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New Virescent Cotton Mutant Linked with the Marker Gene Yellow Petals[1]

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ABSTRACT

A new virescent mutant in cotton (*Gossypium hirsutum* L.), which occurred spontaneously, was found in the Cotton Breeding Nursery at the Texas Agric. Exp. Stn., College Station, Texas. Inheritance tests indicate that the phenotypic expression of this mutant is controlled by a recessive gene at a single locus that, when homozygous, results in virescent foliage. The degree of yellowness expressed by this mutant during its period of maximum expression is comparable to the expression of virescent-1 (v_1) or yellow green ($yg_1\,yg_2$) at College Station. Linkage tests indicate that this new virescent mutant is linked about five crossover units from Yellow petals (Y_1), comprising a new linkage group in cotton, and it is independent from 16 other marker mutants tested. It is proposed that this new virescent mutant be named virescent-10 and assigned gene symbol v_{10}, and the new linkage group be designated Linkage Group XII.

***Additional index words:* *Gossypium hirsutum* L.**

A cotton (*Gossypium hirsutum* L.) seedling with yellow foliage was observed in the Cotton Breeding Nursery at the Texas Agric. Exp. Stn., College Station, Texas, in 1969. This aberrant plant appeared spontaneously in an otherwise normal row. The mutant seedling was transplanted to a greenhouse, and as the plant developed, its leaves became normal green in color. This behavior typifies virescent yellow mutant plants, and the aberrant plant was provisionally designated V5-69. Self-pollinated seeds were obtained from this virescent yellow plant, and progeny tests proved that the virescent characteristic was heritable.

MATERIALS AND METHODS

Plants of V5-69 and their subsequent progeny were crossed with appropriate test lines to furnish seeds needed for F_1, F_2, and backcross populations to test for allelism, inheritance, and linkage. Texas Marker-1 (TM-1) (Kohel et al., 1970) was used in this study as the normal green stock. The inbred line (TM-1) was developed from the cultivar 'Deltapine 14' to serve as a standard tester. Allelism tests were conducted to determine the relationship between the V5-69 mutant and the eight previously identified virescent mutants of *G. hirsutum* L. The test consisted of classifying the F_1 progeny of the crosses, V5-69 × identified virescent mutants, V5-69 × V5-69 (virescent check), and V5-69 × TM-1 (green check) for virescent and green leaf color expression. Virescent-7 (v_7) from *G. barbadense* L., the homoeolog of virescent-1 (v_1) in *G. hirsutum* L. (Turcotte and Feaster, 1973), was not included in the test.

Inheritance tests consisted of classifying progeny of the [(V5-69 × TM-1) × V5-69] backcross and (V5-69 × TM-1)F_2 populations for the virescent and green leaf color character expression. In addition, backcross and F_2 segregating populations of the linkage tests were included in the inheritance tests.

The V5-69 mutant was tested for linkage with 17 known monogenic markers; 12 of these markers are included in the multiple marker lines Texas 586 (T586) and a selection of Texas 582 (T582), which were synthesized for this purpose (Kohel, 1972). T586 contains dominant genes at eight loci representing five linkage groups: Linkage Group I—Brown lint (Lc_1) and Petal spot (R_2); Linkage Group II—Okra leaf (L^o); Linkage Group III—Red plant (R_1); Linkage Group IV—Pilose (H_2); Linkage Group XI—Pollen color (P_1); and Independent—Yellow petals (Y_1) and Naked seed (N_1). The T582 selection contains four recessive genes and represents two linkage groups: Linkage Group III—cluster-1 (cl_1); Linkage Group VI—frego bract (fg); and Independent—glandless boll (gl_1) and cup leaf (cu). Linkage Group V—glandless plant-2 (gl_2) and Linkage Group IX—glandless plant-3 (gl_3) (McMichael, 1960) were tested together, because they are a recessive duplicate pair for gossypol gland density on cotyledons (segregation ratio 13:3). The remaining two dominant and one recessive marker loci were tested individually: Linkage Group VII—Laciniate Leaf (L^L) (Hutchinson, 1934); Linkage Group VIII—mosaic leaf (ml) (Lewis, 1958); and Linkage Group X—Ragged leaf (Rg) (Kohel and Lewis, 1962). Backcross populations were primarily used to test dominant loci and F_2 populations were used to test recessive loci. These data were analyzed for linkage by the methods outlined by Mather (1951).

Plant populations were grown from seeds germinated individually in peat pellets in a greenhouse. The seedlings were transplanted within 3 weeks, either to the field or to individual pots that remained in the greenhouse. Field rows were 1 m wide, and plants were spaced 46 cm apart within the row. Seedlings were classified for virescent and mutant marker expression in the greenhouse and in the field throughout the growing season.

The mutant V5-69 has seedlings with cotyledons that vary from pale green to normal green. The first true leaf, and subsequent leaves through the 6 to 8-week stage of development, has a yellow phenotype. After that stage of development the leaves begin to turn green. The greening process is accelerated, with the new leaves progressively less yellow. Newly expanded leaves are green, and the presence of any yellowness is difficult to detect after 10 weeks. The degree of yellowness during the period of maximum expression is comparable to the expression of virescent-1 (v_1) and yellow green (yg_1yg_2) at College Station. The size and conformation of the V5-69 mutant plants are not appreciably different from those of normal green plants.

RESULTS AND CONCLUSIONS

The results of the allelism tests show that V5-69 is not an allele of any of the six monogenic or two digenic virescent mutants of *G. hirsutum* (Table 1)

Table 1. Allelism tests of the V5-69 mutant with eight identified virescent mutants, classification of F_1's with V5-69 and parental lines in cotton.

Virescent mutant and TM-1	Classification: F_1 with V5-69		Classification: Parental line		Reference
	Green	Yellow	Green	Yellow	
	no. plants				
v_1	8	--	--	4	Killough and Horlacher, 1933
v_2	10	--	--	5	Duncan and Pate, 1967
v_3	10	--	--	5	Percival and Kohel, 1974
v_4	10	--	--	5	Quisenberry and Kohel, 1970
v_5v_6†	9	--	--	5	Kohel, 1973
v_8	10	--	--	5	Kohel, 1974
v_9	10	--	--	5	Percival, 1974
yg_1yg_2†	10	--	--	4	Rhyne, 1955
V5-69	--	10	--	10	
TM-1	10	--	10	--	

† Digenic virescent.

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Table 2. Classification of backcross and F_2 population segregation of the virescent mutant V5-69 of cotton and chi-square analysis.

Population	Classification		Chi-square analysis	
	Green	Yellow	χ^2 (ratio tested)	P
	no. plants			
Backcross generation			1:1	
[(V5-69 × TM-1) × (V5-69)]BC_1	50	55	0.24	0.50-0.70
[(V5-69 × T586) × (V5-69)]BC_1	70	67	0.07	0.70-0.80
[(V5-69 × LG III) × (V5-69)]BC_1	44	48	0.17	0.50-0.70
[(V5-69 × LG VII) × (V5-69)]BC_1	44	53	0.84	0.30-0.50
[(V5-69 × LG X) × (V5-69)]BC_1	34	39	0.34	0.50-0.70
Total	242	262	0.79	0.30-0.50
Heterogeneity			0.86	0.90-0.95
F_2 generation			3:1	
(V5-69 × TM-1)F_2	75	23	0.23	0.70-0.80
(V5-69 × T582)F_2	50	21	0.79	0.30-0.50
(V5-69 × T582)F_2	31	6	1.52	0.20-0.30
(V5-69 × LG V)F_2	62	24	0.39	0.50-0.70
(V5-69 × LG VI)F_2	57	19	0.00	1.00
(V5-69 × LG VIII)F_2	73	20	0.61	0.30-0.50
Total	348	113	0.06	0.80-0.90
Heterogeneity			3.36	0.30-0.50

Table 3. Chi-square linkage deviations and recombination percentages of V5-69 with mutant loci in cotton.

Marker locus	No. plants	Linkage χ^2	P	Ratio tested	Recombination
	[(V5-69 × T586) × V5-69)]BC_1			1:1/1:1	%
Y_1	90	60.84	<0.01		8.89
Y_1	132	120.17	<0.01		2.27
R_1	137	0.18	0.50-0.70		51.82
H_2	136	1.06	0.30-0.50		45.59
L^0	137	0.18	0.50-0.70		48.18
R_2	132	3.67	0.05-0.10		58.33
P_1	132	3.03	0.05-0.10		42.42
Lc_1	134	0.12	0.70-0.80		48.51
N_1	134	0.75	0.30-0.50		46.27
	(V5-69 × T586)F_2			3:1/3:1	
Y_1	79	45.06	<0.01		6.84
R_1	79	0.32	0.50-0.70		54.38
H_2	79	0.00	0.90-0.95		50.14
L^0	79	3.38	0.05-0.10		67.90
R_2	79	1.53	0.20-0.30		61.13
P_1	79	1.54	0.20-0.30		52.29
Lc_1	79	1.54	0.20-0.30		56.47
N_1	79	1.18	0.20-0.30		60.12
	(V5-69 × T582)F_2			3:1/3:1	
cl_1	102	1.34	0.20-0.30		40.78
fg	103	1.17	0.20-0.30		43.04
gl_1	108	3.70	0.05-0.10		35.39
cu	108	2.42	0.10-0.20		37.46
	[(V5-69 × LG III) × (V5-69)]BC_1			1:1/1:1	
R_1	92	0.54	0.30-0.50		46.15
	(V5-69 × LG V)F_2			3:1/13:3	
gl_2	86	1.00	0.10-0.20		57.90
	[(V5-69 × LG VII) × (V5-69)]BC_1			1:1/1:1	
L^L	97	0.26	0.50-0.70		52.58
	(V5-69 × LG VIII)F_2			3:1/3:1	
ml	93	0.14	0.70-0.80		46.21
	(V5-69 × LG IX)F_2			3:1/13:3	
gl_3	86	2.21	0.10-0.20		58.83
	[(V5-69 × LG X) × (V5-69)]BC_1			1:1/1:1	
Rg	71	0.69	0.30-0.50		45.07

because all of the F_1 progeny were green. Self-pollinated seeds of the eight virescents used as parents and V5-69 all produced seedlings that expressed a virescent yellow leaf color. These results established V5-69 as a new virescent mutant.

The inheritance tests indicated that the phenotypic expression of V5-69 is controlled by a recessive gene

Table 4. Segregation and estimation of the recombination value of the coupling linkage of V5-69 [v with Yellow petals (Y_1)] and heterogeneity chi-square.

Data set	Type of population and expected segregation	$V\ Y_1$	$V\ y_1$	$v\ Y_1$	$v\ y_1$	Recombination
						%
1	BC_1 (1:1:1:1) (1973)	65	3	0	64	2.27 ± 1.4
2	BC_1 (1:1:1:1) (1974)	35	7	1	47	8.89 ± 3.0
3	F_2 (9:3:3:1) (1973)	59	2	3	15	6.84 ± 2.8
Combined populations†						5.00 ± 1.27

† Heterogeneity (2 df) χ^2 = 5.50, P = 0.05-0.10.

at a single locus that, when homozygous, results in virescent foliage. This conclusion was made from homogeneous data of five backcross (to the mutant parent) and six F_2 segregating populations totaling 965 plants (Table 2). Backcross (to the mutant parent) and F_2 segregating populations did not deviate significantly from a green:yellow 1:1 and 3:1 ratios, respectively.

The results of linkage tests with known mutants indicated that the V5-69 mutant is linked with the marker, Yellow petals (Y_1), a previously independent and unassociated mutant. It was not associated with any of the 16 other markers tested. Recombination between Yellow petals (Y_1) and V5-69 in the two backcross populations [(V5-69 × T586) × V5-69] was 8.89 and 2.27%, and the recombination estimated in the (V5-69 × T586) F_2 population was 6.84% (Table 3). A combined estimate of the recombination value using Fisher's scoring method, as outlined by Allard (1956), yielded a value of 5.00 ± 1.27% (Table 4). The linkage of V5-69 with Yellow petals (Y_1) establishes a new linkage group in cotton.

It is proposed that this new virescent mutant be named virescent-10 and assigned gene symbol v_{10}. Since there are 11 previously reported linkage groups, each independent of v_{10}, the new linkage between Yellow petals (Y_1) and virescent-10 (v_{10}) is designated Linkage Group XII.

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