



CLCuD Infinity Affects Yield and Retards Growth Pattern of *Gossypium hirsutum* L.

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Abstract

Cotton leaf curl disease is the devastating disease in the sub-continent. There are huge seed cotton yield and economic losses due to it. There is dire need to establish such a breeding program that contains morpho-fiber strong base of the genotypes. The present study is designed to evaluate the morphological and fiber quality traits of cotton. The significant variation is seen in all the studied traits. The CLCuD retards the plant growth. However, some genotypes later recover. The genotypes CRIS-134, CRIS-543, CRIS-129 and CRIS-134 needs to be exploited and used in the breeding programs to develop better genotypes under CLCuD infinity with strong performance.

Keywords: Cotton Leaf Curl Disease; *Gossypium hirsutum* L.; Genetic Diversity; Morphology; Fiber; PCA; Variation; Seed Cotton Yield; Hot Climate

Abbreviations

CLCuD: Cotton Leaf Curl Disease; PH: Plant Height; BpP: Bolls Per Plant; SpPPS: Ympodial Branches Per Plant; BW: Boll Weight; SCY: Seed Cotton Yield; GOT: Ginning Outturn Percentage; LI: Lint Index; SL: Staple Length; MIK: Mike (Staple Fineness); STR: Fiber Strength; FM: Fiber Maturity.

Introduction

Cotton leaf curl disease (CLCuD) is the most devastating major limiting biotic factor to cotton. In subcontinent cotton production is severely compromised due to this endemic disease. The insect white fly (*Bemisia tabaci*) serves as a vector in transmitting

the disease. The symptoms associated with CLCuD are stunting growth, vein swelling, leaves enation and upward or downward leaves curling. The disease was first reported in Africa (1912) from Nigeria affecting *Gossypium peruvianum* and *Gossypium Vitifolia*. Secondly, the symptoms were observed in Sudan (1924) and thirdly, in Tanzania (1926). In Pakistan CLCuD was first observed near Multan region (1967) and it became prominent in (1973) [1]. At that time disease occurred in late season fairly on the upper portion of the plant. Gradually, the disease spreads throughout the whole area of country causing huge economic losses and damages 32-42% of crop [2].

The disease affects the crop plant from the very early growth days and keeps under stress conditions throughout the season. The disease severity is mainly associated with sowing time, genotypic resistance and environmental conditions. The early sowing of crop faces less disease attack as comparative to late sowing. The different genotypes show varying level of disease resistance depending upon the genetics and genetic makeup of every genotype. The temperature and humidity plays significant role in the environment for disease spreading (Ahmed., *et al.* 2017). The top fresh emerging leaves are more susceptible. The CLCuD damage varies on different plant parts ultimately affecting seed cotton yield (Raza., *et al.* 2016). It damages directly and indirectly the crop plant. The direct affect can be seen on the morphology and fiber quality.

The breeder remains in the efforts of developing new genotypes that perform better but side by side naturally insects, pests also getting stronger. Presently there is no such genotype that shows complete resistance to the cotton leaf curl disease. All the genotypes are vulnerable and responsible for low yield projections [3]. The exploitation of the germplasm is necessary at this stage.

There is a need to develop germplasm that have more resistance to CLCuD. To make effective and higher cotton production morpho-

fiber changes must be studied. The present study is designed to evaluate the morphology and fiber quality under the infinity of CLCuD.

Material and Method

There were 20 genotypes collected from germplasm of cotton research institute, Multan and grown in the randomized complete block design with two replications. These were planted under same identical agronomic practices without any biasing keeping plant to plant distance 30cm and row to row 75cm. Later seedlings were thinned to one plant after fourteen days. All the season the crop was kept at zero spray. The data was recorded for different morphology and fiber quality parameters from selected plants in each genotype and in each replication. The morphological parameters were cotton leaf curl disease (%), plant height (cm), bolls per plant, sympodial branches per plant, boll weight (g) and seed cotton yield (g). The fiber parameters are ginning outturn (%), lint index, staple length (mm), mike (µg/inch), fiber strength (g/tex) and fiber maturity. The morphology parameters were taken on crop maturity while CLCuD was taken when crop has peak disease incidence using scale prescribed by (Nazeer., *et al.* 2014), by formulae:

$$\text{Percent disease index} = \frac{\text{Sum of all disease ratings}}{\text{Total plants}} \times \frac{100}{\text{Maximum grade}}$$

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

Table 1: CLCuD rating scale. (Nazeer., *et al.* 2014).

Results

Analysis of variance for component parameters

Analysis of variance was carried out for 12 traits *i.e.* CLCuD (%), PH (cm), BpP, SpPP, BW (g), SCY (g), GOT (%), LI, SL (mm), MIK (µg/inch), STR (g/tex), FM. The data subjected to the analysis revealed highly significant differences of morphological traits bolls

per plant, seed cotton yield and percentage disease index. Among fiber traits ginning outturn and fiber strength showed significance.

Correlation of morphology and fiber quality traits in *Gossypium hirsutum* L.

The correlation studies showed high positive correlation of morphological traits seed cotton yield and boll weight, fiber traits lint index and ginning outturn, respectively.

	Traits	Replication	Genotypes	Error
	Degree of freedom	1	19	19
Morphological traits	CLCuD	527.8	110.7**	40.5
	PH	384.4	711**	5.2
	BpP	36.1	295.8**	1.8
	SpPP	63	71.6**	0.3
	BW	0.09	0.4	0.03
	SCY	39.8	221.7**	0.6
Fiber traits	GOT	0.3	30.3**	3.3
	LI	0.3	1.2*	0.04
	SL	2.5	8.3**	0.4
	Mik	0.4	0.3	0.04
	STR	4.4	15.5**	0.3
	FM	0.3	4.2**	0.2

* = Significant at 5 % probability level.

** = Significant at 1 % probability level.

Table 2: Mean squares values for morphological and fiber quality parameters of (*Gossypium hirsutum* L.).

	CLCuD	PH	BpP	SPpP	BW	SCY	GOT	LI	SL	Mik	Str
PH	0.03										
BpP	0.14	0.42									
SPpP	0.07	-0.23	-0.03								
BW	-0.23	0.20	0.34	0.16							
SCY	-0.21	0.18	0.33	0.16	0.99**						
GOT	-0.18	0.18	-0.01	-0.04	0.06	0.06					
LI	-0.28	0.33	0.00	-0.01	-0.03	-0.02	0.78**				
SL	-0.18	-0.31	-0.02	0.19	0.46**	0.46**	0.21	-0.20			
Mik	0.09	-0.30	0.07	0.07	0.19	0.17	0.24	0.17	0.27		
Str	0.14	-0.19	-0.15	-0.01	0.42	0.43	-0.20	-0.30	0.41	0.44	
FM	0.31	0.31	0.35	0.43	0.37	0.36	-0.02	-0.03	-0.15	-0.07	0.24

Table 3: Correlation results.

Genetic divergence

Principal components analysis

The principal component analysis is a multivariate statistical technique, to extract the important information from the data table and simplify the description of the data set. To discern patterns of variation, PCA was performed on all the morphology and fiber quality variables.

Morphological traits

Out of 6 principal components, three components had extracted eigen value of >1. This contributed 81.1% of the variation among the 20 cotton genotypes. The remaining 19.9% of the total variability was contributed by other components.

The first principal component explained 39% of the total variation with boll weight (0.619) and seed cotton yield (0.613) as the major variability contributing trait. This PC had maximum positive factor loading for bolls per plant followed by plant height and sympodial branches per plant while negative effect towards CLCuD. The second principal component explained 23% of the total variation with boll weight (0.168) as the major variability contributing trait. This PC had positive factor loading for seed cotton yield while negative effect towards plant height, bolls per plant, CLCuD and sympodial branches per plant. The third principal component explained 18% of the total variations with sympodial branches per plant (0.745) as the major variability contributing trait. This PC had positive factor loading for bolls per plant while negative effect towards plant height, CLCuD, boll weight and seed cotton yield.

Variable	PC1	PC2	PC3	PC4	PC5	PC6
CLCuD	-0.154	0.337	0.726	0.509	-0.276	-0.024
PH	0.271	0.603	-0.118	-0.463	-0.579	0.006
BpP	0.371	0.463	0.267	-0.173	0.739	0.018
SPpP	0.08	-0.48	0.622	-0.604	-0.107	0.008
BW	0.619	-0.196	-0.01	0.238	-0.111	-0.714
SCY	0.613	-0.201	0.002	0.276	-0.135	0.7
Eigenvalue	2.3554	1.3988	1.111	0.6211	0.5094	0.0043
Proportion	0.393	0.233	0.185	0.104	0.085	0.001
Cumulative	0.393	0.626	0.811	0.914	0.999	1

Table 4: PCA results of morphological traits.

Fiber traits

Out of 6 principal components, three components had extracted eigen value of >1. This contributed 80.8% of the variation among the 20 cotton genotypes. The remaining 19.2% of the total variability was contributed by other components.

The first principal component explained 33% of the total variation with fiber strength (0.395) and staple length (0.142) as the major variability contributing trait. This PC had maximum positive factor loading for fiber strength followed by staple length

and fiber maturity while negative effect towards ginning outturn, lint index and mike. The second principal component explained 30% of the total variation with fiber maturity (0.013) as the major variability contributing trait. The third principal component explained 19% of the total variations with staple length (0.343) as the major variability contributing trait.

Effect of CLCuD on seed cotton yield

The genotypes CRIS-129, CRIS-134, CRIS-494, VH-289, VH-300, VH-305 and VH-327 performed better comparative with other under disease infinity.

Variable	PC1	PC2	PC3	PC4	PC5	PC6
GOT	-0.608	-0.296	-0.054	-0.311	0.009	0.666
LI	-0.663	-0.097	-0.175	0.095	-0.371	-0.612
SL	0.142	-0.537	0.343	-0.63	0.186	-0.377
Mik	-0.056	-0.593	-0.054	0.63	0.495	-0.032
Str	0.395	-0.512	-0.255	0.085	-0.695	0.161
FM	0.113	0.013	-0.884	-0.307	0.316	-0.11
Eigenvalue	1.9593	1.77	1.1182	0.7367	0.3085	0.1073
Proportion	0.327	0.295	0.186	0.123	0.051	0.018
Cumulative	0.327	0.622	0.808	0.931	0.982	1

Table 5: PCA results of fiber quality traits.

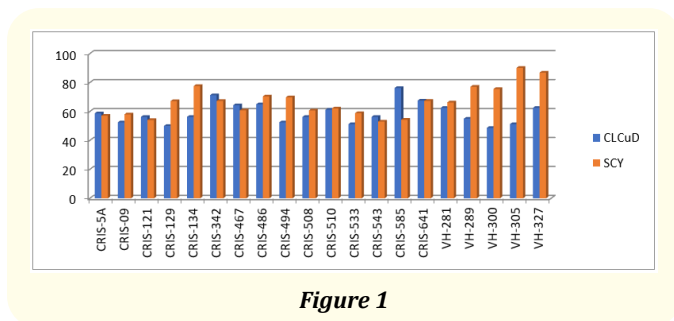


Figure 1

Discussion

Shao, et al. [4], Hussain, et al. [5] and Abdelraheem, et al. [6] also reported similar results of morphological and fiber quality traits. The results are presented in Table 2. This variation can be used in future breeding programs against the disease tolerance and seed cotton yield in the varietal improvement and breeding programs.

The correlation showed high positive correlation of morphological traits seed cotton yield and boll weight. These traits should be kept under notice by the breeder. The fiber traits lint index and ginning outturn also has a key role in genotype success story. The PCA results of morphological traits are similar with Talib, et al. [7], Mugheri, et al. [8] and Gapare, et al. [9]. The PCA results of fiber quality traits were similar with Farooq, et al. [10].

The genotypes CRIS-129, CRIS-134, CRIS-494, VH-289, VH-300, VH-305 and VH-327 can be exploited further in breeding programs.

Conclusion

The CLCuD influences the seed cotton yield by seriously affecting the physiology of the crop plant. The morphology and fiber quality characteristics get reduced. There is dire need to develop resistant genotypes by exploring changes with germplasm and creating variation associated with CLCuD.

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