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Genetic Analysis of Fiber Color Variants in Cotton[1]

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ABSTRACT

Although white is the most common color of fiber in Upland cotton (*Gossypium hirsutum* L.), some lines display brown lint fibers, and others have green lint. Some cottons have white lint and green fuzz. Eleven lines with brown lint, one with green lint and fuzz, and two with white lint and green fuzz were tested for allelism against known genes for lint color, and for chromosomal location of lint color loci. All lines displaying green lint and/or fuzz proved to be alleles at the *Lg* locus. The green fuzz allele was designated Lg^f. Four of the brown-linted lines proved to carry alleles at the Lc_1 locus, and four alleles at the Lc_2 locus. A dark brown phenotype was imparted by an allele at a new locus, Lc_3. The Lc_3 locus proved to be linked with another locus, Lc_5, which harbors alleles for light brown lint color. Alleles at Lc_4 and Lc_6 also impart light brown lint color.

Additional index words: **Mendelian segregation, Linkage, Allelism, Brown lint, Green lint, *Gossypium hirsutum* L.**

At College Station, TX, we maintain an active program in the genetic and cytogenetic identification of the Upland cotton (*Gossypium hirsutum* L.) chromosomes. As part of this program, we seek new genetic variability as spontaneous mutations, induced mutations, and contributions from various cotton researchers throughout the U.S. Cotton Belt. Over the years we have acquired, from various sources, mutant lines with green or brown fibers, and have conducted analyses of these variants to determine their inheritance and chromosomal locations. This report is a consolidation of these tests to integrate current knowledge on the inheritance of fiber color variants of cotton.

MATERIALS

The fiber color variants of unknown genetic control and their source of origin are listed in Table 1. The lines are identified as lint color lines when the lint fibers and fuzz fibers are colored, and fuzz color lines when the lint fibers are white and fuzz fibers are colored. The genetically identified variants used in the tests and their references are listed in Table 2. Because various test procedures were used in this investigation, they will be presented in association with the individual test results.

RESULTS

Green Lint and Fuzz

One green lint with green fuzz and two white lint with green fuzz lines were available for testing for association with the green lint locus (*Lg*). Tests were made for allelism with *Lg* or for linkage with the marker locus veins-fused (*vf*) that is closely linked with *Lg* (Dilday et al., 1975). The green lint line (TA 40) was tested with *Lg*. TA 40 was crossed with *LgLg* and the F_1 backcrossed to white fiber, *lglg*. The F_1 was uniformly green linted and the backcross was uniformly light green linted, characteristic of the genotype *Lglg*. The test results demonstrated that the green lint character in TA 40 was an allele of *Lg*. An additional test was performed by growing out and classifying plants of the cross (TA 40 × *vfvf*)*vfvf* for green lint and veins-fused expression. Recombination between green lint and veins-fused was 11.76% (Table

Table 1. List of potentially new fiber color variants and their origin.

Variants	Origin
Green lint and fuzz	
TA 40	Mutant in Texas cotton producer's field
Green fuzz and white lint	
FGS (Florida Green Seed)	Florida wild cotton
JAL	J. A. Lee transferred from house-yard cotton Wh 219
Dark Brown lint	
AC (Algodon de Catamarca)	Introduction from Argentina
TA 35	Chinese introduction, unknown source
TA 36	Unknown source
LB (Louisiana Brown)	Old variety grown in Louisiana, from B. A. Waddle, Arkansas
Morrilli Brown lint	Transferred from *G. hirsutum* race morrilli, Texas no. 92. Reported under the designation Lc_yLc_z
Light Brown lint	
TT	Spontaneous mutant from cytogenetics program
G255	Stock designated as Lc_4 from C. L. Rhyne
AD_3	Texas mutant collection, transferred from *G. tomentosum*
Higginbotham	B. A. Waddle, Arkansas
Brymer	Texas mutant collection
YSL	Transferred from *G. hirsutum* race *yucatanense*

Table 2. Genetic mutant stocks and testers used in tests, and their reference.

Symbol	Name	Reference
yv	yellow veins	Kohel, 1983
ark-1	-	Unpublished
Rl_3	Round leaf	Percival et al., 1976
v_8	virescent	Kohel, 1978b
Vf^h	Veins-fused	Kohel, 1967
Crp	Crumpled leaf	Kohel, 1978b
Dw	Dirty white lint	Kohel, 1973
H_3	Pilose	Kohel, 1978b
Lc_1	Brown lint	Kohel, 1978b
Lc_2	Brown lint	Kohel, 1973
Lg	Green lint	Kohel, 1973
Li	Ligon Lintless	Kohel, 1978b
ms_2	male-sterile	Kohel, 1978b
Ms_4	Male-sterile	Kohel, 1978b
Ms_7	Male-sterile	Kohel, 1978b
mt	mottled leaf	Kohel, 1973
N_1	Naked seed	Kohel, 1978b
ob	open bud	Kohel, 1978b
Rd	Red dwarf	Kohel, 1978b
v_3	virescent	*Kohel, 1978b*
v_4	virescent	Kohel, 1978b
vf	veins-fused	Kohel, 1973
T582		
cl_1	cluster	Kohel, 1978b
cu	cup leaf	Kohel, 1978b
fg	frego bract	Kohel, 1978b
gl_1	glandless stem and boll	Kohel, 1978b
v_1	virescent	Kohel, 1978b
TM-1	Texas Marker 1	Kohel et al., 1970

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Table 3. Segregation and analysis of green lint and veins-fused in the population (TA 40 × *vfvf*)*vfvf*.

Phenotype	No. of plants	Chi-square analysis Source	Chi-square
veins-fused, white lint	18	Normal vs. veins-fused	0.12
veins-fused, Green lint	0	Green vs. white lint	2.94
Normal veins, white lint	4	Linkage	19.88
Normal veins, Green lint	12		
	34	Recombination = 11.76%	

Table 4. Segregation and analysis of green fuzz and veins-fused in the population TM-1 (FGS × Vf^hVf^h).

Phenotype	No. of plants	Chi-square analysis Source	Chi-square
Veins-fused, white fuzz	46	Veins-fused vs. normal	0.39
Veins-fused, Green fuzz	3	Green vs. white fuzz	2.78
normal veins, white fuzz	8	Linkage	53.26
normal veins, Green fuzz	35		
	92	Recombination = 11.96%	

Table 5. Segregation of JAL green fuzz line in a population of [(Green fuzz × Green lint, Naked seed) normal lint and fuzz].

Phenotype	No. of plants
Naked seed, Green lint	13
Naked seed, white lint	13
Green fuzz, Green lint	19
Green fuzz, white lint	26
white fuzz, Green lint	0
white fuzz, white lint	0
	71

3). These results establish TA 40 as a line bearing the *Lg* allele.

The white lint with green fuzz line, Florida Green Seed, had dark green fuzz, and the white lint with green fuzz line, J.A. Lee, was a lighter green. Unpublished observations indicated that FGS was an allele of *Lg*, so FGS was checked for linkage with a dominant allele at the veins-fused locus (Vf^h). Recombination between FGS and Vf^h in the backcross population was 11.96% (Table 4), which verified the FGS character as an allele of the *Lg* locus.

The green fuzz line (JAL) was crossed with the *G. hirsutum* genetic standard with white lint and fuzz (TM-1) and a small F_2 population segregated as a single dominant (JAL $\chi^2_{3:1} = 0.04$, 38 plants). The JAL line was crossed to a green lint (*Lg*) line and backcrossed to normal white fiber. The green lint line also had Naked seed (N_1). The progeny segregated for green vs. white lint, and naked vs. green fuzzy seeds (Table 5). These data indicate that the green fuzz character of JAL is determined by an allele at the *Lg* locus. Because variations in fuzz-color intensity were noted, more than one green fuzz allele might have been present; however, I have frequently found that green lint color often varies in intensity with genetic background. In some backgrounds, *LgLg* has a phenotype that approaches the expression commonly associated with *Lglg*, and *Lglg* is sometimes difficult to distinguish from *lglg*. Until the identification of multiple green fuzz alleles, green fuzz variants should be represented by Lg^f, a single allele at the *Lg* locus. Thus, all green fiber variants tested

Table 6. F_2 segregation in allelic tests of new dark brown linted lines with the three identified brown lint loci of cotton.

New brown lint lines	Identified brown lint loci: Lc_1 Brown	Lc_1 White	Lc_2 Brown	Lc_2 White	Dw Brown	Dw White
	no. of plants					
Algodon de Catamarca	40	0	–	– –	–	–
TA 35	20	0	16	3	14	5
TA 36	19	0	11	3	15	4
Louisiana Brown	33	0	28	9	30	9

Table 7. F_2 segregation of light brown lint lines.

	G255 Brown	G255 White	AD_3 Brown	AD_3 White	Higginbotham Brown	Higginbotham White	Lc_2^B Brown	Lc_2^B White
	no. of plants							
TT	16	5	17	2	22	1	22	3
G255			12	1	19	3	15	2
AD_3							23	0
Higginbotham							25	0

were conditioned by alleles at a single locus, *Lg*, located on chromosome 15 in the D subgenome.

Brown Lint

Dark Brown Lint. In the College Station, TX, collection of brown linted cottons are several sources that vary in color intensity. The first group that I shall consider is dark brown lint, consisting of Algodon de Catamarca (AC), TA 35, TA 36, and Louisiana Brown (LB). These four lines were tested for allelism with the three described brown lint loci, Lc_1, Lc_2, and *Dw* (Table 6). All four lines proved to carry alleles at the Lc_1 locus. Louisiana Brown was unusual in that it carried a gene for light brown lint at an additional locus. The parental LB line has a more intense brown color than lines carrying only the Lc_1 locus. I isolated a line from LB that was a very light brown color, but it was too faint to score accurately in segregating populations.

Light Brown Lint. The College Station collection includes six lines with light brown lint in addition to the lines with dark brown lint. These are TT, G255, AD_3, Higginbotham, Brymer, and YSL. Among the presently identified brown lint lines of *G. hirsutum*, Lc_2 is the only light brown. Brymer Brown is the phenotype that has been used to typify the Lc_2 locus, and it is the only genetically designated light brown allele known to date in *G. hirsutum*. Linkage of Pilose (H_2) with Brymer Brown and subsequent monosome tests placed Brymer Brown at Lc_2 (Endrizzi and Kohel, 1966). The light brown lint lines of this group were tested inter se to determine if there was allelism (Table 7). This test was performed before YSL was discovered. Subsequently, a monosomic test established that YSL brown lint was on chromosome 6 and presumably Lc_2. The cross was TM-1 (H6XYSL). The monosomic F_1 was crossed as male to TM1, and all 35 of the resulting progeny had heterozygous light brown lint.

The reported recombination between Lc_2 and H_2 varies widely (Endrizzi and Kohel, 1966; Stephens, 1955), so Higginbotham brown lint was tested for

Table 8. Linkage analysis of Higginbotham brown lint and H_2 in the cross (Lc^H, h_2 × lc, H_2) Lc^H, h_2.

Phenotype	No. of plants	Chi-square analysis	
		Source	Chi-square
Brown lint, nonpilose	49	Pilose vs. nonpilose	5.45
white lint, nonpilose	11	Brown vs. white lint	0.50
Brown lint, Pilose	3	Linkage	49.08
white lint, Pilose	34		
	97	Recombination = 14.43%	

linkage with H_2. I obtained a 14.43% value (Table 8) compared with prevoius tests between Brymer and H_2 (Recombination % = 22.00) (Endrizzi and Kohel, 1966). Because of the discrepancy of recombination values the cross (Brymer × Higginbotham) TM-1 was made, and all 250 progeny were phenotypically uniform for heterozygous light brown lint.

The tests of lines with light brown lint established Brymer (Lc_2^B), Higginbotham, and AD_3 as Lc_2 alleles (Table 7). The AD_3 line was derived from Hawaiian cotton (*G. tomentosum* L.) $(AD)_3$, and was expected to be an Lc_2 allele because $(AD)_3$ is homozygous for Lc_2 and H_2. That left TT and G255 as carrying potentially new brown lint loci. The TT line bears the lighter brown of the two, and field classification is unreliable. However, it was successfully checked against *Dw* and found to be nonallelic. The cross was (TT × *Dw*)TT and the observed and expected segregation was dark brown 11(9.5):light brown 3(4.75):white 5(4.75), $\chi^2 = 0.89$. The expected segregation was 2:1:1 for independence.

Brown Lint from G. Hirsutum Race Morrilli. A line with dark brown lint was recovered in a day-neutral line from *G. hirsutum* L. race morrilli, that was selected initially because it carried the mottle leaf gene (*mt*) (Lewis, 1960). The intensity of brown color suggested it was probably allelic to Lc_1 or *Dw*. Morrilli brown lint was crossed with Lc_1 and the F_1 backcrossed to a white linted line (TM-1). A population of 135 plants was grown; 25 white lint and 110 brown lint plants were observed. The recovery of white lint segregants proves that morrilli brown lint is not allelic with Lc_1.

Morrilli brown lint was then crossed with the dark brown lint gene *Dw*. The F_1 was backcrossed to TM-1; 21 of the resulting 39 backcross progeny were white lint, proving that these browns are not allelic. Morrilli brown lint was then crossed with the light brown Lc_2. The F_1 was backcrossed to TM-1. There were nine white lint plants in a backcross population of 40 plants; therefore, morrilli brown lint is not allelic with Lc_2. Morrilli brown lint is not allelic to any of the designated brown lint loci of *G. hirsutum* L.

Segregation in the above allelic tests suggested that alleles at a single locus conditioned morrilli brown lint but the populations were small and difficult to interpret with the presence of a second brown lint factor. Thus, an inheritance study of morrilli brown lint was initiated. An initial population from the backcross TM-1 (Brown lint × TM-1) had 45 white lint plants and 55 brown lint plants. Although these observations did not deviate significantly from that expected for dominant alleles at a single locus, I doubted that a single locus was involved. The 55 brown segregates bore at least two obvious color classes of brown lint. The following year the remnant seeds were planted, along with seeds for a small F_2 population. The results were the same as before; however, the separation of white vs. brown lint suggested dominant alleles at a single locus.

Table 9. Segregation of morrilli brown lint in backcrosses involving white lint lines.

Population	Segregation			Chi-square
	Brown	White	Total	(1:1 ratio)
	no. of plants			
TM-1 (Brown lint × TM-1)	55	45	100	1.00
TM-1(Brown lint × TM-1)	56	37	93	3.88
(Brown lint × T582)T582	41	56	97	2.32
(Brown lint × T582)T582	94	99	193	0.13
TM-1(Brown lint × TM-1)	115	73	188	9.38
(Brown lint × T582)T582	44	34	78	1.28
(Brown lint × TM-1)TM-1	48	34	82	2.39
(Ms_4 × Brown lint)B.R.	54	46	100	0.64
(Ms_7 × Brown lint)B.R.	44	54	98	1.02
(Brown lint × Crp)B.R.	55	54	99	0.81
(Brown lint × Rl_2)B.R.	54	45	99	0.81
Pooled	650	577	1227	4.34 ($P = 0.05$–0.02)
Heterogeneity				19.32 ($P = 0.05$–0.02)

Field classification of lint color was not adequate to consistently rate the variation present. The random distribution of colors among plants, variations in the time of boll openings, and different degrees of weathering complicated classification. During the following 3 yrs., in addition to the field classification, three-boll samples from each plant were harvested at the end of the season and ginned lint was classified in the laboratory. The samples were classified on a cotton-classing table providing uniform daylight-type illumination. The lint samples were compared and placed in an appropriate color class. This method refined separation and resulted in more numerous classes. The separation did not result in discrete classes, but led to modal groupings along a continual distribution. In the F_2 brown lint could be separated into about seven modal classes and the backcross into about four. Segregation, in combination with the background genotype and environmental variability, resulted in brown lint phenotypes more closely resembling a continuous distribution rather than suggesting discrete classes.

Based on my experience working with brown lint variants and their segregation, I concluded that the variation in brown lint segregants in the F_2 and backcross populations were due to segregation at more than one locus. The best current explanation for the frequency of white vs. brown lint and the variation within the brown lint class suggests brown lint alleles are segregating at two closely linked loci. Furthermore, the color of the lightest brown lint in the backcross was less intense than heterozygous Lc_2. This observation suggests one locus conditions a lighter brown lint color than a second major dark brown lint color locus.

The segregation of populations of morrilli brown lint crossed with various white lint lines, then backcrossed or testcrossed to a white lint tester is shown in Table 9. In these populations the brown lint classes were consolidated into a single brown lint class. The pooled segregation deviated significantly from a 1:1

Table 10. Segregation of morrilli brown lint in F_2 populations involving various white lint lines.

Population	Segregation			Chi-square
	Brown	White	Total	(3:1 ratio)
	— no. of plants —			
(Brown lint × T582)F_2	72	18	90	1.20
(Brown lint × TM-1)F_2	14	3	17	0.49
(TM-1 × Brown lint)F_2	108	62	170	11.93
(TM-1 × Brown lint)F_2	70	28	98	0.67
(yv × Brown lint)F_2	62	37	99	8.08
(Brown lint × ark-1)F_2	72	27	99	0.27
(Brown lint × Rd)F_2	73	26	99	0.08
(Brown lint × Crp)F_2	72	27	99	0.27
(ms_1 × Brown lint)F_2	73	27	100	0.21
(Brown lint × v_6)F_2	78	20	98	1.10
(ob × Brown lint)F_2	81	17	98	3.06
(v_3 × Brown lint)F_2	82	17	99	3.26
(v_4 × Brown lint)F_2	71	28	99	0.56
Pooled	928	337	1265	1.81 ($P = 0.20$–0.10)
Heterogeneity				29.37 ($P \leq 0.01$)

ratio although there was significant heterogeneity among the populations. Based on the excess frequency of the brown lint class and deficiency in the white lint class, assuming two linked brown lint loci, the loci were linked with 5.94% recombination.

The F_2 segregation of morrilli brown lint (Table 10) did not deviate significantly from that expected for a single dominant brown lint gene. The white lint class was in excess of the expected frequency. Heterogeneity among these F_2 populations was significantly large. Variation within the brown lint class did support the hypothesis of more than a single brown lint locus. The heterogeneity among these F_2 populations and the excess of plants classed as white lint may reflect the difficulty to visually distinguish between homozygous white lint plants and those carrying one or two alleles at the weak locus.

Linkage Analysis of Morrilli Brown Lint. Morrilli brown lint was tested for linkage with 18 mutants (Table 11). The multiple recessive tester line (T582) included five mutant loci which cup leaf (*cu*) was the only mutant that indicated linkage with brown lint. Four backcross populations were grown. The first two populations gave consistent linkage results of 37.11% and 39.90%, respectively. The third population consisted of the remaining seed from this backcross and had an excessive amount of recombination (60.26%). New crosses were made and a fourth backcross population yielded a recombination value of 54.73%, which resulted in a nonsignificant linkage chi-square in the pool population and a recombination value of 46.70%. This proves cup leaf and morrilli brown lint are considered independent.

Monosomic Analysis of Morrilli Brown Lint. Monosomic analysis of morrilli brown lint, reported under the designation Lc_yLc_z, was found independent of chromosomes 1, 2, 4, 6, and 18 (Kohel, 1978a). The character was tested with the monosome for chromosome 7 to further verify its independence of Lc_1. The F_1 (H7 × Brown lint) was testcrossed to TM-1. The testcross progeny from monosomic and disomic F_1 plants segregated for brown and white lint which verifies that they are not associated with chromosome 7, the chromosome bearing Lc_1.

Table 11. Linkage analyses of morrilli brown lint.

Phenotypic class	No. of plants	Chi-square analysis: Source	Chi-square
(Male-sterile-4 × Brown lint) tester			
Sterile white lint	22	Sterile vs. fertile	0.25
Sterile Brown lint	25	Brown vs. white lint	0.49
fertile white lint	24	Linkage	0.01
fertile Brown lint	28		
	99	Recombination % = 49.49	
(Male-sterile-7 × Brown lint) tester			
Sterile white	27	Sterile vs. fertile	1.44
Sterile Brown	29	Brown vs. white lint	0.64
fertile white	27	Linkage	1.44
fertile Brown	17		
	100	Recombination % = 56.00	
(Brown lint × Crumple leaf) tester			
Crumple white	27	Crumple vs. noncrumple	0.04
Crumple Brown	24	Brown vs. white lint	0.36
noncrumple white	26	Linkage	0.00
noncrumple Brown	23		
	100	Recombination % = 50.00	
(Brown lint × yellow veins)F_2			
Brown Normal	47	Brown vs. white lint	6.45
Brown yellow veins	17	Normal vs. yellow veins	0.21
white Normal	26	Linkage	0.07
white yellow veins	10		
	100	Recombination % = 49.13	
(Brown lint × ark-1)F_2			
Brown Nonark-1	55	Brown vs. white lint	0.21
Brown ark-1	18	Nonark-1 vs. ark-1	0.05
white Nonark-1	21	Linkage	0.07
white ark-1	6		
	100	Recombination % = 51.90	
(Brown lint × virescent-4)F_2			
Brown Green	54	Brown vs. white lint	0.48
Brown virescent	18	Green vs. virescent	0.00
white Green	21	Linkage	0.00
white virescent	7		
	100	Recombination % = 50.00	
(Brown lint × virescent-2)F_2			
Brown Green	66	Brown vs. white lint	3.41
Brown virescent	17	Green vs. virescent	2.61
white Green	16	Linkage	0.64
white virescent	1		
	100	Recombination % = 69.20	
(Brown lint × open buds)F_2			
Brown Nonopen bud	60	Brown vs. white lint	3.41
Brown open bud	22	Nonopen bud vs. open bud	0.05
white Nonopen bud	16	Linkage	2.56
white open bud	1		
	100	Recombination % = 73.85	
(Brown lint × Crumpled leaf)F_2			
Crumple Brown	52	Crumple vs. noncrumple	2.61
Crumple white	16	Brown vs. white lint	0.05
noncrumple Brown	22	Linkage	0.87
noncrumple white	10		
	100	Recombination % = 56.70	
(Brown lint × virescent-8)F_2			
Brown Green	62	Brown vs. white lint	1.10
Brown virescent	16	Green vs. virescent	0.67
white Green	15	Linkage	0.22
white virescent	5		
	98	Recombination % = 46.42	
(Brown lint × Round leaf-2) tester			
Round white	19	Round vs. nonround leaf	5.76
Round Brown	19	Brown vs. white lint	1.00
nonround white	26	Linkage	1.00
nonround Brown	36		
	100	Recombination % = 45.00	

(continued)

Table 11. Continued.

Phenotypic class	No. of plants	Chi-square analysis Source	Chi-square
tester (Brown lint × Ligon lintless)			
Brown nonligon	22	Ligon vs. nonligon	0.19
white nonligon	23	Linkage	0.02
- Ligon	41		
	86	Recombination % = 51.11	
(Brown lint × Red dwarf)F_2			
Red Brown	54	Red vs. green	0.01
Red white	19	Brown vs. white lint	0.01
green Brown	29	Linkage	0.04
green white	6		
	98	Recombination % = 48.45	
(Brown lint × cup leaf) cup leaf			
white cup	133	Brown vs. white lint	0.28
Brown cup	110	Noncup vs. cup	1.74
white Noncup	131	Linkage	2.24
Brown Noncup	142		
	516	Recombination % = 46.70	
(Brown lint × glandless stem) glandless stem			
white glandless	83	Brown vs. white lint	0.27
Brown glandless	83	Glanded vs. glandless	3.52
white Glanded	106	Linkage	0.27
Brown Glanded	96		
	368	Recombination % = 51.36	
(Brown lint × frego bract) frego bract			
white frego	83	Brown vs. white lint	0.27
Brown frego	86	Nonfrego vs. frego	2.44
white Nonfrego	106	Linkage	0.70
Brown Nonfrego	93		
	368	Recombination % = 52.17	
(Brown lint × cluster fruiting) cluster fruiting			
white cluster	76	Brown vs. white lint	0.27
Brown cluster	67	Noncluster vs. cluster	18.27
white Noncluster	113	Linkage	0.17
Brown Noncluster	112		
	368	Recombination % = 48.91	
(Brown lint × virescent-1) virescent-1			
white virescent	76	Brown vs. white lint	0.27
Brown virescent	74	Green vs. virescent	12.56
white Green	113	Linkage	0.10
Brown Green	105		
	368	Recombination % = 50.32	
(male-sterile-2 × Brown lint)F_2			
Fertile Brown	57	Fertile vs. sterile	1.33
Fertile white	23	Brown vs. white	0.21
sterile Brown	16	Linkage	0.64
sterile white	4		
	100	Recombination % = 56.76	

DISCUSSION

The results of the analysis of 14 fiber color lines showed that the three green fiber alleles tested reside at a single locus. The *Lg* allele conditions green lint and fuzz fibers while the Lg^f allele conditions the white lint and green fuzz lines.

The dark brown lint lines tested were conditioned by alleles at the Lc_1 locus, except for morrilli brown lint. There was no evidence of more than one Lc_1 allele. Louisiana Brown carries a second brown lint locus, but the expression of the allele at the locus was so weak that when isolated it could not be identified readily in segregating populations.

Morrilli brown lint (tentatively designated Lc_yLc_z, Kohel, 1978a) is conditioned by dark brown lint alleles at one new locus that is closely linked to a second new locus carrying light brown alleles. The dark brown locus is assigned the gene symbol Lc_3. The second locus having light brown lint was assigned the symbol Lc_5.

The light brown lint lines AD_3, Higginbotham, Brymer Brown, and YSL carry alleles at the Lc_2 locus. The lines G255 and TT are independent of all other brown lint loci. Since G255 was tentatively designated Lc_4, it is assigned the gene symbol Lc_4, and TT is assigned the gene symbol Lc_6.

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