A Genetic Study of Number of Involucral Bract Teeth in Cotton[1]

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ABSTRACT

Texas 207 is a photoperiodic accession of cotton, *Gossypium hirsutum* L., that has many toothed involucral bracteoles (bracts) that enclose the flower bud more completely than do the few-toothed bracts of modern cultivars. This character could possibly be of value in deterring small insects, such as thrips, *Frankliniella* spp., from damaging very small flower buds. The inheritance of number of bract teeth was studied in a series of crosses with Texas 207 as one founder parent ($\bar{X}$ = 17.3 teeth/bract) and a cultivar, Stoneville 7A (St 7A) as the other ($\bar{X}$ = 8.7). From a cross of a day neutral selection of (T-207 × St 7A) with St 7A, quantitative and qualitative genetic analyses taken together suggested that those two parents differed by at least three pairs of genes which acted additively in concert. Narrow-sense heritability, estimated in F_2 on a plant basis, was 46%. I failed to transfer a high number of bract teeth into the 7A background apparently because certain advanced-generation populations from backcrosses to St 7A were too small to recover the many bract-teeth phenotype. However, the genetic analyses suggest that it should be possible to recover that phenotype by growing larger populations of BC_nF_2.

Additional index words: Gossypium hirsutum L., Host plant resistance, Quantitative inheritance, Additive variance, Heritability.

I N a search for characters of possible value for resistance to insects in cotton, *Gossypium hirsutum* L., I observed a photoperiodic race stock, Texas 207 (T-207) that possessed normal-sized involucral bracteoles (hereafter referred to as bracts) that have many more bract teeth than do those of commercial cultivars. In T-207, the bracts enclose the flower bud more completely than in the cultivars examined. This character could possibly afford better protection to very small flower buds from the attack of small insects such as thrips, *Frankliniella* spp. (6).

Subsequently, I attempted to transfer the high number of bract teeth character into a cultivar background, while simultaneously studying the inheritance of this character. Number of teeth per bract, along with other characters studied previously (9,10,11), seemed to provide model genetic systems which could be studied both quantitatively and qualitatively.

The inheritance of number of bract teeth apparently has not been reported previously. Bridge (2), however, observed genetic variability for number of bract teeth among 17 cultivars of upland cotton. A related trait, bract size (area), has been studied in some detail because bract trash in lint has been implicated in byssinosis, a lung disease associated with textile mill employees (cf. 1 for earlier references).

The objectives of the studies reported in this paper were to determine 1) the inheritance of number of bract teeth and 2) the ease of transfer of a high number from a primitive race stock into an improved agronomic background to study its effect on insect attack.

MATERIALS AND METHODS

Texas 207 (T-207) is a photoperiodic stock of *G. hirsutum* "race" *latifolium* collected by C.W. Manning and J.O. Ware in Guatemala in 1948 (M. W. 67; PI 163666). I crossed T-207 to several cultivars, among them 'Stoneville 7A' (St 7A) in a greenhouse at the Western Cotton Research Laboratory, Phoenix, AZ, during 1974-1975. At that time, I noticed that T-207 had many teeth per bract ($\bar{X}$ = 17.3) and St 7A had relatively few ($\bar{X}$ = 8.7). Number of teeth per bract was estimated by counting the teeth on all three bracts of one or two large squares per plant. These squares were taken from an upper sympodium of plants at the peak stage of flowering.

Soil type in the field at Phoenix, where the plants were grown, was Avondale clay loam (fine-loamy, mixed [calcareous], hyperthermic Typic Torrifluvent). The 20 plants of (T-207 × St 7A) F_1 did not flower in the field in 1975, so they were pruned, uprooted, and moved into the winter greenhouse for seed production. An F_2 population of 131 plants grown in the field in 1976 arose from one F_1 plant. In that F_2, 49 plants flowered; of those, 11 had the number of teeth per bract in the range of St 7A and eight had the number in the range of T-207.

One F_2 plant was selected for few bract teeth, and one was selected for many bract teeth (Table 1). All F_3 plants from the two selected F_2 plants flowered in the field in 1977. The F_3 plant, from the many bract-teeth population, that had the highest number of bract teeth was designated $P_{1,1}$. It was used in two crosses (Table 1), as follows: Cross 1 = $P_{1,1}$ × $P_{2,1}$ [$P_{2,1}$ = St 7A $\bar{X}$ = 8.7]; Cross 2 = $P_{1,1}$ × $P_{2,2}$ [$P_{2,2}$ = the (T − 207 × St 7A) F_3 plant, from the few bract-teeth population, that had the fewest teeth per bract.] The F_1 plants from Crosses 1 and 2 were grown at the National Cotton Council winter nursery in Mexico in 1977-1978 and were selfed and backcrossed to the parents involved in each cross.

In 1978, six generations from Crosses 1 and 2 were grown in the field at Phoenix in unreplicated rows; plants were spaced 46 cm apart in rows 1 m wide. Generations were designated as follows: P_1 = the many toothed parent; P_2 = St 7A or the few toothed parent; B_1 = the backcross to the many toothed parent; B_2 = the backcross to St 7A or to the few toothed parent; F_1 and F_2 generations from Crosses 1 and 2 were also grown. All plants were scored for number of bract teeth. Also in 1978, a backcrossing program was initiated to transfer few and many bract teeth into the St 7A background.

Cross 3, $P_{1,3}$ × $P_{2,3}$, was made in 1982. The $P_{1,3}$ parent was a plant (which originated from T-207 × St 7A) from the many toothed BC_3F_2 ($\bar{X}$ = 11.9) and $P_{2,3}$ was one from the few toothed BC_4F_2 [$P_{2,3}$ ($\bar{X}$ = 8.0)]. The F_1 plants from Cross 3 were selfed and backcrossed to both parents in Mexico in 1982-1983. The six generations were grown at the Arizona State University Farm Laboratory (ASU) in 1983 in the same-sized plots as in 1978 and scored for number of bract teeth. Soil type at ASU is Contine clay loam (fine, mixed, hyperthermic Typic Haplargid).

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Table 1. Number of teeth per bract in parents and selections of cotton plants.

| | | | Teeth/bract | |
			Few	Many
Parent or hybrid	Generation	Year	Mean no. ± SE†	
Texas 207 (T-207)	P_1	1976–1977	–	17.30 ± 0.40
Stoneville 7A (St 7A)	P_2	1976	6.13 ± 0.21	–
(T-207 × St 7A)	F_2	1976	6.33	17.67
St 7A	[$P_{2,1}$‡]	1977	8.39 ± 0.11	–
(T-207 × St 7A)	F_3	1977	7.47 ± 0.53 [$P_{2,1}$§]	15.89 ± 0.27 [$P_{1,1}$‡§]
(T-207 × St 7A)	F_4	1978	10.58 ± 0.31	16.33 ± 0.43
(F_4 × St 7A)	BC_1F_2	1979	7.50 ± 0.30	16.33 ± 0.45
(BC_1F_2 × St 7A)	BC_2F_2	1980	7.58 ± 0.20	15.03 ± 0.19
(BC_2F_2 × St 7A)	BC_3F_2	1981	7.70 ± 0.18	11.89 ± 0.42 [$P_{1,3}$¶]
(BC_3F_2 × St 7A)	BC_4F_2	1982	7.14 ± 0.22 [$P_{1,3}$¶]	–

† Means accompanied by their standard errors (SE) are means of all the selected plants of a given progeny, while those unaccompanied by standard errors are means of the single plants in F_2 that were selected for crossing or carrying forward.

‡, §, ¶ Parents of Cross 1, 2, and 3, respectively.

A generation-mean analysis (5,7) was performed for the six-generations from Cross 1, but not from the other two crosses because $P_{2,2}$ and $P_{1,3}$ probably were not homozygous.

For Cross 1, the formula of Cavalli-Sforza and Bodmer (3) was used to estimate the number of genes conditioning bract teeth inheritance: $[1/2\ (\overline{P}_1 - \overline{P}_2)]^2\ /2V_A$, where $\overline{P}_1$ and $\overline{P}_2$ are the parental means and V_A is the additive genetic variance, calculated as follows: $V_A = 2\ V_{F_2} - (V_{B1} + V_{B2})$. An independent estimate of gene number was made by calculating the frequency of occurrence of the St 7A phenotype in the F_2 and testcross (backcross to St 7A) populations (4). Chi-square tests were used to test the goodness of fit of calculated to expected segregation ratios. Both of these estimates of gene number assume equal effects for all genes, no linkage, and no nonadditive genetic effects. Narrow-sense heritability was estimated using the following formula: V_A/V_{F_2}. No attempt was made to estimate number of genes or heritabilities in Crosses 2 and 3.

RESULTS

Selection for few bract teeth was apparently effective through BC_4, but the F_4 mean was inexplicably anomalous (Table 1). On the other hand, the many bract teeth phenotype of T-207 was not recovered past F_2. An apparently stable phenotype with significantly fewer bract teeth was selected in F_3 and carried through F_4 and BC_1F_2 (T-207 = 17.30, F_3 = 15.89; t = 2.71, P < 0.01, 55 df). Means declined thereafter.

Generation-mean analysis of Cross 1 showed that only the additive genetic effect was significant (Table 2). The narrow-sense heritability estimate was 46%. According to the Cavalli-Sforza and Bodmer formula, estimated number of genes was 2.4. From the frequency-distribution analysis, the observed testcross ratio of 7:1 (3-gene model) agreed well with this estimate, but the observed F_2 ratio of 9.6:1 did not fit well either a 15:1 (2-gene) or the expected 63:1 (3-gene) ratio (Table 3).

DISCUSSION

Results of early crosses indicated that it should have been relatively easy to transfer both high and low numbers of bract teeth into a St 7A background. In (T-207 × St 7A) F_2 (49 flowering plants) and in BC_1F_2 to St 7A (160 plants), 16 and 8%, respectively, of the plants were selected that apparently had as many teeth

Table 2. Number of teeth per bract in parental and hybrid generations of three crosses and a generation-mean genetic analysis of Cross 1.

| Parent or hybrid generation | Cross† | | | | | |
| | 1 | | 2 | | 3 | |
	N	Bract teeth	N	Bract teeth	N	Bract teeth
		Mean ± SE		Mean ± SE		Mean ± SE
P_1‡	20	16.33 ± 0.43	20	16.33 ± 0.43	38	10.86 ± 0.14
B_1	20	14.25 ± 0.58	99	14.82 ± 0.20	213	10.93 ± 0.08
F_1	66	12.63 ± 0.33	54	14.90 ± 0.29	42	9.81 ± 0.19
F_2	361	12.50 ± 0.14	128	15.45 ± 0.16	213	9.67 ± 0.11
B_2	184	11.47 ± 0.14	159	12.47 ± 0.16	210	8.72 ± 0.08
P_2‡	40	8.54 ± 0.23	20	10.58 ± 0.31	38	8.02 ± 0.18

| Source | Genetic effects |
	Mean ± SE
Additive (A)	3.90 ± 0.24**
Dominance (D)	4.37 ± 3.85
Epistasis:	
(A × A)	1.43 ± 1.32
(A × D)	−2.24 ± 1.30
(D × D)	−2.75 ± 2.60

** Genetic effect significant at the 0.01 level of probability.

† Crosses 1 and 2 were made in 1977; parental and hybrid data were obtained in 1978. Cross 3 was made in 1982; data were obtained in 1983.

‡ See Table 1 for parents of Crosses 1, 2, and 3.

Table 3. Segregation ratios for number of bract teeth in cross 1.

| | Generation | |
Comparison	F_2	B_2
	No. plants	
In St 7A (P_2) range	34	27
Above P_2 range	327	157
Chi square	146.30 (63:1)	0.80 (7:1)
P	<0.01	0.40–0.30

per bract as did T-207. Also, 22% of the F_2 plants had no more teeth per bract than did St 7A. Subsequent experience showed that it was easy to retain the few toothed phenotype. However, no plants in the F_3 or in subsequent generations had as many bract teeth as did T-207. On the other hand, the stable many toothed phenotype selected in F_3 averaged only one bract tooth per bract lower than the T-207 phenotype but had twice as many bract teeth as did St 7A.

Apart from my failure to recover the desired high-parent genotype after the first backcross to St 7A, the data yielded some genetic information that allowed me to postulate the inheritance pattern of

number of bract teeth in Cross 1. The combined results from the generation-mean analysis (additive effects only) with those of the testcross segregation ratio of 7:1 and estimated gene number of 2.4, led to the predicted genotype $AABBCC$ for $P_{1,1}$ and $aabbcc$ for $P_{2,1}$. This conclusion assumes that the parents were homozygous and that all three pairs of genes segregating in cross 1 contributed equally to the bract teeth phenotype.

For Crosses 2, and 3, it is evident that the parents differed genetically but the possibility of parental heterozygosity did not allow me to partition the genetic effects.

Even though this genetic analysis is probably simplified and approximate, the results support the idea that the day-neutral, many bract teeth segregate of (T-207 $\times$ St 7A $= P_{1,1}$) differed from St 7A in at least three gene pairs that acted additively. According to Sedcole (8), 191 F_2 plants would have to be grown to provide a 95% chance (assuming 100% heritability) of recovering one plant having the parental genotype in the 3-gene system indicated by the data from Cross 1. Obviously, the BC_2F_2 and BC_3F_2 populations (81 and 144, respectively) were too small to recover the desired genotype. Therefore, it should be possible to incorporate a high number of bract teeth in St 7A background by growing larger backcross populations in the future. Judging from results in BC_1F_2, a BC_nF_2 population of ca. 160 plants should be sufficient to recover the high bract teeth phenotype of 16 + bract teeth per bract. Apparently a larger population, however, would be needed to recover the T-207 phenotype.

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