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Genetic Analysis of a New Virescent Mutant in Cotton[1]

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ABSTRACT

A spontaneous mutant in cotton (*Gossypium hirsutum* L.) is described, and the results of its genetic analysis are reported. This mutant was called virescent-splash-leaf because it showed a typical virescent expression, and portions of the leaf surface had a splash-leaf appearance resulting from abnormal palisade cell development. Expression of the virescent phenotype was consistent, but the splash-leaf expression was variable. The incidence of the splash-leaf expression was associated with cool temperatures.

The mutant was conditioned by recessive alleles at a single locus. Because it was non-allelic with any known virescent mutants, it was designated as *virescent-8* and assigned the gene symbols v_8v_8.

Linkage analysis of virescent-8 did not reveal any significant association with the marker loci: cup leaf, glandless-1, frego bract, cluster-1, virescent-1, Okra leaf, Red plant, Pilose, Petal spot, Yellow petals, Pollen color, Brown lint-1, Naked seed, or Green lint.

Additional index words: Linkage, Inheritance, Phenotypic expression, Temperature effect.

SEEDS from a mutant cotton line were sent to the author by E. N. Duncan. The original mutant plant appeared spontaneously in the cotton genetics nursery at Knoxville, Tennessee. The mutant was described as a virescent plant, in which about 25% of the leaf area surface contained abnormally developed palisade cells. The abnormal palisades formed an irregular pattern of whitish color on the yellow leaves, and the mutant was called virescent-splash-leaf.

Results of inheritance and linkage tests of the virescent-splash-leaf mutant and the variability associated with its mutant expression are described in this report.

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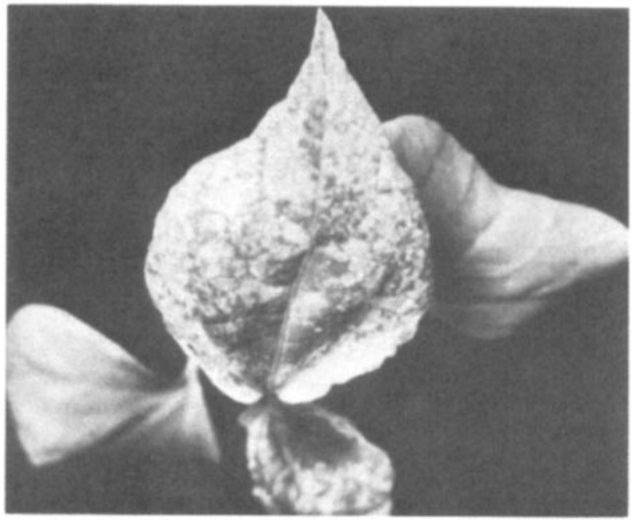

Fig. 1. Virescent-splash-leaf seedling growing in the winter in a greenhouse, showing extreme "splash-leaf" expression.

MATERIALS AND METHODS

The inheritance of virescent-splash-leaf was determined in the segregating backcross and F_2 generations of crosses between the mutant and the tester lines Texas Marker-1, Texas 582, and Texas 586. Texas Marker-1 (TM-1) is a genetic standard for *Gossypium hirsutum* L. (Kohel, Richmond, and Lewis, 1970). Texas 582 and T586 are multiple marker lines (Kohel, 1972) that were used for the linkage analysis of the mutant, in addition to the inheritance studies. Texas 582 is a multiple recessive marker line containing the following loci: cluster-1 — *cl*, (Linkage Group III), frego bract — *fg* (Linkage Group VI), cup leaf — *cu*, glandless-1 — *gl*, and virescent-1 — v_1. Texas 586 is a multiple dominant marker line containing the following loci: Brown line — Lc_1 (Linkage Group I), Petal spot — R_s (Linkage Group I), Okra leaf — L^o (Linkage Group II), Green line — *Lg* (Linkage Group II), Red plant — R_1 (Linkage Group III), Pilose — H_s (Linkage Group IV), Yellow petal — Y_1, Pollen color — P_1, and Naked seed — *N*.

Materials grown in the field were germinated in expandable peat pellets in the greenhouse and transplanted to the field after 2 to 3 weeks growth. In the field, 20 plants were placed in each row with 46 cm spacing between plants and 101 cm spacing between rows. Routine cultural practices of the Cotton Genetics Nursery at College Station, Texas, were followed. A portion of the inheritance tests was conducted in the greenhouse. This material was germinated in the same manner as material taken to the field, but the seedlings were classified and discarded.

RESULTS

Mutant Expression. The description of virescent-splash-leaf plants furnished by E. N. Duncan stated that about 25% of the leaf area of mutant plants grown at Knoxville, Tenn., had abnormal palisade cells. Progenies of the mutant were virescent, but in our initial plantings, the mutant progeny did not show the "splash-leaf" characteristic associated with abnormal palisade cell development. It was not until we grew the mutant seedlings during the winter in the greenhouse that we observed the abnormal palisade cell development (Fig. 1). Subsequently, we have observed seasonal variability in the expression of the splash-leaf characteristic, but it does not persist beyond the seedling stage at College Station. At Knoxville, the splash-leaf characteristic persisted throughout the growing season (E. N. Duncan, personal communication). I assume that the abnormal palisade cell development is initiated or enhanced by cool temperatures.

Table 1. Segregation in F_2 and backcross populations in the inheritance tests of the virescent-splash-leaf ($v_s v_s$) mutant of cotton.

Population	Segregation by class			χ^2 analysis	
	Normal	Mutant	Total	χ^2	P
	No. of plants				
F_2					
$(v_s v_s \times$ TM-1)F_2	124	40	164	0.03	0.9-0.8
$(v_s v_s \times$ T582)F_2	51	19	70	0.17	0.7-0.5
Total	175	59	234	0.01	0.8-0.7
Heterogeneity				0.19	0.7-0.5
Backcross					
(TM-1 $\times$ $v_s v_s$)$v_s v_s$	27	38	65	1.86	0.2-0.1
$v_s v_s$ ($v_s v_s \times$ T586)	72	57	129	1.74	0.2-0.1
($v_s v_s \times$ T586)$v_s v_s$	16	23	39	1.26	0.3-0.2
($v_s v_s \times$ T586)$v_s v_s$	54	46	100	0.64	0.5-0.3
Total	169	164	333	0.08	0.8-0.7
Heterogeneity				5.42	0.2-0.1

Inheritance Analysis. Virescent-splash-leaf mutant plants were crossed with all the described virescent mutants and several new virescent mutants under investigation, as shown below.

Virescent testers	Reference
virescent-1	Killough and Horlacher (1933)
virescent-2	Duncan and Pate (1967); Kohel (1973b)
virescent-3	Percival and Kohel (1974)
virescent-4	Quisenberry and Kohel (1970)
virescent-5, 6	Kohel (1973a)
yellow green-1, 2	Rhyne (1955)
New virescent lines under investigations 1 to 8	Unpublished

As suggested by its unique phenotypic expression, virescent-splash-leaf was not allelic to any of the virescent mutants. All of the F_1 plants had normal green phenotypes.

Virescent-splash-leaf plants were then crossed to TM-1, Texas 582, and Texas 586. The F_1 hybrids with TM-1 and Texas 582 were self-pollinated to produce the F_2 generation, and F_1's with TM-1 and Texas 586 were backcrossed to virescent-splash leaf (Table 1). Segregation in the F_2 populations and backcross populations conformed to the expectations of recessive alleles at a single locus, controlling the virescent-splash-leaf expression.

Linkage Analysis. The F_2 population with Texas 582 and the backcross populations with Texas 586 were classified for segregation of virescent-splash-leaf in association with the 14 genetic markers of the multiple marker lines (see Materials and Methods). No significant linkage associations were detected, and the resulting recombination values and chi-square deviations for linkage are presented in Table 2. The segregation of virescent-splash-leaf could not be distinguished when the plants were also homozygous for virescent-1, so the linkage chi-square represents the chi-square deviation for segregation of virescent-splash-leaf among the non-virescent-1 plants.

DISCUSSION

The mutant called virescent-splash-leaf was found to be a new, simply inherited, recessive virescent mutant, and it is not allelic with v_1, v_2, v_3, v_4, v_5, v_6, yg_1,

Table 2. The chi-squared deviations for linkage and the recombination percentages between virescent-splash-leaf and the genetic markers in the F_2 population with T582 and the backcross populations with T586.

Marker locus	Linkage	Recombination
	χ^2	%
Linkage Group I		
Brown lint-1	0.14	50.8
Petal spot	0.09	50.9
Linkage Group II		
Okra leaf	0.01	50.4
Green lint	2.54	45.1
Linkage Group III		
cluster-1	0.31	45.2
Red plant	3.82	44.0
Linkage Group IV		
Pilose	2.92	55.2
Linkage Group VI		
frego bract	0.77	57.1
Independent		
cup leaf	0.77	39.7
glandless-1	0.01	49.3
virescent-1	0.17	-
Yellow petal	1.22	48.3
Pollen color	0.31	50.9
Naked seed	0.06	49.3

or yg_2. The mutant gene v_7 is a new mutant which interacts with the phenotypic expression of v_1 (Turcotte and Feaster, 1973). It is proposed that this mutant be named virescent-8 and be assigned the symbols v_8v_8.

Linkage analysis of the mutant did not detect any significant linkage association with the 14 marker loci tested. The association between virescent-8 and Red plant approached significance ($P=0.05<P<.10$). Since the association with cluster-1 was not significant, and Red plant and cluster-1 loci are 17 recombination units apart in Linkage Group III, association of virescent-8 with this linkage group would place it on that side of the Red plant locus opposite to the cluster-1 locus. The data in support of linkage are weak, but the possibility will be tested further.

Monosome analysis of this mutant (Kohel and Douglas, 1974) showed it to be independent of chromosomes 2, 4, 17, and 18; these chromosomes do not contain any of the marker loci included in the linkage analyses reported in the present paper.

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