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Characterization and Performance Evaluation of Frego Bract Isolines of Cotton[1]

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ABSTRACT

The effect was measured statistically of introgressing the morphological character frego bract *(fg)* into a cotton (*Gossypium hirsutum* L.) genetic standard Texas Marker-1 (TM-1) to evaluate the performance of two isolines. Two frego bract *(fg)* sources and their normal-allele *(Fg)* counterparts were synthesized into TM-1 isolines through a multiple backcross and selfing program. Five sub-lines were isolated within each isoline. The sub-line within each isoline did not vary significantly. Tests of the isolines showed that they differed significantly in seven of the 13 agronomic characters measured (date of first flower, seed cotton yield, lint yield, boll size, seed index, lint percentage, and lint index). The introgression of frego bract *(fg)* into the standard background delayed the date of first flower (indicating lateness) and reduced boll size, lint percentage, and lint index. The other three characters, seed cotton yield, lint yield, and seed index, were affected by the TM-1 background of the isolines.

Additional index words: **Pleiotropy, Breeding for insect and disease resistance.**

IN cotton (*Gossypium hirsutum* L.), frego bract *(fg)* (Green, 1955) is classified as a simply inherited recessive mutant that causes narrow, literally rolled bracts when homozygous and bracts intermediate between frego and normal when heterozygous. The morphological change in the bract caused by homozygous frego bract imparts resistance to boll weevil (*Anthonomus grandis* Boheman) (Jones et al., 1964; Lincoln and Waddle, 1965; Jenkins and Parrott, 1971) and boll rot resistance (Jones et al., 1968-1969) to cottons having this character. However, undocumented reports persist that breeders using frego bract in their programs have found that frego bract cottons were late and susceptible to the lygus bugs (*Lygus* spp.) and cotton fleahopper (*Pseudatomoscelis seriatus* Reuter). The study reported in this paper was designed to (1) isolate frego bract *(fg)* and its normal allele *(Fg)* in isolines (Atkins and Mangelsdorf, 1942) to evaluate the pleiotropic or linkage effects of frego bract; and (2) help to determine the influence of this character in a breeding program. However, the disadvantage of testing only on one genetic background should not be overlooked. The same test using other cultivars with different genotypes might have different effects.

MATERIALS AND METHODS

Isolines carrying frego bract *(fg)* from two sources and their normal allele *(Fg)* were synthesized by a multiple backcross method that had Texas Marker-1 (TM-1) (Kohel et al., 1970) as the recurrent parent. TM-1 was introduced in its 29th generation of inbreeding. The first frego bract source (A) was obtained from the collection maintained at College Station, Tex. which traces to the original frego bract mutant found in Arkansas in 'Stoneville 2B.' The second frego bract source (B) was found in plants from a production field of 'Deltapine Smooth leaf.' A frego bract A plant was crossed to TM-1, and for each of seven generations a heterozygous frego bract plant was backcrossed to TM-1. One heterozygous plant was then selected and selfed, from which S_1 seeds were recovered. These S_1 seeds were then grown at College Station, where segregating S_1 plants of frego bract *(fg)* and normal bract *(Fg)* were selfed. S_2 seeds were recovered and grown at Iguala, Mexico as S_2 plants. From these S_2 plants five plants of each type were randomly selected and selfed to provide S_3 (sub-lines) seeds for a performance test at College Station. The same scheme was used to isolate the S_3 frego bract (B) sub-lines, except that only five backcrosses were made. TM-1 was grown and selfed each generation of the isolation scheme.

A performance test was grown in the cotton genetics nursery of the Texas Agric. Exp. Stn. Brazos Valley Farm at College Station. Excellent insect control was maintained at this location, and thus we avoided confounding the test variables with the effect of insect susceptibility.

Each entry (isolines or genotypes of frego bract and their normal counterparts) of sources A and B and the TM-1 recurrent parent were grown in five-row (sub-lines) plots, with each row 1 × 10 m. The test was replicated four times. The five sub-lines within each entry were grown to estimate the genetic variability within each isoline and in the TM-1 recurrent parent. Thirteen agronomic characters were measured: (1) Date of first flower, with 1 January = day 1; (2) Seed cotton yield, from total seed cotton weight (g); (3) Lint yield, total lint weight (g); (4) Percent first harvest, percent of total yield harvested on the first pick; (5) Boll size, mean weight of seed cotton (g) from a 10-boll sample; (6) Seed index, weight (g) of 100 seed (two lots of 50 seed); (7) Lint percentage, ratio of lint to seed cotton expressed as a percentage; (8) Lint index,

Table 1. ANOVA model A to test the genetic variability within sub-lines of isolines of cotton introgressed with two frego bract sources and the TM-1 recurrent parent.

Source of variation	df†	EMS	F
a Reps	3	$\sigma^2_\epsilon + 25\,\sigma^2_R$	
b Entries (Isolines)	4	$\sigma^2_\epsilon + 5\,\sigma^2_S + 5\,\sigma^2_{R\times E} + 20\,\sigma^2_E$	b/(c+d−e)
c Reps × Entries	12	$\sigma^2_\epsilon + 5\,\sigma^2_{R\times E}$	c/e
d Sub-lines (within entries)	(20)17	$\sigma^2_\epsilon + 4\,\sigma^2_S$	d/e
e Reps × Sub-lines (within entries)	(60)46	σ^2_ϵ	
Total	(99)82		

† Numbers in parentheses are degrees of freedom with no missing data.

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weight (g) of lint from 100 seeds; (9) Micronaire, a measure of fiber fineness in micronaire units (smaller number = finer fiber); (10) T_1, the breaking strength (mN/tex) of a fiber bundle measured with a 3.2-mm gage stelometer; (11) E_1, percentage elongation of the fiber bundle before breakage; (12) and 13) 2.5 and 50% span length, the length (mm) at which the given percentage of fibers in an array are that long or longer.

The ANOVA model A (Table 1) allowed the test for genetic variability within the entries. Kohel and Richmond (1971) found significant variation within entries even after eight generations of backcrossing, and thus we expected variation within entries in this test. In ANOVA, model B (Table 2) the sub-lines (within entries) were pooled as sources of variability into the error term to strengthen the power of the test for the other sources of variability.

RESULTS AND DISCUSSION

The ANOVA model A showed no significant variation within entries among sub-lines indicating that genetic stability had been attained in these entries for the 13 agronomic characters measured. (In retrospect this result was not unusual as both frego selections and TM-1 were derived from Delta-type cottons that were probably stable and similar to begin with.)

ANOVA model B showed that the entries (genotypes) differed significantly for seven of the 13 characters measured: date of first flower, seed cotton yield, lint yield, boll size, seed index, lint index, and lint percentage (Table 3).

Table 2. ANOVA model B to test the genetic variability among isolines of cotton introgressed with two frego bract sources and the TM-1 recurrent parent.

Source of variation	df†	EMS	F
a Reps	3	$\sigma^2_\epsilon + 25\,\sigma^2_R$	a/d
b Entries	4	$\sigma^2_\epsilon + 5\,\sigma^2_{R\times E} + 20\,\sigma^2_E$	b/c
c Reps × Entries	12	$\sigma^2_\epsilon + 5\,\sigma^2_{R\times E}$	c/d
d Reps × Sub-lines	(80)63	σ^2_ϵ	
Total	(99)82		

† Numbers in parentheses are degrees of freedom with no missing data.

Four nonorthogonal contrasts were used to compare the performance of the entries (isolines and TM-1) (Table 4). The significance of contrasts (a) and (c) and the nonsignificance of contrasts (b) and (d) would indicate pleiotropic or tight linkage effects.

A later date of first flower and a lower lint index were associated with frego bract. The delay in flowering by 1 to 2 days might not appear agronomically important, but the consequence was visually apparent at maturity. Percent of total yield at first harvest, another measure of lateness, probably would have confirmed this effect. However, we could not detect a difference because fall rains caused us to telescope the three harvests, which led to a confounded interpretation of the data. The two frego bract lines had significantly lower lint indexes than the normal isolines, which showed that the presence of frego bract caused a reduction in lint production per unit area of seed (Table 4).

Frego bract had no obvious effect on seed cotton yield, lint yield, and seed index. The comparison (b) of normal (*Fg*) vs. TM-1 was significant for the first two characters, and the comparison (a) of normal (*Fg*) vs. frego bract (*fg*) was nonsignificant for all three of these characters (Table 4). This result is the reverse of what would have been expected if frego bract had a direct influence on these characters.

The frego bract isolines had the smallest bolls, the normal counterparts had intermediate-sized bolls, and TM-1 had the largest bolls (Table 5). Jones et al. (1968-1969) also found that frego bract reduced boll size. TM-1 is noted for large bolls, so it is not unusual to find its bolls significantly larger than those of other cottons. The boll size of the normal (*Fg*) counterparts did not reach that of TM-1 in seven backcross generations, indicating that other genes on other chromosomes influenced this character. Reduced boll size of the frego isolines unaccompanied by reduced seed cotton and lint yield showed a compensation in produc-

Table 3. Mean squares of the 13 agronomic characters measured from ANOVA model B for cotton entries.

	df	Date first flower	Seed cotton yield	Lint yield	First harvest	Boll size	Seed index	Lint index	Lint	Micronaire [fineness]	T_1 [strength]	E_1 [Elongation]	2.5% span length	50% span length	F
					%				%						
a Reps	3	7.7654	94,446.0	9,372	137.95*	140.30**	6.55**	1.24**	2.01*	0.7183**	1.2858	0.4710	0.0009**	0.0011**	a/d
b Entries	4	15.5811**	214,776.0*	20,942*	8.19	108.45*	6.56*	2.53*	4.70**	0.0624	1.0693	0.5742	0.0012	0.0015	b/c
c Reps × Entries	12	2.3525	50,125.0	5.259	230.04**	20.32	1.55*	0.28**	0.17	0.1312*	0.5038	0.3383	0.0004*	0.0005**	c/d
d Error (Sub-lines within Entries × Reps)	(80)63†	3.4735	143,632	14,240	43.71	23.25	0.66	0.11	0.72	0.0607	0.6453	2.2004	0.0002	0.0002	
Total	(99)82†														

*,** Mean squares significantly different at the 0.05 and 0.01 levels, respectively. † Numbers in parentheses are degrees of freedom with no missing data.

Table 4. Contrasts of isolines (entries) and the TM-1 recurrent parent for the agronomic characters that were significantly different.

Contrasts	Date 1st flower	Total seed cotton	Lint yield	Boll size (S.C. wt. 10 bolls)	Seed index	Lint	Lint index
						%	
a Fg (Normal) vs. fg (frego)	**	NS	NS	*	NS	**	**
b Fg (Normal) vs. TM-1 (Normal)	NS	**	**	*	NS	*	NS
c fg (frego) vs. TM-1 (Normal)	**	**	**	**	**	NS	**
d fg (A frego) vs. fg (B frego)	NS	NS	NS	NS	NS	**	NS

*,** Mean squares significantly different at the 0.05 and 0.01 levels, respectively.

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Table 5. Mean performance of entries and a commercial check.

	Date first flower	Seed cotton yield	Lint yield	Boll size	Seed index	Lint	Lint index
						%	
fg(A)	194.4	1,900	573	54	12.2	30.2	5.2
fg(B)	195.4	1,881	589	55	12.1	31.1	5.4
Fg(A)	193.3	1,887	580	56	12.3	30.7	5.5
Fg(B)	193.5	1,922	605	57	13.1	31.5	6.0
TM-1	193.6	2,127	652	60	13.3	30.8	5.9
DPL-16†	192.6	2,492	908	57	10.8	36.5	6.1

† DPL-16, 'Deltapine 16,' was added to compare test entries with a currently grown commercial variety.

tion through increased boll number. The many generations of inbreeding of TM-1 with no selection to maintain agronomic performance has resulted in fewer and larger bolls through a transfer of energy from lint production to seed production (Kohel et al., 1970). Thus, reduction in boll size in the isolines was due to the genetic contributions of parental sources A and B as well as to the effects of the frego bract allele.

The contrast (a) (Table 4) of normal (*Fg*) vs. frego bract (*fg*) was significant for lint percentage. Means (Table 5) showed that frego bract was associated with lower lint percentage. Thus, the presence of homozygous frego bract influenced a quantitatively inherited character. The contrast (c) of frego bract vs. TM-1 was not significant for lint percentage. The means of the two frego bract entries were in opposite directions (A below and B above TM-1) and they cancelled one another. The B frego bract isoline was significantly higher than the A isoline, contrast (d), probably because five backcrosses were not enough to eliminate background effects. This result is contrasted with that in isolines from the A source in which seven backcrosses produced the desired result. Contrast (b), normal (*Fg*) vs. TM-1, was significant because the normal bract B isoline had a higher lint percentage, again attributed to residual background effects. The parental differences (entries source of variation in Table 2) in lint percentage were thus probably due to the effect of the frego bract allele added to the effects of quantitative genes distributed among the chromosomes. It was likely that the latter were numerous and each of small effect in influencing lint percentage because no significance was detected among sub-lines. Linkage associations were not apparent because both genotypes (*Fg* and *fg*) of the B source had lower lint percentages than the commercial cultivar from which they were extracted.

The deleterious agronomic effects to maturity, boll size, lint index, and lint percentage due to frego bract are apparently small enough that they do not negate the beneficial effect of boll weevil resistance. Breeders using frego bract in their improvement programs have thus probably compensated for deleterious effects through selection for complementary agronomic types and sources of plant bug resistance.

No significant variability of lines within genotypes was found, indicating that a good set of isolines was developed. This fact would strengthen the probability of frego bract having pleiotropic effects on the characters date first flower, boll size, lint percentage, and lint index.

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