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Linkage Tests in American Pima Cotton[1]

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ABSTRACT

The results of 42 linkage tests involving six American Pima cotton (*Gossypium barbadense* L.) mutants and 15 mutants of *G. hirsutum* L. are reported. Forty of the tests gave no significant evidence of linkage and two tests indicated linkage. A dominant Pima male-sterile mutant (*Msp*) was found to be linked with one of a pair of duplicate factors for glandless (gl_3) with 9.38 ± 0.98% recombination and with naked seed (N_1) with 13.95 ± 1.89% recombination. *Msp* was not allelic with the dominant male-sterile genes Ms_4 and Ms_7. The gene symbol, Ms_{12}, is proposed for the character Pima male-sterility in place of the currently used symbol *Msp*.

***Additional index words:* *Gossypium barbadense* L., Linkage groups, Allelism.**

THE testing of mutant genes for linkage in American Pima cotton (*Gossypium barbadense* L.) is a continuing project. Plants with mutant genes are found in field plantings of Pima cotton. These Pima mutant genes are tested for linkage among themselves and with marker genes in *G. hirsutum* L. This paper reports the results of linkage tests involving six mutants in Pima cotton and 15 mutants in *G. hirsutum*. The results are from tests made since the last summary reported by Turcotte and Feaster in 1972.

MATERIALS AND METHODS

The genes tested for linkage are listed in Table 1. F_1, F_2, and, in some cases, testcross populations were used. As seed became available, segregating populations were grown and scored in progeny rows in a field nursery or in 15-cm pots in a greenhouse at Phoenix, Ariz. Prior experience with linkage studies in cotton (Kohel et al., 1977) showed no reciprocal cross effects, and reciprocal crosses were not made in the present study. Not all possible cross combinations were made. Linkage studies are a continuing project, and data from several combinations either have been reported previously or are yet to be reported.

Linkage was detected by Chi-square analysis. Confidence limits for recombination values were estimated by the maximum likelihood method (Allard, 1956).

Table 1. Marker gene, phenotype, and linkage group of 23 genes in cotton used for linkage tests reported in the present study.

Marker gene	Phenotype	Linkage group	Reference
yg_2†	Yellow-green plant color	I	Kohel, 1973
L^o	Okra leaf	II	Kohel, 1972
cr‡	Crinkled dwarf	II	Turcotte & Feaster, 1972
Dw	Dirty white lint	III	Kohel et al., 1965
R_1	Red plant color	III	Kohel, 1972
yg_1†	Yellow-green plant color	III	Kohel, 1973
H_2	Pilose	IV	Kohel, 1972
Lc_2	Brown lint-2	IV	Kohel et al., 1965
gl_2†	Glandless plant	V	Kohel, 1972
fg	Frego bract	VI	Kohel, 1972
gl_3†	Glandless plant	IX	Kohel, 1972
p_1	Cream pollen	XI	Turcotte & Feaster, 1972
N_1	Naked seed	XIII	Kohel et al., 1977
cu	Cup leaf	Independent	Kohel, 1972
Ms_4	Male-sterility	Independent	Kohel, 1972
Ms_7	Male-sterility	Independent	Kohel, 1973
Msp‡	Male-sterility	Independent	Turcotte & Feaster, 1972
p_2‡	Orange pollen	Independent	Turcotte & Feaster, 1972
rs‡	Rudimentary stigma	Independent	Turcotte & Feaster, 1972
Ru‡	Rugate leaf	Independent	Turcotte & Feaster, 1972
v_1	Virescent-1 plant color	Independent	Kohel, 1972
v_2	Virescent-2 plant color	Independent	Kohel, 1973
v_7‡	Virescent-7 plant color	Independent	Turcotte & Feaster, 1973

† Recessive duplicate genes. ‡ Pima mutant genes.

RESULTS AND DISCUSSION

Results of the linkage tests are given in Table 2. Forty-two combinations were tested for association. Forty tests gave nonsignificant Chi-square values for

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Table 2. Summary of linkage tests involving six Pima mutant genes and 16 mutant genes of *G. hirsutum*. In each combination the upper figure is the population size and the lower figure is recombination percent. F_2 populations are in regular type, and testcross populations are in italics. Combinations reported previously are shown by –. Untested combinations are blank.

Tester genes	Pima mutant genes tested					
	Msp	p_2	rs	Ru	v_7	cr
yg_1yg_2		154 64	120 78	225 56		
L^o	–	–	–	*89* 53	169 42	–
R_1	–	–	–	–	397 51	–
H_2	*227* 49	*155* 49	*111* 55	*276* 50	*411* 51	–
gl_2gl_3	*566* 08	–	–	–	–	
fg		216 48	159 45	99 67	246 54	
p_1	–	–	–	–	133 49	–
N_1	*337* 14	*304* 50	*75* 47	*88* 57	154 56	–
cu	*85* 61	204 47	192 45		233 44	
Ms_4			*219* 51	*91* 63	*264* 47	
v_1	*292* 52		112 45	484 52	–	–
v_2		154 49	150 47			
Msp		–	–	–	–	–
p_2			–	–	–	–
rs				239 53	–	–
Ru					–	–
v_7						409 50
Lc_2		*70* 49		*155* 55		–
Dw		*100* 49		*214* 43		

Table 3. Detailed analyses of linkage tests involving Msp and gl_3gl_3, Ms_4 and gl_2gl_3, Ms_7 and gl_2gl_3, and Msp and N_1.

Genotype	No. plants	Source	Chi-square
Msp-Gl_2-Gl_3-	286	Msp vs. msp	1.59
Msp-$gl_2gl_2gl_3gl_3$	12	Gl_2/Gl_3 vs. gl_2gl_3	0.29
mspmspGl$_2$-Gl$_3$-	144	Linkage	134.56
mspmspgl$_2$gl$_2$gl$_3$gl$_3$	124		
	566		
Recombination %		7.98 ± 1.08	
Msp-Gl$_2$-gl$_3$gl$_3$	18	Msp vs. msp	0.61
Msp-gl$_2$gl$_2$gl$_3$gl$_3$	94	Gl$_2$ vs. gl$_2$	0.27
mspmspGl$_2$-gl$_3$gl$_3$	104	Linkage	108.47
mspmspgl$_2$gl$_2$gl$_3$gl$_3$	20		
	236		
Recombination %		16.10 ± 2.39	
Msp-gl$_2$gl$_2$Gl$_3$-	58	Msp vs. msp	0.00
Msp-gl$_2$gl$_2$gl$_3$gl$_3$	58	Gl$_3$ vs. gl$_3$	0.04
mspmspgl$_2$gl$_2$Gl$_3$-	59	Linkage	0.04
mspmspgl$_2$gl$_2$gl$_3$gl$_3$	56		
	231		
Recombination %		49.35 ± 3.29	
Ms_4-Gl$_2$-Gl$_3$-	39	Ms_4 vs. ms_4	0.09
Ms_4-gl$_2$gl$_2$gl$_3$gl$_3$	11	Gl_2/Gl_3 vs. gl_2gl_3	0.16
ms_4ms_4Gl$_2$-Gl$_3$-	40	Linkage	0.08
ms_4ms_4gl$_2$gl$_2$gl$_3$gl$_3$	13		
	103		
Recombination %		47.45 ± 4.26	
Ms_7-Gl$_2$-Gl$_3$-	84	Ms_7 vs. ms_7	0.06
Ms_7-gl$_2$gl$_2$gl$_3$gl$_3$	57	Gl_3/Gl_3 vs. gl_2gl_3	19.04
ms_7ms_7Gl$_2$-Gl$_3$-	93	Linkage	2.76
ms_7ms_7gl$_2$gl$_2$gl$_3$gl$_3$	44		
	278		
Recombination %		56.63 ± 2.58	
Msp-N_1-	27	Msp vs. msp	0.24
Msp-n_1n_1	146	N_1 vs. n_1	0.07
mspmspN$_1$-	144	Linkage	175.22
mspmspn$_1$n$_1$	20		
	337		
Recombination %		13.95 ± 1.89	

linkage, indicating that the genes tested were on separate chromosomes or that linkage was not detected if the genes were on the same chromosome. Two tests with significant Chi-square values showed linkage between Pima male-sterile (*Msp*) and glandless (gl_2gl_3) and between Pima male-sterile and naked seed (N_1). Detailed analyses of these linkages are presented in Table 3.

The initial linkage tests between Pima male-sterile and glandless involved a glandless stock homozygous for the recessive genes gl_2 and gl_3. A recombination value of 7.98 ± 1.08% was obtained from these data, but the test did not show if the linkage was between *Msp* and gl_2 or *Msp* and gl_3. We then tested *Msp* and two monomeric stocks with the gland genotypes $Gl_2Gl_2gl_3gl_3$ and $gl_2gl_2Gl_3Gl_3$. Results from these tests showed the *Msp* was independent of the gl_3 locus and linked with the gl_2 locus, with a recombination percent of 16.10 ± 2.39. A combined recombination percent of 9.38 ± 0.98 was obtained with data from all tests showing linkage.

The association between *Msp* and gl_2 is a new linkage in cotton. The gl_2 locus has been located in the A genome and forms linkage group V (Kohel, 1972) with the genes ne_1, one of a pair of duplicate genes conditioning nectariless, and bw_1, one of a pair of duplicate genes conditioning withering bracts. The gene order of linkage group V has not been determined.

The allelism of Pima male-sterile (*Msp*) with the dominant male-sterile genes Ms_4 and Ms_7 cannot be determined directly, because sterility prevents them from being crossed. The results of linkage tests between Ms_4 and gl_2gl_3 and between Ms_7 and gl_2gl_3 (Table 3) showed no association. Because *Msp* has been associated with gl_2, it follows that *Msp* should not be allelic with either Ms_4 or Ms_7. *Msp* has not been assigned a gene symbol (Turcotte and Feaster, 1972) in accordance with current rules for genetic nomenclature in cotton (Kohel, 1973). We now propose the name Male sterile-11 with the gene symbol Ms_{11} for this dominant male-sterile trait in Pima cotton.

The second test with a significant Chi-square value for linkage involved *Msp* and N_1. As shown in Table 3, a recombination percent of 13.95 ± 1.89 was obtained. These data indicate that N_1 is also a member of linkage group V, along with Ms_{11}, gl_2, ne_1, and bw_1. Kohel et al. (1977) reported a linkage between N_1 and Leaf fleck (*Lf*), with 9.52% recombination. They designated this association to be linkage group XIII. Neither N_1 nor *Lf* has been tested with marker genes of linkage group V. It would appear from our data that *Lf* might be in linkage group V. This matter remains to be resolved.

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