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Effects of Plant Smoothness on Agronomic Traits of Upland Cotton—Fiber Properties[1]

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ABSTRACT

Glabrousness in upland cotton (*Gossypium hirsutum* L.) confers resistance to certain insects and decreases trash in ginned lint. Such plant smoothness has been associated with reductions in lint percentage and fiber yield, but there is little information on the effects of the phenotype on fiber properties. Two complete diallel sets involving various combinations of smoothness and pilosity alleles were grown in randomized, complete blocks in North Carolina in 1982 in four replications per location. The first set was generated by intercrossing the allelic pairs, Sm_1^{sl} and sm_1, and Sm_2 and sm_2 in all possible combinations, and the second by intercrossing the allelic pairs Sm_2 and sm_2, and Sm_3 and sm_3^k. Increasing the number of *Sm* alleles in a given cotton increases plant smoothness, whereas the completely recessive phenotype (all *sm* alleles), imparts normally pubescent, the phenotype of 'Coker 310', the cultivar used as background. Within the two diallels 2.5% fiber span length varied from 26.9 to 30.1 mm with the lowest values associated with the Sm_2 allele. Fifty percent span length varied from 13.0 to 14.3 mm but was significantly various only in the first diallel, and the variation for 50% span length in that particular set did not relate to degree of plant smoothness. The entries with the shortest 2.5% span length tended to have the highest fiber uniformity index. Micronaire values above 5 were associated with some of the entries homozygous for Sm_2, and fiber tenacity showed a deficiency where the Sm_1^{sl} allele was homozygous. There were significant estimates for general and specific effects for some of the traits, particularly with entries harboring the $Sm_2 \times sm_2$ contrasts, and evidence for maternal and reciprocal (maternal × embryonic) effects for some traits. There was no consistent evidence that degree of plant smoothness related to disturbances in any fiber trait, but evidence that specific smoothness alleles were accompanied by fiber quality deficits.

***Additional index words:* *Gossypium barbadense* L., *Gossypium hirsutum* L., *Gossypium tomentosum* Nutt. ex Seem., General Effects, Specific Effects, Maternal Effects, Reciprocal Effects, Trichomes.**

TYPICALLY, cultivars of upland cotton, *Gossypium hirsutum* L., have trichomes liberally distributed over the surfaces of leaves, on the margins of leaves, on stems and petioles, and on the outer surfaces of the bracteoles. There are phenotypes of *G. hirsutum* in which the trichomes on vegetative parts are reduced progressively in a clearly discernable pattern, the loss beginning on the lesser stages of leaf-vein branching and culminating in plants that are entirely glabrous. Such semi, and entirely, glabrous cottons have been described as being smooth-leaved (6).

Potential uses for glabrousness include reduction of vegetative trash in ginned lint and curtailment of the attacks of certain insect pests (3, 10, 14, 17). Unfortunately, certain of the smoothness alleles have been associated with agronomic deficits, particularly reduced lint percentage (gin out-turn) and yield of fiber (2, 7, 17).

There is evidence that degree of pubescence density in upland cotton is sometimes associated with alterations in fiber properties. Perhaps the best known example is the effects of Simpson's fuzzy leaf, or Pilose, allele (15). Pilose imparts dense tomentum on leaves and stems while simultaneously shortening lint and increasing micronaire (4, 5, 15). The H_2 allele from *G. tomentosum* Nutt. ex Seem., which is allelic with Pilose, and imparts a similar phenotype on upland background, shortened lint very little and increased micronaire not at all in the upland cultivar Empire (8). To further confound the issue, Dark (1) reported that the Pilose allele did not alter fiber length of the *G. barbadense* L. cultivar Domains Sakel.

Worrell (18) reported a negative relationship between density of tomentum and fiber length in stocks of upland cotton adapted for production in South Africa, but stated that jassid-resistant, tomentose stocks with acceptable fiber length could be selected. Therefore, Worrell's correlation must have been weak, or else spurious.

Smith (16) counted the trichomes on the abaxial surfaces of the leaves of upland cultivars and found a three-fold difference in the density of pubescence. Although Smith's data were not accompanied by information on the comparative fiber properties of the stocks examined, Americans upland cottons at the time (1964) had a modal length of about 27 mm upper-half mean length and micronaire in the 3.5 to 5 range, properties demanded by fiber markets at the time. Therefore, except for the prominant case of the Pilose allele, there is scant evidence for a direct relationship between grade of plant vestiture and the fiber properties of hirsute cottons.

Information on the fiber properties of glabrous cottons is even more scarce than such data for pubescent cottons. The Delta Smooth allele, sm_3, confines trichomes to the principal leaf veins, leaf margins, petioles, and stems, a semismooth phenotype, as it were. The sm_3 allele has been used in American upland cultivars for decades to improve fiber grade, and Ewing et al. (3) did not report any fiber quality deficits associated with the allele. Davis (2) using the D_2 smooth morph of Sm_1^{sl}, a gene that confines trichomes largely to the margins of mature leaves, found no fiber quality deficits associated with the allele in the backgrounds of 'Deltapine' and 'Acala' cottons. The Coker Pedigreed Seed Company once offered a cultivar Coker 413 that was homozygous for what was very likely the *G. barbadense* morph of Sm_1^{sl} as a quality cotton, which meant that fiber length and tenacity were better than average for the time, the 1960s.

Two additional smoothness genes have been extracted from a wild accession of *G. hirsutum*, WH-219, and introgressed into upland background (6). One, Sm_2, imparts a phenotype similar to that of the Sm_1^{sl} allele, and the other, Sm_3, a phenotype similar

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Table 1. Means and Tukey's honestly significant differences for fiber properties for Exp. 1.

Entry no.	Genotype	2.5% span length	50% span length	Uniformity index
		mm		%
1	2 (a_1b_0)	28.7 ab*	13.0 b	44.8 c
2	× a_0b_1	28.4 ab	13.2 ab	45.8 bc
3	× a_1b_1	28.3 ab	13.0 b	45.5 bc
4	× a_0b_0	28.7 ab	13.5 ab	46.3 bc
5	2 (a_0b_1)	26.9 c	13.2 ab	49.0 a
6	× a_1b_0	29.1 a	13.6 ab	46.1 bc
7	× a_1b_1	28.8 ab	13.7 a	46.9 abc
8	× a_0b_0	28.5 ab	13.2 ab	45.5 bc
9	2 (a_1b_1)	27.9 bc	13.2 ab	46.9 abc
10	× a_1b_0	28.8 ab	13.7 a	47.1 abc
11	× a_0b_1	27.5 bc	13.4 ab	47.8 abc
12	× a_0b_0	28.4 ab	13.4 ab	46.5 abc
13	2 (a_0b_0)	29.1 a	13.4 ab	46.0 bc
14	× a_1b_0	28.8 ab	13.4 ab	45.8 bc
15	A a_0b_1	28.3 ab	13.7 a	47.9 abc
16	× a_1b_1	28.2 ab	13.2 ab	46.5 abc
Tukey's HSD (0.05)		1.0	0.6	2.6

Entry no.	Genotype	Tenacity	Micronaire	Elongation
		$kNmkg^{-1}$	$\mu g\ in^{-1}$	%
1	2 (a_1b_0)	176.1 c	4.4 b	7.3 a
2	× a_0b_1	186.1 abc	4.8 ab	7.1 abc
3	× a_1b_1	184.4 bc	4.7 ab	6.6 abcd
4	× a_0b_0	189.2 ab	4.4 b	7.2 ab
5	2 (a_0b_1)	191.8 ab	5.1 a	7.3 a
6	× a_1b_0	184.0 bc	4.6 ab	7.0 abc
7	× a_1b_1	189.3 ab	4.8 ab	6.3 cd
8	× a_0b_0	186.4 abc	4.5 ab	6.5 abcd
9	2 (a_1b_1)	190.2 ab	4.7 ab	6.0 d
10	× a_1b_0	184.4 bc	4.7 ab	6.8 abcd
11	× a_0b_1	195.2 ab	4.8 ab	6.7 abcd
12	× a_0b_0	196.2 a	4.4 b	6.5 abcd
13	2 (a_0b_0)	193.8 ab	4.3 b	6.6 abcd
14	× a_1b_0	184.2 bc	4.4 b	6.8 abcd
15	× a_0b_1	196.3 a	4.6 ab	6.8 abcd
16	× a_1b_1	192.1 ab	4.4 b	6.4 cd
Tukey's HSD (0.05)		11.7	0.6	0.8

* Means followed by a common letter within the same column do not differ significantly at the 0.05% probability level.

to that of the Delta Smooth allele. Although stocks bearing these genes have been disseminated widely, and the genes have been used in breeding programs, there are no formal reports on the effects, if any, of the genes on fiber properties in upland cotton backgrounds. The current report supplies such data taken from estimating the effects of various combinations of smoothness and pilosity alleles in the background of 'Coker 310', a productive, medium-stapled upland cultivar adapted for production in North Carolina and adjacent regions.

MATERIALS AND METHODS

The data reported herein were taken from fiber samples saved from experiments on the influence of plant smoothness on lint percentage and associated traits. Briefly, there were two 4 × 4 complete diallel sets generated from combining, in all possible combinations, the alleles Sm_1^{sl} (a_1) and sm_1 (a_0), and Sm_2 (b_1) and sm_2 (b_0) in the first set, and Sm_2 and sm_2, and Sm_3 (c_1) and sm_3^h (c_0) in the second set. Monomeric and dimeric smooth and normally pubescent parental stocks, $a_1a_1b_0b_0c_0c_0$, $a_0a_0b_1b_1c_0c_0$, $a_1a_1b_1b_1c_0c_0$, and $a_0a_0b_0b_0c_0c_0$ in the first set, and $a_0a_0b_1b_1c_0c_0$, $a_0a_0b_0b_0c_1c_1$, $a_0a_0b_1b_1c_1c_1$, and $a_0a_0b_0b_0c_0c_0$ in the second set, were selected from F_2 populations derived from crossing monomeric smooth stocks that had been fixed in the upland cultivar, Coker 310, the maternal background. A random sample of parental segregates were then intercrossed to generate the diallels. The normally pubescent stock in each diallel set, $a_0a_0b_0b_0c_0c_0$, was designated as the control entry.

The diallels were grown at two locations in North Carolina in 1982 in randomized, complete blocks with four replications per location. Plot size, row width, locations and soil types used are discussed fully in Lee (7) and need not be repeated here.

A 15 g sample of fiber was taken from each plot at each location and sent to the AMS-USDA Fiber Laboratory, Clemson, S.C., where data were taken on the following fiber properties: i) 2.5% fiber span length—the distance in mm on a test specimen spanned by 2.5% of the fibers scanned at the initial starting point; ii) 50% span length—the distance in mm spanned by 50% of the fibers treated as in (i); iii) uniformity index—100 times the ratio of 50% span length to 2.5% span length; iv) tenacity—the force required to break a flat bundle of fibers divided by the linear distance when the jaws of the breaking device are spaced 3.2 mm apart, expressed as kilonewtons per m in kg of force; v) micronaire—a measure of airflow through a specimen of fiber that relates to the surface area of the fibers that is exposed to the air, and vi) elongation—the percentage elongation at breakage of the center 3.2 mm of the fiber bundle assayed for tenacity.

The data were processed through ANOVA to secure error terms for the estimation of Tukey's honestly significant differences, and the sums of squares for entries partitioned for individual degrees of freedom comparisons of general (additive), specific (dominance and epistasis), maternal, and reciprocal (maternal × embryonic) effects according to procedures developed by Cockerham [Lee et al. (9)] who also outlined the expectations for the effects.

RESULTS AND DISCUSSION

Experiment 1

Means and Tukey's honestly significant differences for the various fiber measures are given in Table 1. When entry 13, the normally pubescent control, was used as the standard for comparison, entries 5, 9, and 11 were significantly deficient in 2.5% fiber span length at the 0.05 level of probability. Two of the three were homozygous for b_1 (Sm_2) and the third was heterozygous for the allele. Note that a_1 (Sm_1^{sl}), a gene conferring essentially the same level of smoothness as b_1, was not associated with a reduction in 2.5% span length in the monomeric state (entry 1).

None of the smooth parental entries, 1, 5, and 9, differed significantly from entry 13 in 50% span length. Entry 5, the entry with the lowest 2.5% span length, was nearly equal to the control in 50% span. Apparently the loss in 2.5% span noted in monomeric b_1 was attributable to truncation of fiber span at the upper limits of length distribution, perhaps accompanied by less fiber breakage during ginning, rather

Table 2. Individual degrees of freedom comparisons for fiber properties for Exp. 1; Sm_i^{sl} vs. $sm_1 = a$, and Sm_2 vs. $sm_2 = b$.

Effect	Mean squares for: 2.5% span length	Fiber tenacity	Micronaire	Elongation
General				
α_a	2.33*	1066.83**	0.01	0.02
α_b	12.78**	542.30**	3.71**	2.25**
$(\alpha\alpha)_{ab}$	0.05	1179.90**	0.98**	8.12**
Specific				
δ_a	2.15*	158.11	0.08	0.01
δ_b	2.82**	0.28	0.06	0.18
$(\alpha/\alpha)_{ab}$	2.64**	5.18	0.06	0.60
$(\alpha\delta)_{ab}$	1.05	34.07	0.28**	0.28
$(\alpha\delta)_{ba}$	1.76*	0.44	0.08	0.14
$(\delta\delta)_{ab}$	1.32	0.05	0.01	0.09
Maternal				
θ_a	3.10**	292.33**	0.02	0.81*
θ_b	3.06**	58.31	0.08	0.02
$(\theta\theta)_{ab}$	0.60	124.93	0.01	0.22
Reciprocal				
$(\theta\theta)_{ab}$	0.04	132.51	0.00	0.74*
$(\delta\theta)_{ba}$	0.77	22.82	0.02	0.33
$(\delta\theta\theta)_{aab}$	2.48**	30.44	0.02	0.55
Error (90 df)	0.36	43.11	0.03	0.18

*,** 0.05 and 0.01 level of significance, respectively.

than a general shortening of fibers over much of the span.

The uniformity index of entry 5 was the highest in the array of entry means, and was significantly various from that of the control. When I plotted uniformity index against 2.5% span, entries 5 and 11, both homoygous for b_1, tended to be outliers.

Tenacity measures provided some unanticipated results. Entry 1 displayed significantly lower tenacity than the control entry, and three other entries homozygous for a_1 were intermediate in fiber tenacity. Such a result seems odd in view of the fact that the a_1 allele stems from Coker 413, a cotton that assayed 200.5 $kNmkg^{-1}$ from material grown in the field in 1982. Six backcrosses into Coker 310 seemingly reversed that relationship, associating the a_1 allele with a level of tenacity not acceptable in a quality cotton.

The a_1 allele was fixed in Coker 413 mostly to curtail vegetative trash in ginned lint. Therefore there was no reason to suspect, a priori, that the gene would be associated with either a high or a low level of fiber tenacity. Still, finding the allele associated with low fiber tenacity in Coker 310 background was somewhat of a surprise. Such a result suggests the possibility that the a_1 allele is linked with germplasm that imparts weak fiber on some backgrounds, effects that were masked—apparently reversed—in Coker 413 background. If there is a didactic in the above, it must be that transferring a particular allele, or germplasm linked with the allele, into a new background sometimes results in a phenotype not predictable from the phenotype of the donor stock.

Entry 5 displayed significantly higher micronaire than the control, and the trend was that the higher micronaire counts were associated with entries homozygous for b_1. Ramey (13) stated that micronaire is an indirect measure of the air permeability of a fiber specimen of fixed mass in a chamber of fixed dimensions, the permeability varying inversely as the square of the surface area of the fibers exposed to airflow. Recognizing the relationship outlined above, Lord (11) showed that, given a constant fiber perimeter, micronaire can vary with changes in fiber wall thickness and linear density which change the relative proportions of the cell surfaces exposed in a compressed sample. Therefore, for a given sample, micronaire cannot be interpreted in terms of fiber fineness without additional fiber measures.

Ramey (13) pointed out that there is often a modest negative association between fiber tenacity and fiber perimeter in upland cotton. The fact that the fiber in entry 5 did not suffer a loss in tenacity when compared with the control suggests that the fiber was more mature than that of the control. Still, the introduction of a gene from a "wild" *G. hirsutum* accession into an adapted cotton cultivar affords the potential for novel expressivity. Therefore, in the absence of additional data on fiber fineness, the question as to what caused the perturbation in entry 5 must remain moot.

Mean square estimates for general, specific, maternal, and reciprocal effects for 2.5% span length, tenacity, micronaire, and elongation, along with error terms from the ANOVA tables, are given in Table 2. There were highly significant additive effects associated with both allelic pairs for 2.5% span length. There were also highly significant maternal effects associated with each pair of alleles. Approximately one-half of the primary maternal effects confound estimates of additivity in Cockerham's [Lee et al. (9)] analysis. Maternal effects were large enough to make the additive estimate for the *a* pair suspect, whereas the estimate for the *b* pair appeared to remain robust. Cockerham also showed that significant reciprocal effects tend to confound estimates of dominance and epistatis.

The term (α/α) was significant for 2.5% span length in Table 2, whereas the term $(\alpha\alpha)$ was not. The first term estimates the contribution to additive × additive effects from the *trans* arrangements of doubly-heterozygous entries, and the second the contributions from the *cis* arrangements, i.e., both a_1 and b_1 contributed by the same gamete. The actual contributions by the *cis* and *trans* entries were not various (MS = 0.81). The major difficulty stemmed from the fact that the *trans* entries were sufficiently larger than the *cis* entries to combine with inequalities among parents, particularly that between entries 5 and 9, to produce a significant *trans* effect.

Fiber tenacity showed significant additive effects for both allelic pairs, plus unbalanced contributions for additive × additive effects. There was some evidence for a maternal effect associated with the *a* pair, but probably not enough to confound the primary estimate for additivity.

The *b* pair of alleles displayed a large, highly significant additive effect for micronaire, a highly significant estimate of the a × b term for epistasis, and unbalanced estimates for additive × additive effects. Elongation likewise showed a highly significant additive effect for the *b* pair, unbalanced estimates for additive × additive effects, and some evidence for specific and maternal effects. There was no evidence that elongation tracked degree of plant smoothness.

Table 3. Means and Tukey's honestly significant differences for fiber properties for Exp. 2.

Entry no.	Genotype	3.5% span length	50% span length	Uniformity index
		mm		%
1	2 (b_1c_0)	27.4 d*	13.9 a	49.8 a
2	× b_0c_1	29.0 bc	14.2 a	46.9 bc
3	× b_1c_1	29.6 abc	13.9 a	46.4 bc
4	× b_0c_0	29.9 ab	14.1 a	45.8 bc
5	2 (b_0c_1)	29.3 abc	14.1 a	46.9 bc
6	× b_1c_0	29.2 abc	13.6 a	45.9 bc
7	× b_1c_1	28.9 c	13.5 a	45.4 c
8	× b_0c_0	29.6 abc	13.8 a	45.4 c
9	2 (b_1c_1)	29.4 abc	13.8 a	46.3 bc
10	× b_1c_0	28.8 c	14.1 a	48.1 ab
11	× b_0c_1	29.7 abc	13.8 a	45.4 c
12	× b_0c_0	29.4 abc	13.6 a	45.8 bc
13	2 (b_0c_0)	30.1 a	14.0 a	45.6 c
14	× b_1c_0	30.0 a	14.3 a	46.8 bc
15	× b_0c_1	29.9 ab	13.9 a	45.5 c
16	× b_1c_1	29.4 abc	13.7 a	45.5 c
Turkey's HSD (0.05)		0.9	0.9	2.3

Entry no.	Genotype	Tenacity	Micronaire	Elongation
		$kNmkg^{-1}$	$\mu g\ in^{-1}$	%
1	2 (b_1c_0)	192.8 a*	5.3 a	7.4 a
2	× b_0c_1	182.8 ab	4.7 cde	6.8 bcde
3	× b_1c_1	186.9 ab	5.1 ab	6.5 ef
4	× b_0c_0	188.0 ab	4.7 cde	6.8 bcde
5	2 (b_0c_1)	195.0 a	4.6 cde	6.7 cdef
6	× b_1c_0	189.7 ab	4.6 cde	6.9 bcd
7	× b_1c_1	187.5 ab	4.6 cde	6.9 bcd
8	× b_0c_0	189.8 ab	4.5 de	7.0 bc
9	2 (b_1c_1)	178.3 b	5.1 ab	6.4 f
10	× b_1c_0	186.8 ab	5.1 ab	7.1 ab
11	× b_0c_1	185.3 ab	4.6 cde	6.4 f
12	× b_0c_0	183.2 ab	4.9 bc	6.6 def
13	2 (b_0c_0)	190.8 ab	4.4 e	6.7 cdef
14	× b_1c_0	187.3 ab	4.8 cd	6.6 def
15	× b_0c_1	188.7 ab	4.5 de	6.9 bcd
16	× b_1c_1	186.6 ab	4.8 bcd	6.6 def
Tukey's HSD (0.05)		12.5	0.3	0.3

* Means followed by a common letter within the same column do not differ significantly at the 0.05% probability level.

The presence of significant maternal and reciprocal effects with the current material came as somewhat of a surprise. Although the maternal parent, Coker 310, is not known to be a pure line, variations in cytoplasmic expression within such a cultivar are not expected. Nonetheless, the evidence, although not overwhelming, is there.

Experiment 2

Means and Tukey's honestly significantly differences for the various fiber measures for the second experiment are given in Table 3. Fiber length—2.5% span—averaged 1 mm longer in Exp. 2 than in Exp. 1, a difference that equalled, or exceeded, the HSDs for the trait in the two trials. Entry 1, the b_1 monomeric, displayed significantly lower 2.5% span length than any other entry in the array. Three other entries, 2, 7, and 10, all either homozygous or heterozygous for b_1, also differed significantly from entry 13, the control. Thus the b_1 allele was associated with reduced 2.5% span length in both experiments even though the parental monomerics were prepared through somewhat divergent routes. As in Exp. 1, the b_1 monomeric displayed higher uniformity index than most of the remaining entries.

Table 4. Individual degrees of freedom comparisons for fiber properties for Exp. 2; Sm_2 vs. $sm_2 = b$, and Sm_3 vs. $sm_3^h = c$.

Effect	Mean squares for: 2.5% span length	Fiber tenacity	Micronaire	Elongation
General				
α_b	13.87**	384.16**	5.82**	2.10**
α_c	0.00	160.97	0.24**	0.08
$(\alpha\alpha)_{bc}$	11.47**	370.56**	0.00	1.96**
Specific				
δ_b	1.01	136.33	0.32**	0.16
δ_c	0.01	33.92	0.03	0.03
$(\alpha/\alpha)_{bc}$	4.25**	326.71**	0.42**	0.30**
$(\alpha\delta)_{bc}$	2.18**	96.63	0.03	0.29**
$(\alpha\delta)_{cb}$	6.06**	62.21	0.13*	0.20
$(\delta\delta)_{bc}$	5.28**	0.51	0.11	0.00
Maternal				
θ_b	0.18	190.10	0.05	0.23
θ_c	0.87	5.18	0.00	0.79**
$(\theta\theta)_{bc}$	0.15	17.12	0.06	0.02
Reciprocal				
$(\delta\theta)_{bc}$	2.14**	0.16	0.01	0.53**
$(\delta\theta)_{cb}$	0.72	120.72	0.03	0.11
$(\delta\theta\theta)_{bbc}$	1.79**	2.76	0.10	0.32**
Error (90 df)	0.24	48.95	0.03	0.07

*,** 0.05 and 0.01 level of significance, respectively.

None of the entries in the second experiment differed significantly from the control in fiber tenacity. Even so, I found it difficult to reconcile the low tenacity of entry 9, the dimeric smooth entry, with the significantly higher tenacity of entries 1 and 5, the monomerics for b_1 and c_1 respectively. Based upon the evidence at hand, one might conclude that the increased smoothness from combining b_1 and c_1 in the homozygous state had a negative effect upon fiber tenacity. However, the effct could not have been general because the equally smooth dimeric entry in Exp. 1 did not differ significantly from the control in that trial and exceeded the tenacity of the lowest parent. Thus the results from the two experiments are contradictory.

As in Exp. 1, high micronaire tracked entries homozygous for b_1, and presumably the causes for the increased micronaire values were the same. Elongation was significantly various among entries, and, again, there was no evidence that changes in elongation tracked degree of plant smoothness.

Individual degrees of freedom comparisons for 2.5% span length, tenacity, micronaire, and elongation, along with error terms, are given in Table 4. As in Exp. 1, the *b* pair of alleles displayed highly significant additive effects for 2.5% span length. Moreover, there were balanced and significant estimates for additive × additive effects. However, the highly significant estimates for reciprocal effects cast doubt upon the validity of the significant estimates for epistatis.

There was a highly significant estimate of additive

effects for fiber tenacity for the *b* pair of alleles and balanced additive × additive effects. The significant additive effects for the *b* pair of alleles seems curious in light of the fact that the parental entries 1 and 13 had essentially equal tenacity means. The significant additive estimate arose from the fact that the average of the entries homozygous for b_1 was significantly less than that of the entries homozygous for b_0, there being an especially large contribution from entry 9, the only entry in the array with exceptionally low tenacity. The apparently aberrant behavior of entry 9 also generated the large additive × additive interactions terms.

There was a large, highly significant, estimate of additive effects for micronaire with the *b* pair of alleles, and a lesser, though still significant, estimate for the *c* pair. Curiously, the latter was caused mostly by the relatively large contribution of entry 1, which was also responsible for the disequilibrium in the additive × additive effects.

The only seemingly valid estimate of general effects for elongation in Experiment 2 was significant additivity for the *b* pair of alleles. The b_1 allele was thus related to most of the disturbances in elongation noted in both experiments, but even then not all entries homozygous for b_1 showed increased elongation.

General Conclusions

In both experiments the b_1 (Sm_2) allele, or possibly germplasm linked with the gene, conditioned significant departures from the control in 2.5% span length, uniformity index, micronaire, and elongation (this report) and in lint percentage in an earlier report (7). The a_1 (Sm_1^{s1}) allele was associated with a lesser effect upon lint percentage (7), and, rather surprising, I thought, a large effect upon fiber tenacity. The third smoothness allele, c_1 (Sm_3), was not associated with significant effects upon either fiber properties or lint percentage when compared with the control entry.

There was scant evidence that variations in fiber properties related directly to level of plant smoothness. Entry 9 in Table 3, $2(b_1c_1)$, did assay an unexpectedly low level of tenacity, but the equally smooth entry 9 on Table 1, $2(a_1b_1)$, had tensile strength not inferior to the control and significantly higher than the a_1 parent. Therefore, the contribution of degree of plant smoothness to this one fiber trait remains moot. For the other properties sampled there is good reason to believe that the disturbances noted related mostly to two of the alleles that imparted glabrousness and not to the degree of smoothness imparted by the genes, or combinations thereof.

Although there was no consistent evidence that degree of plant smoothness altered fiber properties in any specific way, the question of whether or not the alterations recorded were attributable to pleiotropic effects of the genes in question or to linked germplasm remains moot. However, the fact that b_1 is associated with various quality deficits after many generations of backcrossing and some pedigree selection would seem to provide a strong argument for pleiotropic effects for that particular allele. Still, I know of no intensive efforts to match the gene with better gin out-turn and fiber properties. Knowledge of the deficits likely to be encountered should be helpful in choosing a scheme for dealing with the problems. Perhaps the intermating techniques proposed by Miller and Rawlings (12) would be a productive alternative to backcrossing.

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