

Genetic Analysis of Virescent Mutants in Cotton¹A. E. Percival and R. J. Kohel²

ABSTRACT

Seven potential yellow-foliage mutants were found in Upland cotton (*Gossypium hirsutum* L.), and progeny tests proved three to be genetically controlled. These three mutants were classed as virescents, two of which were found to be alleles of known virescent mutants, virescent-2 (v_2) and virescent-4 (v_4). However, results indicate that the remaining mutant is not an allele of any of the known virescent-yellow mutants. It is a complete recessive and is controlled by a single locus that causes virescent-yellow foliage when the recessive alleles are homozygous. Linkage tests indicate that it is an independent mutant, not linked to any of the known mutants tested. It is proposed that this new virescent mutant be named virescent-3 and assigned the gene symbol v_3 ; the homozygous mutant genotype will thus be v_3v_3 .

Additional index words: Inheritance, Linkage, *Gossypium hirsutum* L.

THE diverse and varied material in the Upland cotton (*Gossypium hirsutum* L.) breeding nursery of the Texas Agricultural Experiment Station is searched each spring for potential mutants. The nursery is screened in the seedling stage before thinning.

Seven potential yellow-foliage mutants were found during the spring of 1968. Progeny tests proved three of these seven to be genetically controlled mutants, and the remaining four were environmentally induced phenocopies. The three mutants were classed as virescents because they showed yellow or yellowish as seedlings and young plants, but became completely green at maturity. These three mutants were assigned temporary symbols bv-2, bv-3, and bv-7. Of the three, bv-2 and bv-7 were found to be alleles of the known yellow mutants, virescent-2 (v_2) (4), formerly called golden crown (1), and virescent-4 (v_4) (7), respectively. This paper reports the results of allelism tests of bv-2, bv-3, and bv-7, and inheritance and linkage tests of bv-3.

DESCRIPTION OF THE MUTANT

The cotyledons of bv-3 seedlings are normal green color, and the yellow phenotype is first expressed when the 4th or 5th leaf has formed. The yellowness of this particular virescent is concentrated at the terminal portion of the plant and decreases downwards and outwards. Although 1 to 3 terminal leaves show a very yellow color, 1 or 2 of the adjacent leaves show an irregular blending of yellow-green throughout the leaf and the rest of the plant has normal green leaves. This leaf characteristic of bv-3 is different from those of most other virescent cotton mutants which, when showing their particular mutant expression, are uniform in color. The area of the plant that expresses in bv-3 resembles virescent-2 (v_2) (4), although the color intensities are different in these two mutants.

Accompanying this unique yellow expression of bv-3 is a slight-to-moderate overall reduction in plant size. This reduction is especially noticeable in populations that involve bv-3 crossed with the multiple-genetic-marker lines used in the study.

¹ Received Dec. 3, 1973.

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MATERIALS AND METHODS

The virescent mutant (bv-3) was self-pollinated in the field, and appropriate crosses were made to furnish seed for the F_1 , F_2 , and backcross populations.

The inbred tester line, Texas Marker-1 (TM-1) (6), was used as a normal green stock, along with F_2 and backcross populations of the linkage study, to test for inheritance. Seeds were germinated individually in peat pellets in the greenhouse and transplanted to the field about 3 weeks later. Field rows were 1 m wide, and plants were spaced 46 cm within the row. Seedlings were scored in the greenhouse for character expression, where possible, and scoring was continued in the field throughout the growing season.

Eighteen known monogenic markers were used in the linkage tests. The markers tested and their respective linkage groups were as follows: Linkage Group I: Petal spot (R_1) and Brown lint (L_1); Linkage Group II: Okra leaf (L^o), Green lint (L_g), and crinkled leaf (cr); Linkage Group III: Dirty white lint (Dw), Red plant (R_1) and cluster-1 (cl_1); Linkage Group IV: Pilose (H_1); Linkage Group VI: accessory involucre (ia), frego bract (fg); and Linkage Group X: round leaf (rl). Independent genes tested were Naked seed (N_1), Pollen color (P_1), Yellow petals (Y_1), glandless boll-1 (gl_1), cup leaf (cu), and virescent-1 (v_1). The linkage tests were facilitated by using two multiple marker lines synthesized at the Texas Experiment Station for this purpose. Multiple recessive marker T582 (5) carries cl_1 , fg , gl_1 , cu , and v_1 . Multiple dominant marker T586 (5) carries dominant markers listed above, except Dw and L_g . Those loci not included in the multiple markers T582 and T586 were tested with the following linkage group tester lines: LG II (L_g) and (cr); LG III (Dw); LG VI (ia); and LG X (rl).

An inheritance study was made of reciprocal crosses of bv-3 with TM-1 and crosses between bv-3 and the multiple marker lines. The appropriate F_1 's were backcrossed to bv-3 and self-pollinated.

The linkage test used backcross populations to test dominant loci, and F_2 populations with recessive loci. An exception to this was bv-3 \times LG II, which was backcrossed to bv-3, and the BC_1 plants were self-pollinated to score cr in the selfed progeny.

RESULTS AND CONCLUSIONS

The six virescent mutants (Table 1), which were each crossed with bv-2, bv-3, and bv-7, furnished F_1 's for a test of allelism (Table 2). F_1 's of bv-3 with the six virescents were all green. Thus of seven different plants originally selected, only bv-3 emerged as a possible new mutant.

Results (Table 3) indicated that the phenotypic expression of virescent bv-3 is controlled by a recessive gene at a single locus. Possible linkage was shown between bv-3 and Petal spot (R_2) from the backcross population of bv-3 \times T586. However, the F_2 data from this same F_1 progeny dispelled this possibility. These data indicated that bv-3 is independent of all 18 markers tested.

Table 1. List of known virescent mutants of cotton.

Mutant	Gene symbols	Reference
virescent-1	v_1	2
virescent-2 (golden crown)	v_2	4
virescent-4	v_4	7
Virescent splash leaf	vs_1^*	4
yellow 6	v_5v_6	3
yellow-green	yg_1yg_2	8

* Temporary designation.

Table 2. Allelism tests of three potentially new virescent mutants in cotton.

Mutants and F ₁ hybrids	Number of plants	
	Green	Yellow
bv-2	-	6
bv-3	-	10
bv-7	-	3
v ₂ (virescent-2)	-	9
v ₄ (virescent-4)	-	9
v ₅ v ₆ (Yellow 6)	-	7
y _{g1} y _{g2} (yellow green)	-	10
vs1 (Virescent splash leaf)	-	4
bv-2 × v ₁	9	-
bv-2 × v ₂	-	10*
bv-2 × v ₄	10	-
bv-2 × v ₅ v ₆	10	-
bv-2 × vs1	10	-
bv-2 × y _{g1} y _{g2}	10	-
bv-3 × v ₁	10	-
bv-3 × v ₂	10	-
bv-3 × v ₄	10	-
bv-3 × v ₅ v ₆	7	-
bv-3 × vs1	8	-
bv-3 × y _{g1} y _{g2}	9	-
bv-7 × v ₁	6	-
bv-7 × v ₂	7	-
bv-7 × v ₄	-	10*
bv-7 × v ₅ v ₆	9	-
bv-7 × vs1	9	-
bv-7 × y _{g1} y _{g2}	10	-

* Allelism indicated.

Table 3. Parental populations and segregation of the virescent mutant bv-3 in F₂ and backcross populations of cotton.

Populations	Segregation by class, #			χ^2 (ratio tested)
	Green	Yellow	Total	
TM-1	9	-	9	-
bv-3	-	10	10	-
(bv-3 × TM-1)	10	-	10	-
F ₂ populations:				(3:1)
(bv-3 × TM-1)F ₂	36	18	54	2.0000
(bv-3 × T582)F ₂	77	21	98	0.6667
(bv-3 × T582)F ₂	59	18	77	0.1083
(bv-3 × T586)F ₂	26	13	39	1.4444
(bv-3 × T586)F ₂	59	30	89	3.5992
(bv-3 × LG III)F ₂	111	29	140	1.3715
(TM-1 × bv-3)F ₂	68	31	99	2.1044
(TM-1 × bv-3)F ₂	70	28	98	0.6667
Total	506	188	694	1.6157
Heterogeneity				10.2455
Backcross populations:				(1:1)
[(bv-3 × TM-1) × bv-3] BC ₁	56	58	114	0.0351
[(TM-1 × bv-3) × bv-3] BC ₁	26	32	58	0.6207
[(bv-3 × T586) × bv-3] BC ₁	28	33	61	0.4098
Total	110	123	233	0.7254
Heterogeneity				0.3402

Test results showed that bv-3 is not an allele of any of the known virescent mutants tested. It is controlled by recessive alleles at a single locus, which results in virescent foliage when homozygous. The results of linkage tests (Table 4) indicated that bv-3 is an independent mutant not linked to any of the known mutants tested. It is proposed that this new virescent mutant be named virescent-3 and assigned gene symbols *v₃v₃*.

Table 4. Chi-square linkage deviations and recombination percentages of bv-3 with mutant loci in cotton.

Marker locus	Number of plants	Linkage χ^2	Ratio tested	Recombination, %
(bv-3 × T582)F ₂	175	2.06	3:1	40
v ₁	172	2.99		37
cl ₁	172	0.84		42
fg ₁	175	0.14		52
gl ₁	175	0.28		46
cu				
(bv-3 × T586) × bv-3 BC ₁	61	0.02	1:1	51
R ₁	61	2.77		61
H ₂	61	0.41		46
L ₃	61	4.74		36
R ₂	61	0.15		48
P ₁	61	0.80		56
Y ₁	61	0.15		48
LC ₁	61	0.80		44
N ₁				
(bv-3 × T586)F ₂	89	3.00	3:1	35
R ₁	83	2.03		39
H ₂	82	0.44		65
L ₃	77	0.64		50
R ₂	77	0.01		54
P ₁	77	0.17		55
Y ₁	76	0.21		46
LC ₁	76	0.00		50
N ₁				
Populations with linkage group tester lines				
LG II (bv-3 × LG II) × bv-3 BC ₁	94	0.52	1:1	54
L ₂	90	0.04		49
LG	94	0.00		50
P ₁	77	1.05		44
cr				
LG III (bv-3 × LG III) × bv-3 BC ₁	97	0.01	1:1	51
R ₁	97	3.72		40
Dw				
(bv-3 × LG III)F ₂	140	0.05	3:1	50
R ₁	128	0.13		46
Dw	128	1.39		37
cl ₁				
LG VI (bv-3 × LG VI)F ₂	81	1.19	3:1	53
la				

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