

**RESEARCH REGARDING THE GENETIC CONTROL
OF THE MAIN AGRONOMICALLY USEFUL GENETIC TRAITS IN COTTON**

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Abstract

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The cotton involves a large quantity of useful variability. The experiments have been performed during 2000-2001, in Romania, at ARDS Teleorman, Branceni center and had in view the elucidation of some aspects regarding the genetic control of the main agronomically useful quantitative genetic traits in cotton. Ten parental genotypes in C_7 in-breeding generation and 45 direct hybrids obtained by $n(n-1)$ diallel crossing in F_1 generation were tested. The results led to the hypothesis that the genetic control of the main traits in cotton is of type: total dominance for the insertion height of the first sympodium expressed in nodes; partial dominance for the distance between cotyledonal node and insertion one of the first sympodium (cm) and for the fiber length; overdominance for the weight of early yield from the total one, early yield, capsule weight, fiber content and total yield. The tested traits have large heritability excepting the capsule weight. The results are strictly available for the utilized genitors.

Key words: cotton, earliness, genetic control, raw cotton yield, fiber content, fiber length, capsule weight

Introduction

The cotton contains a large quantity of genetic variability (Miller, 1959; Murray and Verhalen, 1970; Baker and Verhalen, 1973). Meredith (1984) presents the relative weight of additive and dominance components as well as dominance degree obtained by different researchers in some quantitative genetic traits in cotton. So, White and Kohel (1964) communicate complete dominance for cotton yield while Al-Rawii and Kohel (1964) partial one and Verhalen (1971) overdominance for the same genetic trait. Similar results are quoted for other traits, too: fiber content, capsule weight and fiber length. In the case of *Gossypium hirsutum* x *Gossypium barbadense* L. interspecific crossing, the study of Ana Stoilova (1987) shows that the transmission of the insertion node of the first sympodium is closely correlated with heterosis effect, more rarely with genitor partial dominance.

Thus, the statistical results regarding the heredity mechanisms of a given genetic trait are available only for the tested biological material

MATERIAL AND METHODS

During 2000-2001, at ARDS Teleorman, Branceni center, experiments with 10 cotton lines (C_7) and their direct hybrids in F_1 generation, obtained by $n(n-1)/2$ diallel crossing have been performed. The earliness components (insertion height of the first sympodium, early yield weight and raw cotton early yield), components regarding the productivity (fiber content, capsule weight, total yield) and fiber length were tested.

The determinations were made on 50 plants x 3 reps and the yields were calculated by plant yield totalizing expressed in t/ha. The analysis of variation coefficients (Ceapoiu, 1968), variance analysis for experiment groups (Ceapoiu, 1968), half diallel table analysis (Walters and Morton, 1978), estimation of genetic variance components and heredity coefficients (Jinks, 1954, Hayman, 1954a; 1954b, Mather and Jinks, 1974) have been analyzed.

RESULTS AND DISCUSSION

The average values of tested genetic traits corresponding to parental genotypes had enough variability for the proposed aim (Table 1).

Table 1. Mean values of the quantitative genetic traits, agronomically useful, tested in cotton, ARDS Teleorman, 2000-2001 average

Parental genotype	Insertion height of the first sympodium (nodes)	Distance from cotyledonal node to the first sympodium (cm)	% early yield from total one (arcsin $\sqrt{\%$)	Early yield (t/ha)	Capsule weight (g)	Fiber content (%)	Total yield (t/ha)	Fiber length (mm)
T-045	5.15	16.00	52.39	1.82	5.50	45.30	2.90	30.38
T-0225	6.13	21.60	50.48	1.87	6.87	41.18	3.13	29.90
T-0320	7.20	22.50	49.17	1.61	5.10	44.87	2.81	29.85
T-0419	3.33	14.60	58.86	2.45	6.23	39.93	3.35	29.37
T-0435	3.30	12.50	60.68	1.90	6.57	35.80	2.49	35.23
C-0438	4.95	17.03	50.92	1.98	5.93	43.50	3.29	30.93
T-0535	4.93	17.53	55.56	1.56	6.18	40.80	2.29	29.55
C-0572	6.90	19.55	51.36	1.58	6.10	41.85	2.59	28.95
T-0575	5.03	18.88	55.10	1.82	6.87	41.30	2.33	32.28
C-0577	4.13	14.88	55.86	1.88	6.57	37.75	2.74	31.97
Average	5.11	17.51	54.04	1.85	6.19	41.23	2.79	30.84
S x	0.0941	0.3817	1.0123	0.1142	0.1190	2.7965	0.2272	0.2149
LSD 5%	0.42	0.86	1.39	0.47	0.47	2.30	0.66	0.64
LSD 1%	0.56	1.13	1.83	0.62	0.63	3.03	0.97	0.84
LSD 0,1%	0.71	1.44	2.34	0.77	0.80	3.87	1.24	1.08

The variance analysis for all tested traits emphasized that the differences between parental genotypes were distinctly significant in F test vs. error variant, the variability coefficient being of 5.57-17.34% depending on the tested genetic trait (Table 2 and Table 3).

The estimation of genetic variance components and heredity coefficients based on covariance and variance of hybrid rows with a common parent led to the obtainment of the following genetic parameters: D, H_1 , H_2 , F and h^2 and of some proportional values among them with certain genetic significances depending on the tested trait (Table 4):

- for all tested genetic traits, the results emphasize the fact that the values of genetic parameters are significant, proving the fact that these traits are not too much affected by environmental conditions;

- the very significant values of D parameter (which estimates the additivity effects) as well as H_1 , H_2 , F and h^2 ones (which estimate the dominance effects) confirm the fact that both effect types are present into tested trait heredity, the dominance effects having prevalent role;

Table 2. ANOVA for earliness indicators in cotton, ARDS Teleorman, 2000-2001 average

Variability cause	GL	Insertion height of the first symposium (nodes)			Distance from cotyledonal node to the first symposium (cm)			Early yield from total one (arcsin√%)			Raw cotton early yield (t/ha)		
		SP	s ²	F	SP	s ²	F	SP	s ²	F	SP	s ²	F
Blocks	3	0,28			1,55			6,25			0,12		
Genotypes	54	267,9	4,96	55,11**	1426,27	26,41	69,5**	2151,94	39,85	39,46	28,85	0,53	4,68**
Error	162	15,24	0,09		61,83	0,38		163,99	1,01		18,50	0,11	
Variability coefficient (%)		6,50			6,49			11,83			17,34		

**significantly for 1%

Table 3. ANOVA for capsule weight, fiber content, total yield and fiber length, ARDS Teleorman, 2000-2001 average

Variability cause	GL	Capsule weight (g)			Fiber content (%)			Total yield (t/ha)			Fiber length (mm)		
		SP	s ²	F	SP	s ²	F	SP	s ²	F	SP	s ²	F
Blocks	3	0,35			23,39			0,21			0,43		
Genotypes	54	38,22	0,71	5,95**	753,84	13,96	5,04**	49,08	0,91	4,00**	361,25	6,69	31,13**
Error	162	19,29	0,12		448,35	2,77		36,80	0,23		34,81	0,21	
Variability coefficient (%)		5,57			13,95			16,45			11,48		

**significantly for 1%

Table 4. Values of genetic variance components for cotton earliness factors, capsule weight, fiber content, raw cotton total yield and fiber length, ARDS Teleorman, 2000–2001 average

Nr. crt.	Genetic parameters	Insertion height of the first sympodium		Early yield from total one (arcsin%)	Raw cotton early yield (t/ha)	Average weight of capsule (g)	Fiber content (%)	Raw cotton total yield (t/ha)	Fiber length on seed (mm)
		nodes	cm						
1.	D	1,77±0,07	10,08±0,14	14,38±0,81	1,02±0,01	0,29±0,01	7,91±0,24	0,04±0,002	3,42±0,06
2.	H ₁	1,80±0,14	6,19±0,29	28,23±1,72	0,64±0,03	0,46±0,01	9,76±0,50	0,07±0,004	2,34±0,13
3.	H ₂	1,63±0,12	5,33±0,25	23,51±1,46	0,55±0,02	0,41±0,01	8,23±0,43	0,06±0,004	2,08±0,11
4.	F	0,99±0,16	-0,46±0,02	9,67±1,86	0,03±0,02	0,14±0,01	5,88±0,55	0,02±0,005	1,38±0,14
5.	h ²	0,83±0,08	0,07±0,17	5,26±0,98	0,03±0,01	0,04±0,01	3,32±0,29	0,001±0,003	1,75±0,07
6.	(H ₁ /D) ^{1/2}	1,00	0,79	1,40	1,26	1,27	1,11	1,42	0,83
7.	Vr/Wr	1,01	0,85	1,80	1,55	1,81	1,62	1,78	0,87
8.	H ₂ /4H ₁	0,23	0,22	0,21	0,21	0,22	0,21	0,19	0,22
9.	(4DH ₁) ^{1/2} +F (4DH ₁) ^{1/2} -F	1,27	0,94	1,63	1,26	1,47	2,01	1,54	1,64
10.	$\frac{1}{2}F$ [D(H ₁ -H ₂)] ^{1/2}	0,90	0,08	0,59	0,31	0,56	0,85	0,42	0,73
11.	h ² /H ₂ Heredity coeff.: - in narrow sense - in large sense	0,51	0,01	0,22	0,04	0,10	0,40	0,02	0,84
12.		0,43	0,77	0,41	0,47	0,31	0,84	0,52	0,61
		0,93	0,95	0,91	0,85	0,63	0,96	0,94	0,89

·the positive and significant value of F parameter suggests the fact that the presence of dominant genes is in excess vs. recessive gene one for all tested traits excepting the distance from cotyledonal node to insertion one of the first sympodium at which, the recessive gene frequency is in excess vs. dominant gene one;

·the ratios $(H_1/D)^{1/2}$ and Vr/Wr emphasize a genetic control of type:

- complete dominance for height insertion of the first sympodium (nodes);
- partial dominance for height insertion of the first sympodium (cm) and fiber length (mm);
- overdominance for early yield from total one (arc sin v%), early yield (t/ha), capsule weight (g), fiber content (%) and total yield (t/ha).

·the value, supraunitary and different from 1, of ratio $[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F]$ emphasizes the asymmetry of dominant and recessive gene distribution among parents for insertion of the first sympodium (cm), early yield from total one (arc sin v%), early yield (t/ha), capsule weight (g), fiber content (%), total yield (t/ha) and fiber length, hypothesis confirmed by $H_2/4H_1$ ratio value which estimates the relative distribution of dominant and recessive genes (value<0.25, registered when the genes have equal frequency);

·average degree of dominance variation at the level of different loci is given by the value of $S F/[D(H_1-H_2)]_{1,2}$, which shows that the dominance is not variable for the first sympodium insertion (cm), early yield weight, early yield, capsule weight and total yield but is variable from one locus to another for the insertion node of the first sympodium, fiber content and length;

·for this set of parental genotypes, the h^2/H_2 ratio emphasizes a gene or a group of genes closely associated which demonstrate dominance only for fiber length (0.84) and maybe for insertion node (0.51);

·generally, the heredity coefficients have high values for all tested traits: 0.41-0.84 in narrow sense and 0.85-0.96 in large sense, excepting the capsule weight which registers 0.31 in narrow sense and 0.63 in large one.

CONCLUSIONS

The differences among these 55 cotton genotypes were distinctly significant.

The variability of the tested traits was enough for the proposed study.

The genetic control of the heredity of main agronomically useful genetic traits in cotton is of type:

- complete dominance for insertion height of the first sympodium (nodes);
- partial dominance for insertion of the first sympodium (cm) and fiber length;
- overdominance for early yield from total one, early yield, capsule weight, fiber content and total yield.

The dominant and recessive genes are relatively unequally distributed among parents for all tested traits.

The dominance is not variable from one locus to another for insertion of the first sympodium (cm), early yield from total one, early yield, capsule weight and total yield but is variable from one locus to another for insertion node of the first sympodium, fiber content and fiber length.

For this set of parental genotypes, a gene or a group of genes which demonstrate dominance only for fiber length was emphasized.

Generally, the tested traits have high heredity coefficients in narrow sense as well as in large one.

The results are strictly available for the set of genitors under study.

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