

Genetic Analysis of the *Depauperate* Mutant in Cotton, *Gossypium hirsutum* L.¹

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ABSTRACT

The *depauperate* mutant was conditioned by recessive alleles at a single locus, and the homozygous mutant genotype was assigned the gene symbols *de de*. Linkage analysis failed to detect any linkage association between *depauperate* and the marker loci *cup leaf*, *virescent-1*, *glandless bolls*, *frego bract*, *cluster-1*, *Okra Leaf*, *Red Plant*, *Pilose*, *Petal Spot*, *Yellow Petals*, *Pollen Color*, *Brown Lint*, *Naked Seed*, and *Green Lint*.

Additional index words: Inheritance, Linkage, Texas Marker-1, Texas 582 and 586.

THE cotton (*Gossypium hirsutum* L.) genetics program at College Station, Texas, has the responsibility under Regional Research Project S-77 for the collection, identification, investigation, and maintenance of mutants of *Gossypium hirsutum* L. (Anonymous, 1968). We actively search for and produce mutants, and we solicit the cooperation of fellow researchers to make available aberrant cottons they discover. A mutant strain called *depauperate* was sent to us for study, and this paper reports the results of the inheritance and linkage analysis of this cotton mutant.

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MATERIALS AND METHODS

The *depauperate* mutant was discovered by C. L. Rhyne, Americus, Ga., who sent seeds of the mutant line, backcross populations, and the F₂ population. *Depauperate* is an apt description of the mutant plants. The plants lack vigor and have an overall reduction in size. They have the general appearance of unthrifty plants. Frequently, the young seedlings have chlorotic blotches on the leaves and some puckering of the laminal area.

The genetic standard, Texas Marker-1 (TMI), (Kohel, Richmond, and Lewis, 1970) was used as the normal parent in the inheritance studies of *depauperate* conducted at College Station. The populations that were received from C. L. Rhyne involved several marker loci, but these were duplicated in the linkage analysis.

Two multiple marker lines were used in the linkage analysis of *depauperate*: a multiple recessive marker line, Texas 582, containing the loci *cluster-1*, *cl*, (Linkage Group III); *frego bract*, *fg* (Linkage Group VI); *cup leaf*, *cu*; *glandless boll-1*, *gl*; and *virescent-1*, *v*; and the multiple dominant marker line, Texas 586, containing the marker loci *Brown Lint-1*, *Lc*, (Linkage Group I); *Petal Spot*, *R*, (Linkage Group I); *Okra Leaf*, *L*^o (Linkage Group II); *Green Lint*, *Lg* (Linkage Group II); *Red Plant*, *R*, (Linkage Group III); *Pilose*, *H*, (Linkage Group IV); *Yellow Petals*, *Y*, (Linkage Group I); *Pollen Color*, *P*, (Linkage Group I); and *Naked Seed*, *N* (Kohel, 1972).

Seeds in this study were germinated in 170 ml cups filled with a soil mixture, and after 2 to 3 weeks, seedlings were transplanted to the field or to 25.4-cm (10-in) pots in the greenhouse. In the field, 20 plants were placed in each row with 46-cm spacing between plants and 101-cm spacing between rows. Cultural practices of the Cotton Genetics Nursery were aimed at maximum control of cotton insect pests, and fertilizer and water were applied for optimum plant growth.

Table 1. Segregation of the *depauperate* mutant of cotton in backcross populations.

Population	Segregation by class (number of plants)			$\chi^2(1:1)$
	Normal	Mutant	Total	
<i>depauperate</i> × F_1^*	4	3	7	0.14
F_1 × <i>depauperate</i> *	27	32	59	0.42
(<i>depauperate</i> × TM1) <i>depauperate</i>	27	18	45	1.80
	28	32	60	0.27
<i>depauperate</i> (<i>depauperate</i> × TM1)	11	8	19	0.47
	30	28	58	0.07
(<i>depauperate</i> × T586) <i>depauperate</i>	46	37	83	0.98
	45	41	86	0.18
	67	48	115	3.14
Total	285	247	532	2.71
Heterogeneity				4.76

* Populations from C. L. Rhyne.

RESULTS

In the original backcross and F_2 populations grown from seed sent by C. L. Rhyne, two phenotypes were observed, the *depauperate* mutant and the normal. The segregation indicated that a single completely recessive gene was controlling the expression of the *depauperate* phenotype (Tables 1 and 2).

The *depauperate* mutant was crossed with TM1, and the resulting F_1 plants appeared normal, confirming that *depauperate* was a recessive character. The F_1 hybrids were backcrossed to the *depauperate* parent and self-pollinated to produce larger backcross and F_2 populations to more adequately evaluate the inheritance of *depauperate*. The general unthriftness of the mutant plants was reflected in their low productivity.

Segregation in the backcross populations did not deviate significantly from the expected 1:1 segregation of a single recessive gene (Table 1). The F_2 populations segregated 3 normal:1 *depauperate*, confirming the single recessive gene control of *depauperate* (Table 2). Mutant and normal segregants in the backcross population were self-pollinated to further investigate the inheritance of *depauperate* (Table 2). The progeny from the normal segregants (expected to be heterozygotes) segregated 3 normal:1 mutant, and the mutant progeny bred true for the mutant type. These results further confirm the single gene control of *depauperate*.

The *depauperate* mutant was tested for linkage with the markers, listed above, of Texas 582 and 586. The populations tested and numbers of individuals in the populations are given in Tables 2 and 3. These populations were classified for segregation of *depauperate* and the various genetic markers and were analyzed for any possible linkage associations. Significant linkage deviations were not detected between *depauperate* and the 14 marker loci (Table 3).

Table 2. Segregation of the *depauperate* mutant of cotton in F_2 and progeny test populations.

Populations	Segregation by class (number of plants)			$\chi^2(3:1)$
	Normal	Mutant	Total	
<i>depauperate</i> F_2^*	33	15	48	1.00
(<i>depauperate</i> × TM1) F_2	22	5	27	0.60
(TM1 × <i>depauperate</i>) F_2	50	16	66	0.02
(T582 × <i>depauperate</i>) F_2	72	22	94	0.13
[(<i>depauperate</i> × TM1) <i>depauperate</i>] × normal phenotype				
1.	16	3	19	
2.	11	7	18	
3.	8	2	10	
4.	16	3	19	
5.	17	3	20	
6.	17	3	20	
7.	13	2	15	
8.	15	4	19	
9.	16	3	19	
10.	9	5	14	
11.	16	4	20	
Subtotal	154	39	193	2.36
Total	331	97	428	1.25
Heterogeneity				2.86
[(<i>depauperate</i> × TM1) <i>depauperate</i>] × mutant phenotype				
1.		10	10	
2.		5	5	
3.		9	9	
4.		8	8	
5.		10	10	
6.		9	9	
		51	51	

* Populations from C. L. Rhyne.

Table 3. Chi-square linkage deviations and recombination percentages of *depauperate* with the markers of T582 and T586 in cotton.

Marker locus	Linkage χ^2	Recombination (%)	Marker locus	Linkage χ^2	Recombination (%)
cluster-1	0.57	57.2	Okra Leaf	0.21	48.5
frego-bract	0.38	55.7	Green Lint	0.15	51.5
cup leaf	0.12	52.3	Red Plant	0.11	49.1
glandless-1	1.06	59.3	Pilose	1.53	46.0
virescent-1	1.37	59.2	Yellow Petals	0.61	53.0
Brown Lint-1	0.31	52.1	Pollex Color	0.10	48.8
Petal Spot	1.41	53.9	Naked Seeds	1.02	53.9

DISCUSSION

A new mutant, *depauperate*, is described. Inheritance tests have shown it to be determined by recessive genes at a single locus. The hybrid progeny from crosses between *depauperate* and normal have the normal phenotype, demonstrating the complete recessiveness of the mutant character. The *depauperate* mutant has been assigned the symbols *de de* for the homozygous mutant genotype. *Depauperate* was tested for linkage and found independent of the 14 marker loci of Texas 582 and 586.

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