INT. J. BIOIL. BIOTECH., **8 (1): 135-138, 2011.**

EVALUATION OF (DIVERSE) COTTON GENOTYPES FOR REACTION TO COTTON LEAF CURL VIRUS DISEASE AND YIELD PERFORMANCE UNDER DIFFERENT ECOLOGICAL ZONES

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ABSTRACT

Thirty five advanced cotton lines including nine hybrids in National Coordinated Varietal Trials (NCVT) and twenty six lines in Provincial Coordinated Cotton Trials (PCCT) were planted in order to test their performance related to Cotton Leaf Curl Virus (CLCuD-B) disease and seed cotton yield. These experiments were laid out in core area (Cotton Research Station, Vehari) and in non core-area (Cotton Research Station, Sahiwal) during May, 2008 as per proposed plan. Twenty six coded varieties in NCVT were found with higher CLCuV disease incidence within 85-100% range and a drastic seed cotton yield variation was noticed in seed cotton yield ranging from 654 Kg/ha to 1903.52 Kg/ha. The variety V_{22} (NIBGE-II) out yielded the rest entries with maximum seed cotton yield of 1903.52Kg/ha with 87% CLCUV disease infection. It was followed by V_{13} with 1439.53 Kg/ha seed cotton yield and 100% disease incidence. While nine cotton hybrids in NCHT had 85 to 100% CLCuV disease incidence with yield ranging from 273.63 Kg/ha to 499.69 Kg/ha seed cotton yield. Twenty six advanced lines in PCCT showed severe infection of CLCuV disease up to 79.94% range. The seed cotton yield of these varieties varied from 1435-3588 Kg/ha. Both the coded genotypes V_{11} and V_{26} promised the same highest cotton yield as 3588 Kg/ha with 84% and 89% disease incidence respectively.

Results indicated that core area (Vehari) is an ideal hot spot place/site for appraisal of cotton varieties performance under high pressure of CLCuV disease. Hence the cotton varieties with good yield potential even in presence of CLCuV disease can be better exploited in hybridization program for development of superior cotton varieties.

Key words: Cotton, Cotton Leaf Curl Virus, disease incidence, seed cotton yield.

INTRODUCTION

Cotton as fiber, oil and feed crop occupies prominent position in the Pakistan's economy. It contributes 10.5% of value added in agriculture and in gross domestic products (GDP) and generates vast opportunities of employment. It is termed as white gold that is exported in form of yarn, cloth, readymade garments for earning foreign exchange. In Pakistan, it is cultivated over extensive area of almost 3.08 million hectares with annual production of 12.86 million bales (Anonymous, 2008). The low cotton production is mainly due to cotton leaf curl virus disease which causes colossal loss to the cotton crop every year. The other factors for yield decline are severe pest's infestation and mealy bug damage in recent years and lack of such cultivars which could have wider adaptability against diseases especially CLCuV and sucking pests white fly. CLCuV disease complex is highly devastating and predominant on all cultivars in cotton belt. It is whitefly (*Bemesia tabaci* Genn) transmissible begomo virus complex/syndrome. Both the diseases and vector (whitefly) have the wide range of hosts. Whitefly is the only known vector of the CLCuV which is prevalent in all cotton growing regions where disease occurs (Singh *et. a*l, 1990). This disease is due to Gemini virus which has a single stranded circular DNA(SSDNA) of about 2.8 Kb with twinned germinate particles and belongs to the family germiniviridac genus begomo virus (Fauquet and Thouvend, 1987).

Zhou *et al.* (1998) reported that CLCuV disease in Pakistan is caused by several distinct variants like: CLCuV-Pak1, ClCuV-Pak2, ClCuV-Pak3, and ClCuV-Pak4. No difference exists in the disease symptoms production between Burewala strains and old strains of CLCuV disease. However Burewala strain can produce severe disease symptoms (with grafting and under field conditions) within shorter period of time all previously available germplasm resistant to old strains. This new strain proved disastrous for cotton production and resistance breaking malady. With a view to protect cotton crop from huge yield losses by this disease, the durable and long-term feasible strategy is to breed and develop high yielding/ resistant cotton cultivars. So under this objective an attempt was made to evaluate advance cotton lines in NCVT/NCHT & PCCT for best performance in terms of seed cotton yield and CLCuV tolerance.

MATERIALS AND METHODS

Thirty five advanced cotton lines including nine hybrids in NCVT, NCH**T** and twenty six lines in PCCT were planted in May 2008-09 at Cotton Research Stations Vehari and Sahiwal as per proposed plan. The experimental plot size was 4.5 x 5.3m with row spacing of 75 cm and 30 cm plant to plant distance. All agronomic inputs viz. water, fertilizers, hoeing and plant protection measures were managed in optimal fashion. The irrigations were applied at fortnight intervals with final irrigation in October.

The CLCuV disease was noticed with appearance of characterized symptoms of thickening veins. A small vein thickening is more common feature under our conditions (Mehmood, 1999). These thickening first appears near the leaf margins and then extend inward to form a network (Watkin, 1981, Akhtar *et al*, 2000). The severe attack in form of enations/scaly leaves was also noticed in the highly susceptible lines. Severely infected plants were observed with symptoms of reduced size of leaves and flowers with spirally twisted leaf petioles. Moreover, inter nodal length was found as short and plants affected in early stage become stunted with adverse effect on fruiting. The mild disease infection indicated small group of veins thickening and in medium attack, all veins were found thickening while in case of severe infections, symptoms of curling, enation and stunting were noticed. Data on CLCuV disease incidence was recorded at dense fruiting stage in September, 2009 as per visual observation of symptoms in the disease scale (Akhtar and Khan 2002). The leaves samples from upper, middle and lower portion of the plants in each genotype were taken. A total number of leaves and disease leaves were counted.

A plant with even single leaf infected was considered to be an infected plant. Data on seed cotton yield were recorded after harvesting all the plants and total cotton seed yield of each line per plant was weighed in kilograms and yield was converted in Kg/ha.

Table 1. Cotton Leaf Curl Virus Disease Incidence (%) and Cotton Seed Yield (Kg/ha) of Advanced Cotton lines and Hybrids in NCVT trials at Vehari.

Entries. No.	Genotype/lines	CLCuV disease incidence (%)	Cotton seed yield (Kg/ha)
V_1	FH-942	90	654.00
V_2	CR4SM-38	95	1463.33
V_3	CIM-55	89	1546.61
V_4	CRIS-129	92	773.30
V_5	GH-102	85	1189.70
V_6	NIA-78	87	701.92
V_7	NIAB-852	92	1035.03
V_8	TH-06/2	100	1106.42
V_9	CRSM-2007	100	1332.46
V_{10}	CIM-554(Block1)	90	832.79
V_{11}	NN-3	95	1689.37
V_{12}	CIM-496(Block1)	100	1201.50
V_{13}	VH-172	100	1439.53
V_{14}	BP-900	85	1261.08
V_{15}	GS-14	100	1070.73
V_{16}	NIAB-777	90	1070.73
V_{17}	SLH-317	100	1332.46
V_{18}	GS-1	100	761.40
V_{19}	VH-278	95	1011.24
V_{20}	FH-941	100	368.80
V_{21}	PB-900	85	880.37
V_{22}	NIBGE-II	87	1903.52
V_{23}	CIM-496(Block2)	98	237.94
V_{24}	CIM-554(Block2)	90	904.17
V_{25}	CIM-557	100	951.76
V_{26}	CIM-534	95	499.67

RESULTS AND DISCUSSION

Twenty six advanced cotton lines in NCVT were found with higher disease incidence ranging 85 to 100 %(Table1). Drastic yield variation was noticed in seed cotton yield varying from 654 Kg/ha to 1903.52 Kg/ha. The variety V_{22} (NIBGE-II) out yielded the rest entries with maximum yield of 1903.52 with 87% disease infection. It was followed by $V_{13\ w}$ith 1439.53 Kg/ha cotton yield inspite of 100% disease incidence. Both the varieties exhibited disease tolerance potential with higher yield levels. Whereas nine cotton hybrids had 85-100% disease incidence with the lowest levels of cotton yield within 273.63 Kg/ha to 499.69 Kg/ha. It was apparent that these hybrids showed low yield performance under high disease pressure. These results were found in conformity with the findings of Alam *et al* (2009) who pointed out that other factors including virus infection are also responsible for the seed cotton yield.

Table 2. Cotton Leaf Curl Virus Disease Incidence (%) and Cotton Seed Yield (Kg/ha) of Advanced Cotton lines and Hybrids in NCHT trials at Vehari.

Hybrid	CLCuV Disease incidence (%)	Cotton seed yield (Kg/ha)
H-1	87	475.88
H-2	85	475.88
H-3	100	356.91
H-4	90	475.88
H-5	100	499.67
H-6	94	449.67
H-7	88	356.91
H-8	90	428.29
H-9	100	273.63

Table 3. Cotton Leaf Curl Virus Disease Incidence (%) and Cotton Seed Yield (Kg/ha) of Advanced Cotton lines in PCCTtrials 2008-09 at Vehari.

Entries No.	Genotype/lines	CLCuV disease incidence (%)	Cotton seed yield (Kg/ha)
V_1	FH-942	89	2870
V_2	RH-620	82	3283
V_3	VH-255	85	2956
V_4	CRSM-2007	82	3014
V_5	MG-6	85	3071
V_6	CIM-557	90	3300
V_7	GS-1	88	1435
V_8	VH-277	85	2927
V_9	NIAB-852	87	3300
V_{10}	CRSM-38	83	2066
V_{11}	VH-207	84	3588
V_{12}	SLH-317	82	3014
V_{13}	CIM-496	90	2870
V_{14}	GS-14	85	3014
V_{15}	GS-554	81	2727
V_{16}	PB-900	92	2866
V_{17}	NIAB-777	94	2870
V_{18}	SITARA-008	87	2440
V_{19}	A-ONE	86	2358
V_{20}	FH-941	83	2727
V_{21}	BH-172	81	3100
V_{22}	FH-2015	79	3444
V_{23}	NIAB-2008	82	2583
V_{24}	FH-113	85	3157
V_{25}	NN-3	94	2726
V_{26}	Alseemi-Hybrid	89	3588

Twenty six cotton genotypes in PCCT were severely affected by the CLCuV disease (Table 2). The disease incidence ranged from 79-945 and yield was recorded within the range of 1435 – 3588 Kg/ha. These findings about varied disease incidence were supported by results recorded by Alam et al (2009) while higher seed yield differences within varieties were corroborated by the results of Hassan *et al* (2006) who opined that seed cotton yield variation is due to heterosis in agronomic characteristics of different cotton strains. Among these lines, the genotype/test entry V_{11} promised as higher yield as 3588 Kg/ha in spite of higher disease incidence as 84%. It was followed by V_{26} which gave equal yield as 3588 Kg/ha even with 89% disease. This situation points to the fact that only two varieties had a sufficient disease with standing potential ensuring high yield of cotton. These findings were found in close agreement with the observations by Iqbal *et al* (2009) who reported that high degree of relatedness found among cotton varieties in the field may be one of the reasons. In CLCuV disease necessitating induction of diverse germplasm as recurrent parent. Development of transgenic cotton harboring resistance to CLCuV and identification of new resistance sources against CLCuV or other possible options remain to be exploited to cope with episodic epidemics of this viral disease.

REFERENCES

Akhtar, K. P., M. Hussain, A.I. Khan and M.S.I. Khan (2000) Screening of cotton mutants for resistance against cotton leaf curl virus (CLCuV) *Pak. J. Biol. Sci*. 3(1): 91-94.

Akhtar, K.P. and M.S.I.Khan (2002). Modified scale for assessment of cotton leaf curl virus (CLCuV). *Pak.J.Phytopath*. 14: 88-90.

Anonymous (2008). *Agriculture statistic of Pakistan*, Ministry of Food and Agriculture, Food and Agriculture Division, Economics Wing, Islamabad, Pakistan.

Alam, S.S., M.Hassan, J. Hussain and M.Aslam(2009). Screening of candidate varieties in NCVT (2007-08) for cotton leaf curl virus by a modified disease rating scale. *Int. J. Biol. Biotech*: 6(1-2): 67-70.

Fauquet, J.C. and J.C. Thouvenel (1987) *Plant viral diseases in the Ivory Coast*. Editions de 1,Or STOM Institute Francis, Paris pp:243.

Hassan, M. M.A.Haq, M.Aslam, M.Maqsoopd and S.S.Alam (2006). Evaluation of new cotton (*Gossypium hirsutum* L.) lines for seed cotton yield and leaf curl virus infection. *Int. J. Env. Sci and Tech.*, 2: 319-325.

Iqbal M.Z., U. Ihsan, I. Azhar and Maria (2009) Bt. Cotton in Pakistan: Current Status Abstracts, *3rd National Conference on cotton production*, Nov. 13-14, 2009, NIAB, Faisalabad: pp. 4-5.

Mehmood, T. (1999). Cotton leaf curls virus disease and its present status in Punjab. *The Pak. Cotton Grower* 3:17-18.

Singh, J.A., A.Sohi, S.B.Dulcha, I.Ocngolm, D. Russell and R. Briddon (1990). Management of cotton leaf curl viral disease in India. *Proceedings. ICAC_CCRI. Regional consultation on insecticide resistance management in cotton*, Multan, Pakistan. June 28 to July 1.pp 277-284.

Watkin, G.M. (1981). *Compendium of cotton disease*. The American Phytopath. Soc: 3340. Pilot Knob Road, Minnesota USA, pp-87.

Zhou, X.,Y. Liu,D.J.Robinson and B.D. Harrison (1998). Four DNA-A variants among Pakistan isolates of cotton leaf curl virus and their affinities to DNA-A of Gemini virus isolates from okra. *J.Gen.Viral.*, 79: 915-23.

(*Accepted for publication November 2010*)