Published March, 1983

Genetic Analyses of the Yellow-Veins Mutant in Cotton[1]

R. J. Kohel[2]

ABSTRACT

Eight virescent and morphological mutants were found in a cotton (*Gossypium hirsutum* L.) breeding nursery at College Station, Tex., in 1962. Four of those mutants were conditioned by the same recessive allele. The mutant was named yellow-veins and assigned the symbol *yv*. The phenotype of the mutant is described as is variability associated with expression of the trait. Analyses with 38 other mutant loci provided evidence for linkage of *yv* with Rugate (*Ru*) and virescent-1 (v_1) to establish linkage group XVII, *Ru*-37-*yv*-30-v_1.

Additional index words: **Mendelian segregation, Linkage, Environmental interaction, Spontaneous mutants.**

THE cotton (*Gossypium hirsutum* L.) genetics program at College Station, Tex., includes the acquisition of new genetic mutants. These mutants are obtained from cooperators and from within our program as induced or spontaneous mutants. Through experience, I have found that the diverse materials in developmental breeding programs provide a good source of spontaneous mutants. Observation of breeding plots in the spring frequently yields pigment and morphological mutants expressed in young seedlings which are apparently enhanced by the cool spring weather (Percival and Kohel, 1976). An advantage of spontaneous mutants, as opposed to those induced, is that they are generally free of chromosome aberrations and other confounding factors; and consequently, they are easier to isolate and manipulate.

[1] Contribution from USDA-ARS, College Station, Tex., in cooperation with the Texas Agric. Exp. Stn. Received 2 Nov. 1981.

[2] Research geneticist, USDA-ARS, College Station, TX 77841.

In 1962, eight potential virescent and morphological mutant plants were found in a cotton breeding nursery at College Station. Four of the morphological mutants proved to be allelic, and tests of their inheritance and linkage are the basis of this report.

MATERIALS AND METHODS

The original group of eight mutants were found in 1962 in the Texas Agriculture Experiment Station cotton breeding nursery of Dr. G. A. Niles at College Station. Two of the mutants were virescents; and the remaining six were morphological mutants, four of which were controlled by a single allele. The four came from three different backgrounds.

The mutants were grown and self-pollinated each year for observation and establishment of true breeding lines. In 1970, the first inheritance populations between the mutants and TM-1 (Kohel et al., 1970) were grown; later tests involved various mutant testers.

Allelic relations were established by intercrossing among the four mutants. Linkage relations were tested by crossing to the multiple marker testers, T586 and T582, and to individual mutant marker lines (Kohel, 1972; 1973; 1978a). Recombination values were calculated by the maximum likelihood method for backcrosses (Mather, 1938) and by the product method for F_2 populations (Stevens, 1939).

RESULTS AND DISCUSSION

Description of Mutants

The four original mutant plants were obtained from three different breeding families. The mutant phenotype was not

Table 1. Segregation of the yellow-veins mutant of cotton in backcross populations.

Year	Classification		Chi-square (1:1)	P
	Normal	Mutant		
	no. of plants			
1970	20	21	0.02	0.90-0.80
	17	14	0.29	0.70-0.50
	15	10	1.00	0.50-0.30
	29	24	0.47	0.50-0.30
	21	26	0.53	0.50-0.30
1971	73	63	0.74	0.50-0.30
1974	73	22	27.38	<0.01
	34	32	0.06	0.90-0.80
	41	33	0.86	0.50-0.30
1975	26	40	2.97	0.10-0.05
1976	38	20	5.59	0.02-0.01
	34	39	0.34	0.70-0.50
1977	36	58	5.15	0.05-0.02
Total	457	402	45.40	<0.01
Pooled			3.52	0.10-0.05
Heterogeneity			41.88	<0.01

Table 2. Segregation of the yellow-veins mutant of cotton in F_2 populations.

Year	Classification		Chi-square (3:1)	P
	Normal	Mutant		
	no. of plants			
1970	45	9	2.00	0.20-0.10
	45	9	2.00	0.20-0.10
	35	12	0.01	0.95-0.90
	40	10	0.67	0.50-0.30
1974	87	13	7.68	<0.01
	67	33	3.41	0.10-0.05
	74	25	0.00	0.98-0.95
	82	17	3.24	0.10-0.05
1976	62	21	0.00	0.95-0.90
	61	22	0.10	0.80-0.70
	78	18	2.00	0.20-0.10
	61	27	1.52	0.30-0.20
	60	30	3.33	0.10-0.05
1977	77	12	6.30	0.05-0.01
	73	22	0.17	0.70-0.50
	76	20	0.89	0.50-0.30
	40	17	0.71	0.50-0.30
	70	27	0.42	0.70-0.50
	70	20	0.37	0.70-0.50
	40	12	0.10	0.80-0.70
	47	38	17.60	<0.01
	85	13	7.20	<0.01
	52	22	0.88	0.50-0.30
	85	15	5.33	0.05-0.02
	61	27	1.52	0.30-0.20
	67	25	0.23	0.70-0.50
	82	13	6.49	0.02-0.01
	81	13	6.26	0.02-0.01
Total	1803	542	80.43	<0.01
Pooled			4.45	0.05-0.02
Heterogeneity			75.98	<0.01

identical among the original plants, but subsequent standardization of genetic background resulted in uniform expression. The mutant plants were small, and leaf shape was distorted. The leaves were also small and became leathery with age. The foregoing general description did not distinguish this mutant from several other morphological mutants. However, its most consistent and distinctive characteristics were a slight downward roll to the leaf edges, prominent veins, and a yellowish color of the leaves which was associated more noticeably with the prominent veins.

Table 3. 1970 tests of researcher's ability to classify the heterozygous yellow-veins mutant of cotton.

Population	Classification			Chi-square	P
	Normal	Intermediate	Mutant		
	no. of plants				
Backcross to normal				(1:1)	
	12	10	-	0.18	0.70-0.50
	19	11	-	2.13	0.20-0.10
Total	31	21	-	2.31	0.20-0.10
Pooled				1.92	0.20-0.10
Heterogeneity				0.39	0.70-0.50
F_2				(1:2:1)	
	34	11	9	42.11	<0.01
	17	18	12	3.64	0.20-0.10
Total	51	29	21	45.75	<0.01
Pooled				36.13	<0.01
Heterogeneity				9.62	<0.01

Table 4. Loci tested, recombination percentages, and population sizes for linkage tests between the yellow-veins mutant and 38 other mutant loci of cotton.

Locu tested	Recombination percentage	Number of plants
Backcross to normal		
Crp	47	66
H_2	48	305
Lc_1	54	293
Lg	54	293
L^o2	51	296
Ms_4	48	93
Ms_7	51	161
N_1	46	293
P_1	46	287
R_1	54	296
R_2	49	295
Rd	41	58
Rl_2	58	74
Ru	37*	73
Y_1	49	293
F_2		
ac	57	85
cl_1	70	50
cu	47	145
fg	51	145
gl_1	64	145
ms_1	58	88
ms_2	58	188
n_2	56	95
pg	51	86
Sm_1S	51	93
st_2	79	74
st_3	48	186
v_1	30*	314
v_2	50	57
v_3	51	99
v_4	52	183
v_8	49	182
crd	67	91
dwf	74	98
Lc_4	50	89
mtBrn	43	100
py	50	52
rx	55	90

* Chi-square value for linkage larger than P = 0.05 value.

For the latter reason I named the mutant yellow-veins.

The original description of the mutants and classification of segregating populations were difficult because of its variable expression. Data presented in this paper illustrate part

Table 5. Linkage analyses of yellow-veins, virescent-1, and Rugate mutants of cotton.

Phenotype	Number of plants	Chi-square analysis and recombination: Source	Chi-square	P
($V_1V_1yvyv \times v_1v_1YvYv$) F_2				
Green-normal	172	Green vs. virescent	0.34	0.70–0.50
Green-yellow veins	68	Normal vs. yellow veins	0.34	0.70–0.50
Virescent-normal	68	Linkage	11.72	<0.01
Virescent-yellow veins	6	Recombination	29.78%	
ruruyvyv (*ruruyvyv* × *RuRuYvYv*)				
Normal-rugate	19	Normal vs. yellow veins	0.34	0.70–0.50
Normal-nonrugate	15	Rugate vs. nonrugate	1.66	0.20–0.10
Yellow veins-rugate	12	Linkage	4.94	0.05–0.02
Yellow veins-nonrugate	27	Recombination	36.98%	
ruruv$_1$*v*$_1$ (*ruruv*$_1$*v*$_1$ × *RuRuV*$_1$*V*$_1$)				
Rugate-green	20	Rugate vs. nonrugate	0.06	0.90–0.80
Rugate-virescent	14	Green vs. virescent	1.43	0.30–0.20
Nonrugate-green	20	Linkage	0.06	0.90–0.80
Nonrugate-virescent	16	Recombination	48.57%	

of the problem. Expression of the mutant varied from no discernible phenotypic difference to a pronounced expression of the homozygote with an intermediate response of the heterozygote. Mutant expression within the season and through the various stages of plant development was transitory. In seasons when temperatures were mild and moisture was abundant so that seedling growth was not stressed, mutant expression began at about the third to fifth true leaf and continued until flowering. Under such conditions, the heterozygote exhibited intermediate expression for the trait. In years when seedling growth was associated with environmental stress, the mutant phenotype was not expressed clearly enough for me to classify accurately the mutants in segregating populations. In certain years I could use fall regrowth to classify them.

Tests of Allelism

The six original morphological mutants were grown for a period of 8 years, primarily because of variable expression. Two mutants from the same family were considered identical, and two phenotypic groups began to emerge. The separation into two groups was confirmed by allelic tests. The group I named yellow-veins is described below. The mutants were tested for and found to be alleles and also were independent of strap leaf (*s*) alleles (Dilday et al., 1975).

Inheritance

Backcross and F_2 data for the segregation of yellow-veins are presented in Tables 1 and 2, respectively. In both cases, the pooled results fit the expected segregation for a single recessive gene; however, fit was of relatively low probability. The comparatively poor fit of the pooled data and the large heterogeneity chi-square was associated with a deficiency in the mutant class.

The problem of proper classification was discussed earlier when the mutant was described. Table 3 presents 1970 data classifying the heterozygote. In backcrosses to normal, the intermediate category could be identified; however, in the more complex F_2 populations, I could not accurately identify the expected classes. Therefore, subsequent segregating populations were classified into two categories, i.e., recessive mutant vs. dominant normal.

Linkage Analyses

Yellow-veins was tested for linkage with 38 other mutant loci (Table 4), and it was linked significantly to Rugate (*Ru*) and virescent-1 (v_1); detailed analyses are shown in Table 5. The linkages were 37 and 30 recombination units, respectively. The yellow coloration of the mutant and the difficulty of identifying its expression, particularly on a background such as Rugate, make these exact linkages somewhat tenuous. The mutant loci in question were not associated with specific chromosomes (Kohel, 1978b and unpublished). The data therefore suggest a new linkage group, XVII, consisting of the following loci and order: *Ru*-37-*yv*-30-v_1.

CONCLUSIONS

A new mutant and a new linkage group are described. The mutant called yellow-veins and assigned the gene symbol *yv* is conditioned by homozygous recessive alleles at a single locus. The degree of expression of the homozygous and heterozygous mutant is influenced by seasonal environmental variation.

Linkage analyses indicated yellow-veins as a member of a new linkage group, XVII, composed of *Ru*-37-*yv*-30-v_1. Chromosome or genomic location of this linkage group is not yet known.

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