

INHERITANCE OF COTTON LEAF CURL VIRUS RESISTANCE IN COTTON (*GOSSYPIUM HIRSUTUM* L.)

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Abstract: To study the inheritance pattern of resistance against the Cotton Leaf Curl Virus (CLCuV) in cotton, the Cotton Leaf Curl Virus resistant LRA-5166 and CLCuV susceptible S-12 cotton cultivars were crossed. The generations F1, BC1, BC2 and F2 of the said cross were studied for the inheritance of CLCuV resistance along with their parents. The ratios of the segregating generations indicated that the resistance of CLCuV is controlled by single dominant gene.

Keywords: Cotton, inheritance, leaf curl virus resistance, segregation.

INTRODUCTION

During the work initiated at Central Cotton Research Institute for finding out DNA markers for resistance to Cotton Leaf Curl Virus (CLCuV), the study of the progenies derived from crosses of CLCuV resistant and susceptible cotton cultivars also provided data for inheritance pattern of this virus. Although Ali [1997, 1999] was of the opinion that the CLCuV resistance was controlled by single dominant gene and could be transferred to any cultivar by using back cross technique, yet there was some controversy on this point among the cotton breeders. Therefore, it was necessary to produce the data collected during the present studies for the information of other scientists.

In earlier studies, the British Team of Scientists has given a comprehensive review of their work done on CLCuV in Sudan [Tarr 1951]. According to Knight [1954], a single mass selection in a moderately resistant population was reported to have produced a highly resistant type. According to Tarr [1951], the virus resistance may not always be a stable quality, it was suggested by Hutchinson and Knight [1950] that breeding of resistant types has been accomplished by accumulation of minor genes by repeated selection. Later, Siddig [1968] found that the resistance may be due to a single dominant gene (or closely linked genes). He hoped that the further studies on the disease resistance might help to investigate the mode of inheritance of this disease (single dominant gene or minor genes). He was of the opinion that the inheritance of Leaf Curl Virus (LCuV) resistance was simpler than previously thought. The main objective of the present study is to investigate the pattern of inheritance of resistance in cotton against the Cotton Leaf Curl Virus.

MATERIALS AND METHODS

Two cotton cultivars, one most susceptible to CLCuV i.e. S-12 and one resistant to CLCuV i.e. LRA-5166 were crossed during the cotton season 1999-2000. F1 was selfed and back crosses were made in 2000-2001. In 2001-2002, parents, F1, back crosses and F2 were sown in the field. Line to line distance was 75 cm and plant to plant distance was 30 cm. All the seeds of F1, BC1, BC2 and F2 were sown in an open experimental field at Central Cotton Research Institute, Multan and observations of virus symptoms were taken throughout the plant growth period from June 2002 to December 2002. Inoculum (Virus) pressure to assure the infestation on susceptible plants was created as described by Ali [1997,1999]. A special hot spot in the field was contrived for this purpose. Test plants were planted in between the ratooned rows of S-12 cultivar the sprouts of which provided ready inoculum for immediate transmission to the young test seedlings through whitefly abundantly present in the field. These studies were carried out before the new Burewala virus made its appearance on cotton at Multan.

A plant was considered susceptible to CLCuV if it showed symptoms of disease on whole plant or its any part at any stage of development. A plant with no CLCuV symptoms at all was considered to be virus resistant. To confirm the virus resistance of the plant, all the test plants were kept ratooned. Up till now, no DNA markers or genes are identified for CLCuV in the world. ELISA, PCR, etc. techniques are helpful only, to confirm the presence or absence of virus in the plant tissues and useless for confirmation of virus resistance of the plant. Because it was observed that virus was present in both virus susceptible and virus resistant plants. So, at the present symptomatology is the only criterion to study the CLCuV disease.

RESULTS AND DISCUSSION

All plants of CLCuV susceptible cotton cultivar S-12 were attacked by leaf curl virus and all the plants of cultivar LRA-5166 were observed virus free. F1 was observed resistant to CLCuV. In back cross with virus resistant parent all the plants were observed virus resistant. In back crosses to susceptible parent, almost half the plants were observed virus resistant and half were virus susceptible. Out of the total population of F2 i.e. 524, virus resistant plants were 391 and 133 plants showed CLCuV symptoms. The data recorded susceptibility of plants to CLCuV in various generations are given in Table 1.

The ratio between virus resistant and virus susceptible plants in F2 population was 1:2.94 which is close to 1:3, the ratio of single dominant gene inheritance. The results of backcrosses were also confirmed that the virus resistance in the experiment was controlled by single dominant gene. These findings support to those described by Ali [1997, 1999]. This sound conclusion is based on the fact that CCRI, Multan, is in anticipation

of future developments, practically involved for efficiently evolving series of virus resistant varieties (CIM-443, CIM-448, CIM-1100 etc.) for the country. In earlier studies, Siddig [1969] had stated that the virus resistance was controlled by single gene or closely linked genes and this should be clarified by further studies. The differences among the various research workers are probably due to the effect that the expression of virus tends to vary with the environment. The conclusive results can be obtained only if the environment is controlled to create desired inoculum pressure. In the present study the inoculum pressure was created artificially due to which it is proved that the CLCuV resistance is controlled monogenically.

Table 1: Number of plants susceptible and resistant to CLCuV.

Genotypes	Total Plants	Susceptible	Resistant	Ratio		λ^2 Calculated
				Expected	Observed	
S-12	60	60	-	-	-	-
LRA-5166	60	-	60	-	-	-
F1	35	-	35	-	-	-
F2	524	133	391	1:3	1:2.94	0.12
BC1	54	26	28	1:1	1:1.07	0.13
BC2	49	-	49	-	-	-
λ^2 2df 0.05=5.99		0.01=9.21				

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