

Research Article

Comparative response of Bt. and Non-Bt. cotton germplasm against cotton leaf curl disease and seed cotton yield under hotspots of Multan region

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Abstract

Cotton leaf curl virus is a major impediment for productivity of cotton particularly in areas of Punjab province. A set of 110 cotton genotypes including varieties, and advanced lines, (87 Bt, and 23 Non-Bt) were evaluated at experimental farm of Cotton Research Institute Multan during 2016-17, and explored comparative response of GMO (Bt.) and Non-GMO (Non-Bt.). cotton varieties against leaf curl disease, and seed cotton yield. Under highly tolerant group, CIM-598, PB-82, and FH-312 showed lowest disease index with values 2, 5 and 7, respectively. Among Bt. varieties, under tolerant group, were PB-83, PB-86, MNH-992, FH-242, and NIAB-2008 showed disease index with values 21. Whereas, for non-Bt., four varieties CIM-506, CIM-573, VH-281, and CIM- 473, were tolerant. Highly tolerant Bt. varieties have 7.4% higher seed cotton yield over Non-Bt varieties. Similarly, under tolerant and susceptible group of Bt. varieties produced 16.6%, and 2.6%, higher seed cotton yield over Non-Bt. cotton varieties, respectively. However, seed cotton yield difference between Bt. and Non. Bt. cotton varieties were statistically non-significant. Disease severity showed negative significant correlation with plant height, bolls plant⁻¹. Whereas disease infestation percentage was positively correlated with plant height, monopodial branches plant⁻¹, fruiting branches plant⁻¹, seed mass and boll mass boll⁻¹. Most of the fibre traits were significantly associated with disease severity. Thus, disease severity is more limiting factor affecting morphological and fibre quality traits. The derived information could be valuable to make future breeding strategy against leaf curl virus disease of cotton.

Keywords: Boll and seed mass; Correlation studies; Cotton leaf curl virus; Disease index; Seed cotton yield

Introduction

Cotton is a leading cash crop considered for almost 100 countries, and this important crop is attacked by a number of diseases. Almost 75 disastrous cotton diseases have

been reported that drastically reduce the cotton production [1]. However, viral diseases fetched the attention of global research since last century due to huge economic losses and intricate unpredictable

nature of virus. Various virus-like symptoms related to bated yield and quality, even deprivation of the whole crop have been represented in cotton from diverse peripherals of the world. More than twenty virus-like infections of cotton have been depicted in the American phyto pathological society, "Cotton Disease Compendium" [2, 3], but just a couple have been affirmed to be of viral virulent agent etiology, together with homopteran-transmitted gemini-viruses, Cotton leaf crumple virus (CLCrV) [4-6] and several other strains of the cotton leaf curl complex (India and Pakistan) [7-9]. However, the Begomoviruses are the most damaging and causes the primary plant infectious agent wherever cotton is fully grown [10, 11]. It is estimated that the losses due to these begomoviruses are equal to 60 billion US\$ a year [12].

In Pakistan, the malady referred as cotton leaf curl disease was first observed near Multan in the year 1967 [13] on a few individual plants. [14] reported that in 1987, the incidence was up to 80% in certain fields. In 1988, it damaged the cotton crop on 150 acres in Multan district. Since then it has been increasing every year. It affected 500 acres in 1989 and 2000 acres in 1990 [15]. During the year 1991-1992, the highest cotton production was 12.8 million bales in Pakistan [16]. During the next year, 1992-1993, CLCuD disease appeared in epidemic form, which caused decrease in cotton yield down to 9.05 million bales and was further decreased to 8.04 million bales during 1993-94. The disease caused reduction of 7.1 million bales; CLCuD was the main force behind yield decline in these years [17].

The disease spread throughout the cotton belt of Pakistan, India, and now reported also in South China and India [18-20]. Between 1992 and 1997, the recorded financial losses due to CLCuD, in Pakistan, are up to 5 billion dollars (US) [7]. Also, in the Indian territory of Punjab, this ailment reduced cotton production by nearly 70% in 1998 [21]. [22] identified a reduction of

52.7% in the quantity of bolls and a decrease of 54.2% in boll weight because of CLCuD, whereas the variations in yield loss between resistant and vulnerable cultivars were nearly 50 and 85–90%, respectively. Upland cotton (*G. hirsutum*) has been a good source for fibre quality and seed cotton yield but upland cotton have poor tolerance to CLCuD. Whereas wild species carry novel genes to combat CLCuD and could be used as donor for *G. hirsutum*. Thus, genetic response of available breeding material comprises *G. hirsutum* and wild species is essential to identify breeding line that are resistance/tolerance to CLCuD. Identification of the breeding line conferring resistance to CLCuD will facilitate to formulate breeding strategies for development of cultivar resistant against CLCuD.

Materials and methods

The present research work was carried out at the experimental area of Cotton Research Institute Multan during 2016-17. The plant material consisted of 110 different inter/intraspecific varieties/lines of cotton. The list of these varieties/lines of cotton is shown in (Table 1). The varieties/lines were collected from different Government as well as Private Research institutions working on cotton.

Experiments undertaken

All the 110 genotypes were sown in the field in a RCBD in duplicate with plot size 40 x 5 sq feet/genotype. Randomization was followed in assigning genotype to the experimental unit in each block supporting intra-row spacing @ 75cm and intra-plant @ 30 cm. Three seeds were dibbled manually, and one healthy seedling was retained after thinning. Farm hold practices like hoeing, manuring and irrigation etc. were kept uniform.

Sampling and measurements

Ten randomly tagged plants from each entry per replication were selected and the data were recorded at appropriate time for the following traits.

Disease related traits

Disease infestation % (DI) and disease severity (DS) were calculated as described by [18] and given in (Table 2).

Table 1. List of cotton genotypes available to conduct present study

Bt. Genotypes				Non-Bt
AGC-2	FB-80	FH-330	NIA-NORI	CIM-473
AGC-501	FDH-228	FH-342	OHO-608	CIM-506
AGC-999	FDH-502	FH-444	PB-81	CIM-554
AS-01	FDH-512	FH-490	PB-82	CIM-573
Baghdadi	FH-114	FH-Kahkashan	PB-83	CRIS-09
BH-184	FH-118	FH-Lalazar	PB-84	CRIS-121
BH-185	FH-142	FH-Lalazar (A)	PB-85	CRIS-129
Bt.CIM-598	FH-142	FH-NOOR	PB-86	CRIS-134
Bt.CIM-599	FH-142	Gh-142	PB-896	CRIS-342
Bt.CIM-602	FH-158	IUB-13	RH-647	CRIS-467
CIM-595	FH-159	MNH-1016	SLH-12	CRIS-486
CIM-598	FH-168	MNH-588	SLH-6	CRIS-494
CIM-599	FH-175	MNH-886	SLH-8	CRIS-508
CIM-600	FH-183	MNH-988	VH-283	CRIS-510
CIM-600 (S)	FH-2073	MNH-992	VH-295	CRIS-533
CIM-602	FH-214	MPS-11	VH-305	CRIS-543
CIM-612	FH-242	MS.DK	VH-326	CRIS-585
CIM-616	FH-312	MS-71	VH-327	CRIS-5A
CIM-622	FH-312	Mubarak	VH-329	CRIS-641
CRS-1	FH-313	NIAB 2008	VH-338	MPS-11
Cyto-178	FH-326	NIAB-824	VH-363	VH-281
Cyto-301	FH-327	Niab-Bt-2		VH-289
				VH-300

Table 2. Symptom rating scale for leaf curl virus disease

Disease index (%)	Severity grade	Symptoms	Remarks
0	0	No Symptoms	Resistant
1-20	1	Thickening of only secondary and tertiary veins.	Highly tolerant (A)
21-30	2	Thickening of secondary and primary (mid rib) veins.	Tolerant (B)
31-50	3	Vein thickening (V.T), leaf curling (L.C) or enation (E) or both.	Susceptible (C)
>50	4	Stunting along with vein thickening leaf curling/enation.	Highly susceptible (D)

Plant morphological traits

For recording plant morphological traits, 50 bolls were collected from selected 10 plants in each entry i.e. 5 bolls/plant. Sample weight (seed cotton) was recorded by electrical balance and ginned at laboratory saw gin machine. The lint weight was also recorded after ginning.

Data for plant architecture traits like plant height (PH), monopodial branches plant⁻¹ (MPpP), fruiting branches plant⁻¹ (FBpP), bolls number plant⁻¹ (BpP) were recorded at plant maturity stage.

The observations and measurements for boll size (BS), seed cotton yield plant⁻¹ (SCYpP), lint mass boll⁻¹ (LMpB), seed

mass boll⁻¹ (SMpB) were taken during the trial were as follows:

$$\text{Boll size} = \frac{(\text{Total seed cotton weight})}{(\text{Total number of bolls})}$$

$$\text{Seed cotton yield plant}^{-1} = \text{Total number of bolls plant}^{-1} \times \text{boll size (g)}$$

$$\text{Lint mass per boll} = \frac{(\text{Total lint mass of the sample})}{(\text{Number of bolls in the sample})}$$

$$\text{Seed mass per boll} = \frac{(\text{Total seed mass of the sample})}{(\text{Number of bolls in the sample})}$$

Fibre quality traits

For lint samples HVI Uster HVI 900 was used for following fibre traits, Fibre length (FL, cm), Fibre strength (FS, g/tax); Micronaire (Mic, µg/inch);

Lint percentage (LP)

Lint percentage was calculated as

$$\text{Lint percentage} = \frac{\text{Lint weight}}{\text{Total seed cotton weight}} \times 100$$

Fibre uniformity (FU, %), Fibre Maturity (FM, %), Short Fibre Index (SFI,%), and Fibre reflectance (Rd). The other fibre trait like lint percentage (LP) was calculated by given formula;

Statistical analysis

The data for all the investigated traits were arranged following the manual guide of SPSS17.0 software. The arranged data were subjected to correlation coefficient (r) by using software SPSS17.0 software (<http://www>

[01.ibm.com/software/analytics/spss/](http://www.ibm.com/software/analytics/spss/)).

Results and discussion

Cotton crop is the foremost important textile fibre crop and the second most important oil seed crop in the world [24]. It has been currently grown in more than 100 countries [24] broadly in temperate climates as well [25]. Almost 75 maladiou diseases have been involved in deduction of cotton production [1]. However, cotton leaf curl virus disease fetched the attention of global research due to huge economic losses in Indian Sub-continent. Disease index of cotton leaf curl disease showed that among 110 cotton cultivated varieties, none of the genotype showed completely resistant to cotton leaf curl disease. However varietal response against the

disease was highly tolerant, tolerant, and susceptible. There were 38 Bt. (Fig. 1) and only 2 Non-Bt cotton genotypes were highly tolerant to CLCuD. Under highly tolerant group, CIM-598, PB-82, and FH-312 showed lowest disease index with values 2,5, and 7, respectively. The complete list of highly tolerant varieties is depicted in (Fig. 1). Whereas for non-Bt., only two varieties CIM-554, and MPS-11 with disease index 16 were highly tolerant. Under tolerant group there were 39 Bt, (Fig. 2) and 4 Non-Bt varieties (Fig. 3). Among Bt. varieties, PB-83, PB-86, MNH-992, FH-242, and NIAB-2008 showed disease index with values 21. Whereas, for non-Bt., four varieties CIM-506, CIM-573, VH-281, and CIM- 473, were tolerant. Under susceptible group there were 10 Bt, (Fig 4) and 17 Non-Bt varieties (Fig. 5). The most susceptible Bt. varieties were FH-Lalazar, Mubarak, NIAB-824, RH-647, and FH-114. Whereas among non-Bt. the varieties bearing varietal mark CRIS were most

susceptible under category susceptible group.

The Bt. Cotton varieties under tolerant group have 16.6% higher yield as contrast to Non-Bt cotton varieties. Whereas, highly tolerant Bt. varieties have only 7.4% higher seed cotton yield over Non-Bt varieties. Likewise, under susceptible group of Bt. varieties produced 2.6%, higher seed cotton yield over Non-Bt. cotton varieties, respectively. However, seed cotton yield difference between Bt. and Non-Bt. cotton varieties were statistically non-significant (Table 3). Globally, Bt. cotton enhanced the farm income due to enhanced productivity and efficiency gains. During 2016, biotech cotton covered an area of 11.2 million hectares in India, followed by China and USA [26]. [27] also observed differences of productivity between GMO (Bt.) and Non-GMO cotton fields. Our results also suggest that Bt. varieties, available in Pakistan, are performing better not only in higher seed cotton yield but also in terms of greater tolerance to cotton leaf curl disease. Bt. varieties have maximum 16.6% higher seed cotton yield compared to Non-GMO varieties. Thus, productivity of cotton can be enhanced by encouragement and adoption of new technologies.

The correlation analysis for morphological traits revealed some useful association among the morphological traits. Among plant architecture traits (Table 4), plant height (PH) has positive and significant correlation with BpP, SCYpP, Dis inf, and DS. Monopodia plant⁻¹ (MPpP) had positive and significant correlation with BpP, BS, SCYpP, and DS. Fruit branches plant⁻¹ (FBpP) had positive and significantly correlated with BpP, SCYpP, while negatively correlated with DS. Boll size (BS) had positive significant associated with SMpP, LMpB. Bolls plant⁻¹ (BpP) showed significantly associated only with

SCYpP while negatively correlated with disease infestation. Seed mass boll⁻¹ (SMpB) had positive and significant associated only with LMpB, while lint mass boll⁻¹ (LMpB) was significant positive correlated with DS.

The correlation analysis for fiber related traits (Table 5) revealed some useful association among the fiber traits. Lint-percentage (LP) had positive and significant correlation with LI, and dis infestation. Fibre length (FL) had significant associations with most of the fibre traits like FS, FM, dis inf., while it had negative and significant association with mic. Fiber fineness (Mic) had significant associated with FU and negatively associated with dis infestation. Fiber strength (FS) had positive significant interaction with FU, FM and dis infestation. Fiber uniformity (FU) had negatively significant association with disease infestation.

Various morphological plant traits are usually correlated [28]. Studying the kind and strength of relationship among different attributes causes the plant breeder to choose proper breeding methods for evolving adapted genotypes. Thus, a thorough knowledge of linkage between economic traits decides the cutoff points within which a specific trait might be relinquished for different attributes [29]. As, in cotton, expanded seed cotton yield and fibre quality is a definite target of any breeding program, the correlation analysis for important agronomic and fibre traits provides data regarding the direction and extent of association of assorted traits among each other and with the ultimate objective. Additionally, based on correlation studies, one will opt for the alternate selection criteria for a definite result.

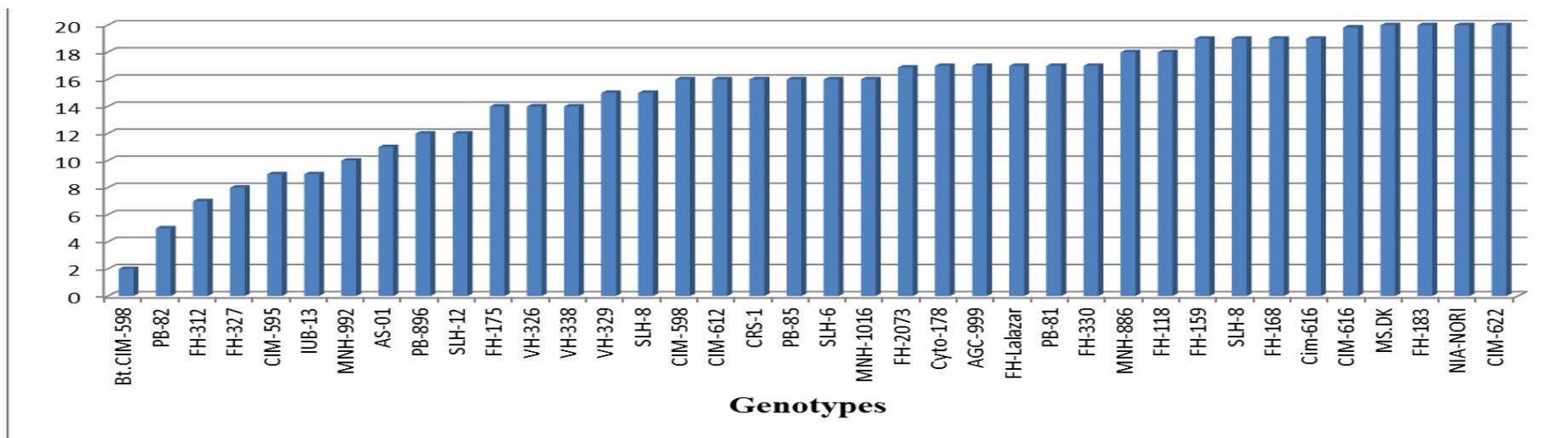


Figure 1. Cotton genotypes (Bt.) highly tolerant to cotton leaf curl disease

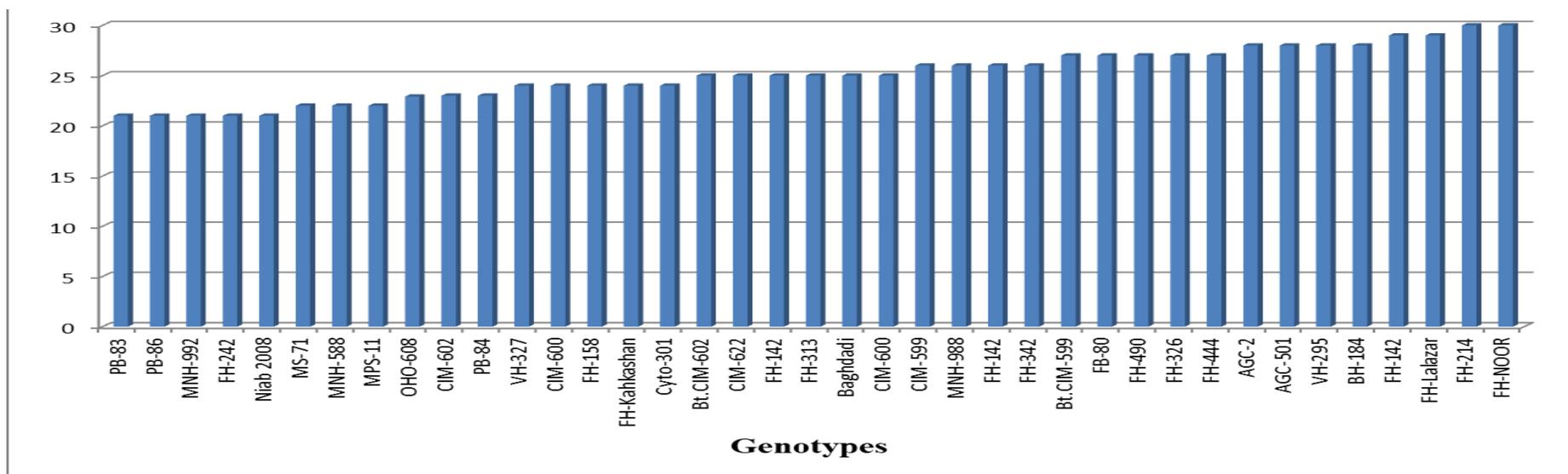


Figure 2. Cotton genotypes (Bt.) tolerant to cotton leaf curl disease

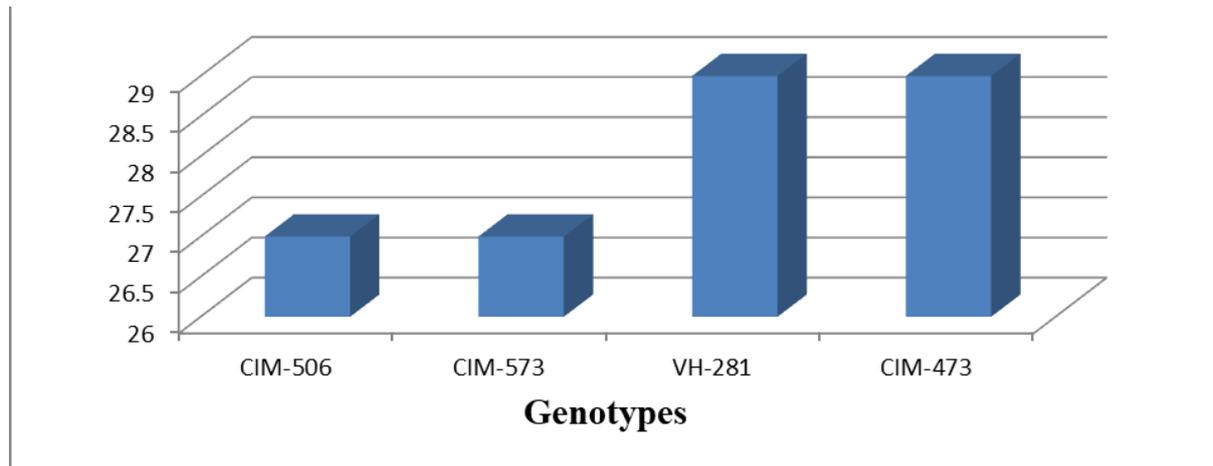


Figure 3. Cotton genotypes (Non-Bt.) tolerant to cotton leaf curl disease

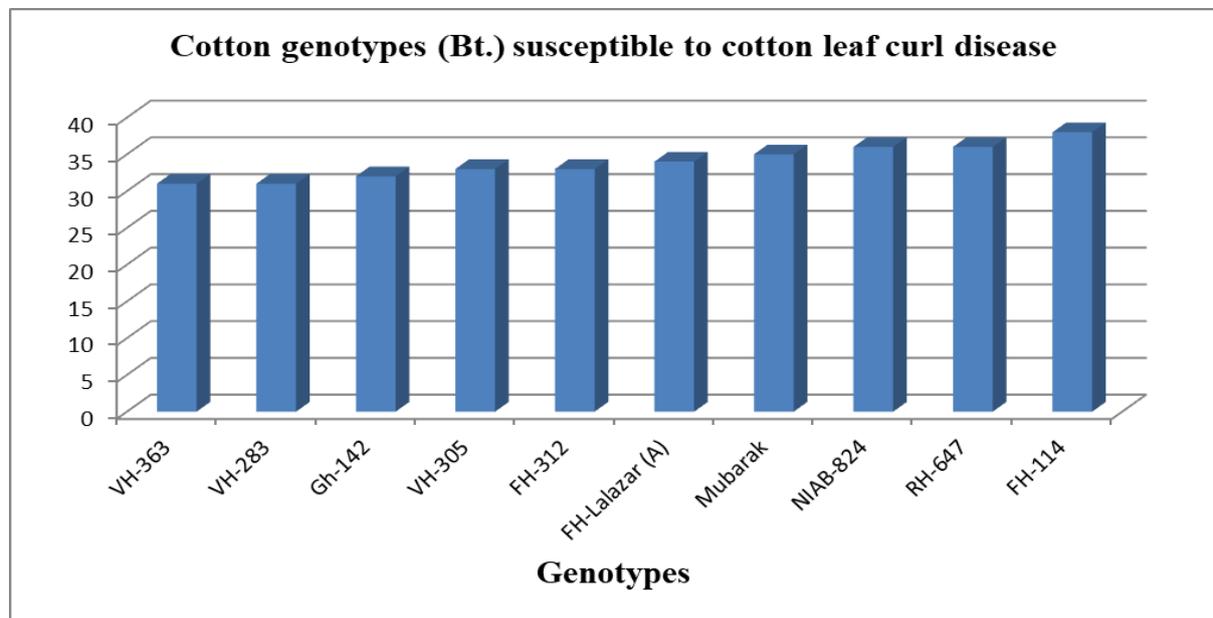


Figure 4. Cotton genotypes (Bt.) susceptible to cotton leaf curl disease

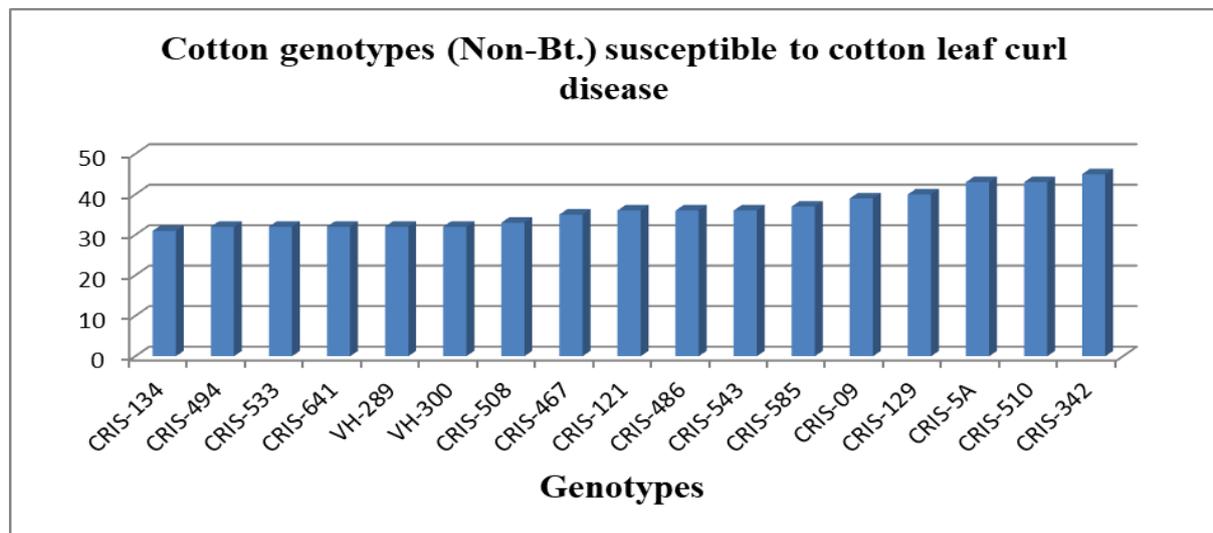


Figure 5. Cotton genotypes (Non-Bt.) susceptible to cotton leaf curl disease

Table 3. Seed Cotton Yield Plant⁻¹ (SCYP⁻¹) for GMO (Bt.) and Non-GMO (Non-Bt.) Cotton Genotypes

Response	Non-Bt		BT		Percent increase (Bt. over Non-Bt.)
	No. of Genotypes	SCYP ⁻¹ (g)	No. of Genotypes	SCYP ⁻¹ (g)	
Highly tolerant	2	71.70	38	77.05	7.47
Tolerant	4	59.68	39	69.63	16.67
Susceptible	17	53.99	10	55.39	2.60
Mean of difference (Bt. and Non-Bt.)				5.57	
SE				2.47	
Confi interval (95%) upper/lower				5.06/16.19	
P value				0.153	

Table 4. Correlation studies among different agronomic and leaf curl disease related traits in cotton

Traits	PH	MpP	FBpP	BS	BpP	SCYpP	SMpB	LMpB	D.S	Dis Inf
MpP	0.095									
FBpP	-0.036	0.123								
BS	-0.144	-0.214*	-0.128							
BpP	0.291**	0.378**	0.434**	-0.191						
SCYpP	0.230*	0.276**	0.360**	0.133	0.835**					
SMpB	0.119	0.169	-0.163	0.252*	0.046	0.122				
LMpB	-0.006	-0.036	-0.098	0.365**	-0.087	0.100	0.761**			
D.S	-0.463**	0.111	0.036	-0.089	-0.202*	-0.112	-0.012	0.022		
Dis Inf	0.212*	0.213*	-0.207*	-0.061	0.108	-0.023	0.399**	0.242*	-0.033	

**Correlation is significant at the 0.01 level (2-tailed), *Correlation is significant at the 0.05 level (2-tailed)

Table 5. Correlation studies among different fibre and leaf curl disease related traits in cotton

Traits	LP	Lint Index	FL	Mic	FS	FU	FM	D.S	Dis Inf
Lint Index	0.794**								
FL	0.038	0.171							
Mic	-0.017	-0.019	-0.254*						
FS	-0.054	0.090	0.614**	-0.108					
FU	0.023	0.026	0.022	0.658**	0.337**				
FM	0.003	0.067	0.391**	0.131	0.537**	0.151			
D.S	0.473**	0.424**	0.313**	-0.440**	0.244*	-0.303**	0.125		
Dis Inf	0.147	0.156	-0.036	-0.060	-0.031	-0.130	0.127	0.458**	

**Correlation is significant at the 0.01 level (2-tailed), *Correlation is significant at the 0.05 level (2-tailed)

Conclusion

There were 38 Bt. cotton genotypes were highly tolerant to cotton leaf curl disease. For Bt. varieties, CIM-598, PB-82, and FH-312 showed lowest disease index whereas for non-Bt., only two varieties CIM-554, and MPS-11 with disease index 16 were

highly tolerant. Under tolerant group there were 39 Bt, and 4 Non-Bt varieties. Among Bt. varieties, PB-83, PB-86, MNH-992, FH-242, and NIAB. Whereas, for non-Bt., four varieties CIM-506, CIM-573, VH-281, and CIM-473, were tolerant. Under susceptible group there were 10 Bt, and 17

Non-Bt varieties. The most susceptible Bt varieties were FH-Lalazar, Mubarak, NIAB-824, RH-647, and FH-114. Whereas among non-Bt. the varieties bearing varietal mark CRIS were most susceptible under category susceptible group. We also suggest that disease severity should be taken into account while dealing with leaf curl disease of cotton. The derived information could be helpful to design future breeding scheme against cotton leaf curl virus disease. The same may be helpful to improve the cotton production by recommending highly tolerant varieties to disease susceptible regions to curtail the losses due to this disease.

Authors' contributions

Conceived and designed the experiments: W Nazeer & ALK Tipu, Performed the experiments: W Nazeer, ALK Tipu & ZU Zia, Analyzed the data: S Ahmad, A Karim, S Ahmad & A Mahmood, Contributed materials/ analysis/ tools: M Naeem, MR Shahid & A Karim, Wrote the paper: W Nazeer & M Basheer.

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