The results from table 2 indicated higher and significant correlation of cotton yield per plant with plant height and CLCuV. Strong and significant correlation was recorded for CLCuV among bolls and yield. Abbas *et al.* (2013) [2] reported that the significant correlation among cotton yield, bolls per plant per plant may be used for the development of higher yielding cotton genotypes. Significant correlation of yield traits may help plant breeders to develop high yielding synthetic and hybrids in crop plants to improve yield and production (ALI *et al*., 2016) [3].

Table 2: Correlation among different traits

Traits	Bolls	Yield	PH
Yield	-0.0359		
PH	-0.1557*	-0.1702*	
CLCuv	-0.3447*	-0.2317*	-0.1070

*= Significant at 5% probability level

Principal component analysis was performed to screen the genotypes for best performing traits, as it helps to explore total variation in the germplasm. Four PCs (Principal Components), PC1, PC2, PC3 and PC4 were recorded as shown in table 3. Higher variation was recorded for traits bolls per plant, plant height, CLCuV infestation and cotton yield per plant. The proportion variation of four PCs PC1 (35.4%), PC2 (27.9%), PC3 (25.2%) and PC4 (11.5%) were recorded for observed traits. FAWAD *et al.* (2015) [6] and ALI *et al.* (2016) [3] working on maze suggested that principal component analysis may help plant breeders in selecting genotypes based on large number of studied traits.

Table 3: Principle Component Analysis for Cotton traits

Eigenvalue	1.41646	1.11447	1.00796	0.46111
Proportion	0.354	0.279	0.252	0.115
Commulative	0.354	0.633	0.885	0.100
Variable	PC1	PC2	PC3	PC4
Bolls	-0.5932	0.1988	0.5688	0.5340
Yield	-0.4054	-0.4727	-0.6568	0.4252
Ph	0.2177	0.7760	-0.4280	0.4090
CLCuV	0.6606	-0.3673	0.2488	0.6057

Table 4: Overall Assessment of Seed quality for yield and CLCuV%

Varieties	Yield kg/ha		Average Variety	CLCuD%		Average Variety	Plant. population/ha		Average Variety
	Breeder seed	Bulk seed		Breeder seed	Bulk seed		Breeder seed	Bulk seed	
FH-142	1681	1576	1628a	16.88	22.17	19.52b	32255	31100	31677
FH-942	745	651	698b	45.02	46.59	45.80a	32080	31050	31565
Treat. average	1213a	1113a		30.95b	34.38a		32167	31075	
LSD (0.05)									

Variety 297 kg/ha, seed classes, 41 kg/ha, interaction,58 kg/ha

Cotton yield per plant is significantly correlated with bolls per plant and infestation by the CLCuV. Bolls per plant strongly correlated with plant height and CLCuV infestation. MEENA *et al.* (2007) [13] and KOTB (2012) [11] suggested that the correlation analysis may be helpful to improve the yield traits to enhance yield and productivitf crop plants. The aim of our study was to evaluate the quality of seed to improve yield and production of crop plant. seed source significantly affected the seed cotton yield and CLCuV%. The seed sources irrespective of varieties affected significantly the seed cotton yield. The breeder seed on an average by yielding 1213 kg/ha proved superior to bulk seed which gave1113 kg/ha seed cotton yield. Similarly, the crop sown by using breeder seed showed significantly less CLCuV% infestation (30.95%) than the bulk seed which exhibited 34.38% CLCuV infestation. FH-142 gave highly significant difference in average seed cotton yield (1576kg/ha) than FH-942 (698kg/ha). Breeder seed has more plant population/ha (32167 plants/ha) than the bulk seed having 31075 plants/ha whereas both the varieties showed at par difference in plant population/ha.

Conclusion

The present study was conducted to evaluate cotton genotypes for cotton yield potential under quality of seed. Analysis was performed to evaluate the yield and it attributed traits for potential of FH-142 and FH-942 cotton genotypes. The genotype FH-142 was found with higher and better performance as compared to FH-942 by using breeder seed and bulk seed. The traits bolls per plant, yield, plant height and CLCuV% per plant were found as most contributing traits towards cotton yield and production. It was also found that Breeder seed has more plant population (32167 plants/ha) than the bulk seed (31075 plants/ha).

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