SHORT NOTE

Genetic analysis of resistance to bacterial in some crosses of cotton (*Gossypium hirsutum L.*)

Ahmed M. Mustafa

Cotton Breeding Program, Gezira Research Station, Agricultural
Research Corporation, P.O. Box 126, Wad Medani, Sudan

Bacterial blight of cotton affects all plant parts during all growth stages. The disease can be extremely damaging under Sudan conditions particularly, to long staple cotton (*gossypium barbadense*). All commercial cotton cultivars grown in Sudan are susceptible to the new race of the bacterium. Breeding for blight resistance has become a major objective in cotton breeding program. Therefore, if improvement of resistance is to be made, and understanding of its genetical basis is essential. Quantitative analysis to bacterial blight indicated additive, dominance, and epistatic gene action (Wallace and El-Zik, 1990). A substantial number of diallel studies indicated the importance of both additive and dominance effects on bacterial blight resistance (Innes and Brown, 1969; Wallace and El-Zik 1990). Estimates of gene effects involved in the inheritance of bacterial blight resistance from four cotton cultivars crosses are reported in this study.

Four cotton cultivars (Acala(93) H, S295, LEBO-1-78 and Tamcot HQ 95) were crossed in a half diallel mating system. These parents were selected on the basis of their moderate resistance to bacterial blight and their different genetic background. Acala(93) H is a newly released cotton cultivar in the Sudan, S295 is a cotton cultivar form Chad, LEBO-1-78 and Tomcot HQ 95 are cotton cultivars from the USA, Parents, F_1,F_2 and F_3 generations were grown at Gezira Reseazed Station field, Wad Medani, Sudan, in July 2000, using a randomized complete block design with three replications.

Field inoculation and scoring of disease severity described by Knight (1946) were used. Disease severity was recorded 21 day after inoculation using a scale of 0-10, where zero represents immunity and 10 represents full susceptibility.

Adequacy of the additive-dominance model was tested using Hayman and Mather scales (1955). Gene effects for resistance to bacterial blight were estimated following Hayman (1958) using the five-parameter model. The significance of gene effects was tested by calculating variances, standard errors, and 't' value separately for each effect.

Analysis of variance indicated significant differences for leaf disease grade among different experimental populations (data not shown). The results obtained by scaling tests and model-fitting procedures to the generation means are shown in Table 1 and 2. A satisfactory fit of expected and observed generation means was obtained with the three-parameter model for all crosses (Table 2) Both simple scaling test C and D were not significant indication the absence of non-allelic interaction, Therefore, the additive dominance model is adequate to explain genetic variability for blight resistance in these crosses.

Table 1. Scaling tests and their standard errors for bacterial blight resistance in five cotton crosses, Gezira Research Station, Wad Medani, Sudan, July 2000.

	Crosses					
Scaling test	1	2	3	4	5	6
C	-0.6±0.8	-0.2±0.8	0.1±1.1	-0.3±1.2	0.4±1.2	-0.3±0.8
D	-0.4±0.7	-1.4±0.7	-0.9±1.2	0.1±1.2	-1.6±0.8	-1.5±0.7
X^2 for joint scaling test Additive dominance	19.2*(2)	14.3*(2)	4.9(2)	4.8(2)	4.8(2)	5.93(2)

- $P< 0.05$

Figure between parentheses indicate degrees of freedom

The joint scaling test indicated the adequacy of the additive dominance model for crosses (3, 4, 5 and indicated inadequacy of the additive dominance model in crosses, (1, and 2) (Table 1). The critical x2 value for

P= 0.05 is 5.99 and the observed x2 values for crosses (1 and 2) were higher, indication the presence of epistasis (Table1). Significant additive genetic effects (d) were detected to all crosses (Table 2). While significant dominance (d) were detected for all crosses (Table 2)> While significant dominance(h0 genetic effects were detected for crosses (2 and6). This indicated the predominance of additive genetic effects in the inheritance of bacterial blight resistance. These results agreed with those of Wallace and El-Zik (1990) who showed that most of the genetic variance was accounted for by additive, dominance, and epistatic gen action.

Table 2. weighted least square estimated and their standard errors for bacterial blight resistance in five cotton crosses, Gezira Research Station, Wad Medani, Sudan, July 2000.

	Crosses					
Parameters	1	2	3	4	5	6
m	4.8±0.20	4.7±0.21	4.4±0.28	4.6±0.28	5.3±0.20	5.0±0.21
d	0.5*±0.09	0.30*±0.07	0.15*±0.07	0.15*±0.08	0.2*±0.09	0.35*±0.09
h	0.47±0.09	1.2*±0.57	0.47±0.92	-0.27±0.92	1.3±0.68	1.2*±0.60
l	0.27±1.70	-1.60±1.90	-1.3±2.70	0.53±2.70	-0.27±2.40	-1.6±01.90
i	1.2*±0.56	1.5*±0.60	0.85±0.88	0.45±0.88	1.5±0.77	1.7*±00.62

- P < 0.05

The additive x additive type of epistatic interaction (fixable component) was significant for crosses (1,2 and 6), while, dominance x dominance type of epistatic interaction was not significant for all crosses (Table 2). This implies the importance of additive x additive type of epistaic interaction in these crosses.

The predominance of additive x additive type of interaction along with prominent additive effects would imply some possibility for selection in the segregating generations. The additive and non-additive components can be utilized by inter-mating of desirable segregates followed by selecting superior genotypes. This study suggests the possibility of breeding for improvement in resistance to bacterial blight disease. Since additive genetic variance was predominant for all crosses for bacterial blight resistance it is expected to be easily fixed and hence a pedigree or bulk selection methods could be followed to improve blight resistance.

REFERENCES

Hayman, B.I. 1958. The separation of epistasis from additive and dominance variation in generation means. Heredity 12:371-91.

Hayman, B.I. and Mather, K. 1955. The description and separation in continuous variation Biometrics 11:69-82.

Innes, N.L. and Brown, S.J. 1969. A quantitative study of the inheritance of resistance to bacterial blight in Upland cotton. Journal of Agricultural Science, Cambridge 73:15-23.

Knight, R.L.1964. Breeding cotton resistant to blackarm disease (Bacterium. Malvacearum). Empire Journal of Experimental Agriculture 14:153-174.

Wallace, T.P. and El-Zik, K.M. 1990. Quantitative analysis of resistance cotton to three new isolates of the bacterial blight pathogen Theoretical Applied Genetics 79;443-448.