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GENETIC ANALYSIS OF A WHITE MUTANT IN COTTON

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Abstract

A cotton, *Gossypium hirsutum* L., mutant with a new phenotype was discovered in the developmental breeding nursery at College Station, TX in which newly formed leaves turned white and subsequently the seedlings died. Seedlings with white leaves were grown under conditions of low light and a seedling greened and developed into a mature plant that provided the basis for further study. Genetic analysis revealed that the expression was controlled by duplicate recessive genes. The aberrant type was called white mutant and assigned the gene symbols *wht*$_1$*wht*$_2$. Linkage analysis revealed no detectable associations with the 14 genetic markers of multiple markers T582 and T586.

THE cooperative cotton research program at College Station, TX includes the acquisition and identification of new genetic mutants. The developmental breeding nursery with segregating generations of crosses between diverse materials frequently have aberrant types (Kohel, 1983; Percival and Kohel, 1976). Observations in the nursery are made after seedling emergence and before hand-thinning of the populations, because new mutants and other variant types may be selectively removed in the thinning process. Therefore, when aberrant seedlings are found, they are transplanted to the greenhouse. The discovery, successful recovery, and genetic analysis of such a mutant is the basis of this report.

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Materials and Methods

Description of mutant.

A seedling with white leaves, a possible mutant. was found. As new leaflets emerged they turned white, and subsequently the seedling died. Similar seedlings were found in a subsequent year. These seedlings were transplanted to the greenhouse and placed under greenhouse benches with no direct sunlight. One seedling's leaves turned green, and it developed into a mature plant. Once the mutant plant greened it was viable and these leaves remained green, but all new growth followed a transition in which the leaves expressed some degree of white expression before becoming green. The white leaf expression is unlike that observed in most virescents or chlorophyll deficient mutants that appear yellow. During the course of this study, other mutant seedlings with white leaves were observed on three separate occasions, but the precise origin was not established. The greened plant described above was used to obtain controlled and selfed pollinations.

Genetic tests.

The single greened mutant plant was crossed with the genetic standard TM-1 (Kohel et al., 1970) for studies of inheritance. The multiple recessive marker T582 was crossed for linkage analysis. The multiple dominant marker T586

was not available to cross with the greened mutant plant, but was crossed to the F_1 of TM-1 × mutant for linkage analysis of dominant markers. Genetic identity of plants possessing the mutant genes was made by progeny tests because of the lethality of the mutant expression.

Results and Discussion

Inheritance

A white mutant plant that was induced to become green was crossed as pollen parent to TM-1 and as female parent to the multiple recessive tester T582. The resulting F_2 plants were then self pollinated and backcrossed to TM-1 and the multiple dominant tester T586. The first F_2 population grown segregated 6 white to 86 green seedlings which fit the segregation expected from duplicate recessive factors ($X^2 = 0.01$, $P = 0.95$-0.90).

Mutant seedlings could not be induced routinely to green and develop into mature plants. The procedure of placing mutant seedlings in subdued light was tried and resulted in sporadic success, but was not dependable for genetic analysis. Therefore, crossing to plants and progeny testing was employed to identify plants heterozygous for the mutant genes.

The ratio of backcross plants not segregating vs. those segregating for the mutant were expected to be 3:1 ratio for duplicate recessive factors. The results of the progeny tests (Table 1) did not deviate significantly from the expected 3:1 ratio of plants not segregating vs. those segregating for mutants. Similarly, the expected segregation, assuming duplicate recessive factors, among the progeny of the normal F_2 plants was 7:8 not segregating vs. segregating progeny. There was consistent deficiency of plants that segregated for mutants in the F_2 progeny, and there was significant deviation from the expected. This deficiency could be due to reduced transmission of the mutant alleles, or the failure to identify all those plants that carried the mutant alleles.

Segregation of mutants in the progeny of the backcross generations was expected to be 15 green to 1 mutant if duplicate recessives control the mutant expression. The results in Table 2 confirm that these families did not deviate significantly from the expected 15:1 ratio.

In the F_2 progeny, one half of individual plants were expected to segregate 3:1 (green to mutant) and one half 15:1 (green to mutant) for an overall ratio of 5.4:1. The families fit the expected 5.4:1 segregation. There was an excess of mutant segregants in both the backcross and F_2 progeny tests.

Table 1. Progeny tests of normal green backcross and F_2 plants from crosses with the white mutant of cotton.

Cross	No segregation	Segregation	Total	X^2 Value	X^2 P
	no. of progeny				
Backcross				(3:1)	
1. (TM1 × white) × TM1	78	20	98	1.10	0.30–0.20
2. (TM1 × white) × TM1	77	17	94	2.40	0.20–0.10
3. (TM1 × white) × TM1	38	17	55	1.02	0.40–0.30
4. (TM1 × white) × T586	12	3	15	0.20	0.70–0.60
Total	205	57	262	1.47	0.30–0.20
Heterogeneity				3.25	0.40–0.30
F_2				(7:8)	
1. TM1 × white	29	11	40	10.72	<0.01
2. TM1 × white	45	36	81	2.57	0.20–0.10
3. White × T582	46	34	80	3.77	0.10–0.05
Total	120	81	201	13.72	<0.05
Heterogeneity				3.34	

Linkage analysis

The multiple recessive markers were tested for linkage in the F_2 of white × T582 by growing the F_2 non-white plants, selfing them, and progeny testing to identify plants heterozygous for the white mutant. Classification of the genetic markers and progeny tests for the white mutants was successful for 80 plants. The expected segregation was 45 normal:15 recessive genetic marker:3 normal for genetic markers and heterozygous for white mutant:1 recessive genetic marker and heterozygous for white mutant. The chi-square values for linkage deviation were not significant for any of the five recessive genetic markers (v_1, *cu*, gl_1, *fg*, and cl_1).

The multiple dominant markers were tested in a similar manner in the cross (white × T586)× TM-1. Seventy-one plants were successfully classified for the genetic marker and progeny tested. The expected segregation was 3 genetic marker:1 genetic marker and heterozygous for white mutant:3 normal and not segregating for white mutant:1 normal and heterozygous for white mutant. No linkage deviation was significantly large for any of the nine dominant genetic markers (R_1, $H_2 = T_1$, $L_2°$, R_2, P_1, Y_1 Lc_1, N_1, and *Lg*).

The mutant is characterized by an apparent lack of pigments giving a white appearance to new leaflets

Table 2. Segregation of normal and mutant plants from plants segregating in the progeny test.

Cross	Normal	Mutant	Total	X^2 Value	X^2 P
	no. of plants				
Backcross				(15:1)	
1. (TM1 × white) × TM1	62	5	67	0.17	0.70–0.60
2. (TM1 × white) × TM1	63	6	69	0.70	0.50–0.60
3. (TM1 × white) × TM1	44	6	51	4.86	0.05–0.02
4. (TM1 × white) × TM1	63	7	70	1.68	0.20–0.10
5. (TM1 × white) × TM1	32	2	34	0.01	0.95–0.90
Total	264	27	291	4.55	0.05–0.02
Heterogeneity				2.87	0.60–0.50
1. (white × T586) × TM1	38	2	40	0.11	0.80–0.70
2. (white × T586) × TM1	60	3	63	0.24	0.70–0.60
3. (white × T586) × TM1	18	3	21	2.31	0.20–0.10
4. (white × T586) × TM1	73	6	79	0.24	0.70–0.60
Total	189	14	203	0.14	0.80–0.40
Heterogeneity				2.76	0.50–0.40
F_2				(5.4:1)	
1. TM1 × white	80	23	103	3.51	0.10–0.05
2. TM1 × white	81	15	96	0.00	>0.99
3. TM1 × white	122	20	142	0.26	0.70–0.60
4. TM1 × white	130	32	162	2.09	0.20–0.10
5. TM1 × white	58	20	78	5.94	0.02–0.01
Total	471	110	581	4.82	0.05–0.02
Heterogeneity				6.98	0.20–0.10
1. white × T582	67	10	77	0.41	0.60–0.50
2. white × T582	114	15	129	1.56	0.30–0.20
3. white × T582	166	25	191	0.93	0.40–0.30
4. white × T582	143	23	166	0.39	0.60–0.50
5. white × T582	125	16	141	1.96	0.20–0.10
Total	615	89	704	4.75	0.05–0.70
Heterogeneity				.6.98	0.20–0.10

and subsequent death of the seedlings. Some seedlings protected from full sunlight can be induced to green, and they are viable and stable once greened. This type of development suggests an aberration in the development of the chloroplast which is subject to photooxidation, but stable chloroplasts are formed once they have developed. The mutant is controlled by duplicate recessive genes with no evidence of linkage associations. It is proposed that the mutant be named white with the corresponding gene symbolization $wht_1wht_1wht_2wht_2$.

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