INHERITANCE OF FIBER LENGTH IN DIALLEL COTTON CROSSES

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Abstract

The studies on genetic control of fiber length are of great importance for breeding of new cotton varieties and germplasm with improved fiber quality. In the period 1993-1995 fourteen cotton varieties and lines of various origin *(G. hirsutum L.* and *G. hirsutum L.* × *G. barbadense L.),* differing significantly in fiber length, were included in a half diallel cross. In 2004-2005 another diallel cross was made with eight other varieties. The diallel schemes included one set of F_1's and parents. It was established that the fiber length in the studied diallel crosses was controlled by additive and dominant genes with a transcendence of additive effects. Complementary epistasis exhibition was also possible subjected to the ecological environments. Some parents were with different dominance in the various years of study which might be explained with the changes in the genes spectrum which determined the fiber length under the influence of the environmental conditions (years). Most parents had high or medium high dominance. Lines *Nos.* 65, 68 and 268, and variety Natalia of *G. hirsutum* × *G. barbadense* origin were with high dominance during all years of study and appeared to be most valuable. The genetic variability was high and reveals an opportunity for successful breeding.

Key words: cotton, diallel analysis, fiber length

Introduction

Diallel analysis is a largely used method in the genetic and breeding research on various crops, including cotton (Carvalho et al., 1994; Xu et al., 1995; Meredith and Brown, 1998; Ashraf et al., 2000). This analysis provides very useful information about the genetic components of inheritance for a fixed set of parents, as well as for their general and specific combining ability, on the base of only one hybrid generation.

The aim of this study was by means of diallel analysis of fiber length of F_1 cotton hybrids to establish some genetic parameters and indexes of inheritance necessary for specifying the breeding strategy by this character and breeding value of parental forms.

Material and Methods

In the period 1993-1995 a half diallel cross was made with 14 cotton varieties and lines of various fiber lengths. The varieties Beli izvor, Ogosta (Bulgarian), T-073 (Romanian), C-9070 (Uzbek) and bred lines *Nos.* 147 and 176 were of *G. hirsutum L.* intraspecific origin. Lines *Nos.* 27, 41, 65, 68, 131, 262, 268 and 273 were of *G. hirsutum L.* × *G. barbadense*

L. interspecific origin. In 2004-2005 another half diallel cross was made with eight other varieties: Chirpan-539, Veno, Darmi, Natalia (Bulgarian); Millenium, Fantom (Greek); Ersan (Turkish); T-073 (Romanian). The diallel schemes included one set of F_1's and parents. The trials were set in three replications and 30 "butterflies" from 10 plants of each replication were measured. The data was processed by application of analysis of variance and diallel analysis appropriate for the diallel scheme (Hayman, 1954; Mather and Jinks, 1971).

Results and Discussion

The results from the analysis of variance for fiber length showed significant genotype differences (dater are not given hire) and confirmed the suitability of data for their inclusion in diallel analysis.

Table 1 shows the results from the statistical analysis for validation of the main hypotheses for representation of the diallel analysis results. In four of five experimental designs the regression coefficient *b* was significantly less than unity, which is an indicator for the presence of complimentary epistasis. Only for F_1-1995 the regression coefficient *b* did not differ significantly from unity, which means this is the regression line of unit slope. There was a statistically significant variation of the parental arrays by the W_r-V_r parameter for F_1-1993 resulting from the influence of non-alleic interactions. The diallel scheme (F_1-1993) with 6 parents removed ensured the most constant values of the differences W_r-V_r, and this means that it already corresponded to the simple model. After removing of lines *Nos.* 68 and 268 from the diallel scheme of F_1-1994, of varieties Ersan and Natalia from the diallel scheme of F_1-2004, and of variety Ersan from the diallel scheme of F_1-2005, the obtained sets of parents satisfied the requirements for diallel analysis.

Table 1. Testing the validity of the null hypothesis for the fiber length character

Diallel cross, year	Removed parents	$b_{Wr/Vr}$±b	0>b>0	1>b>1	$t_{(Wr-Vr)}$
F_1 - 1993	-	0.382±0.104	3.670^{++}	5.905^{+++}	3.993^{++}
	27, 41, 147, 65, T-073, C-9070	0.785±0.223	3.489^{+}	0.946	0.195
F_1 - 1994	-	0.648±0.150	4.429^{+++}	2.411^{+}	1.281
	68, 268	0.728±0.126	5.733^{+++}	2.106	1.368
F_1 - 1995	-	0.896±0.114	7.836^{+++}	0.864	0.152
F_1 - 2004	-	0.596±0.169	3.534^{+++}	2.389^{+}	1.617
	Ersan, Natalia	0.827±0.212	3.898^{+++}	0.815	0.370
F_1 - 2005	-	0.462±0.356	1.295	1.514	0.044
	Ersan	0.940±0.261	3.617^{+++}	0.209	0.520

$^{+}P = 5$ %; $^{++}P = 1$ %; $^{+++}P = 0.1$ %

Fig. 1 shows a graphical diallel analysis of the fiber length of F_1 1993-1995. The regression straight line cuts the ordinate over the origin, in its positive part, and expresses a partial dominant inheritance of this character. There was a certain dislocation of the points when changes occurred in the ecological conditions. The Bulgarian variety Beli izvor having short fiber was with most dominant genes in 1993 and 1994, and comparatively high dominance in 1995 for the fiber length. The Uzbek variety C-9070 possessing long fiber was with lower dominance and the Romanian variety T-073 possessing also long fiber had more recessive genes in 1994. Lines *Nos.* 65, 68, 262, 268 and 273 of *G. hirsutum L.* × *G. barbadense L.* origin carried mainly dominant genes controlling the fiber length. The other genotypes with low mean values for fiber length possessed high (lines *Nos.* 41 and 131) and medium high dominance (the variety Ogosta, lines *Nos.* 131 and 147) or had different dominance (*No.* 176).

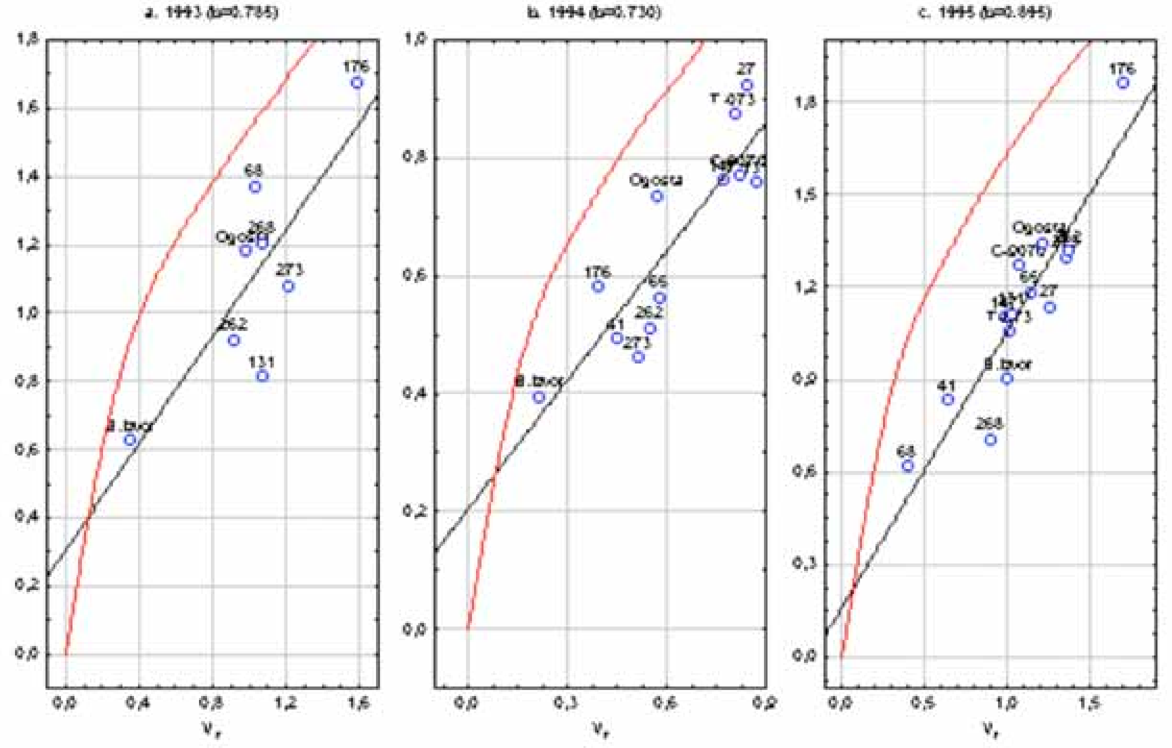

Fig. 1. Graphical Diallel Analysis of Fibre Lenght (1993-1995)

Fig. 2a presents the diallel graph of the fiber length of F_1-2004 without removing any parents, while Fig. 2b presents the graphical data for the same diallel scheme but with respectively excluded the varieties Ersan and Natalia. The graph with the complete set of parents shows that the regression line cuts the Wr-axis near the origin and expresses almost complete dominance. The parental forms are divided into two groups: the varieties Darmi, Veno, Ersan, Natalia and Chirpan-539 are in the more dominant part which expresses dominant genes prevailing over recessive; the varieties Millenium, Fantom and T-073 are about the middle and over which shows equal frequencies of dominant and recessive genes or recessive genes prevailing over dominant. The location of varieties Veno and Darmi outlines them as the parents with most dominant genes. They differed in fiber length, Veno was with short fiber and its dominance was directed to decreasing the character value, while Darmi was with long fiber and its dominance was directed to increasing the fiber length. The variety T-073 with longest fiber had the most recessive genes. We may conclude from the location of T-073 that it being far from the possible respective complete recessiveness. In the diallel graph after removing the varieties Ersan and Natalia, the regression line cuts the ordinate slightly below the origin, i.e. in its negative part, which means weak overdominance. Darmi and Millenium retain their positions, while the other parents were slightly dislocated. According to Mersinkov (2000) the removal of parents only restricts the information obtained from the analysis.

As compared with F_1-2004 there was a significant change in the positions of the parents with F_1-2005 (Fig. 2c and 2d). The regression line crosses the ordinate in its positive part and shows incomplete dominance. Higher number of dominant alleles was seen at T-073, Millenium, Fantom and Natalia. The other varieties located over had more recessive alleles. In the diallel graph after removing the variety Ersan the genotypes dislocation is slow.

The results analysis led to conclude that the variety T-073 had different dominance subject to the environmental conditions. The other varieties had also different ratio of dominant and recessive alleles during the years of research which could be explained with the changes in the genes spectrum which determined the fiber length under influence of the environmental conditions (years).

The genetic components of the fiber length inheritance are given in Table 2. Statistically significant were both the additive and dominant effects. The additive gene action (D) exceeded the dominant and reflects the greater significance of the additive variance in the inheritance of fiber length. An exception was diallel cross F_1-2004, where the dominant gene action surpassed the additive. The H_1/D parameter shows incomplete dominance in the crosses, except for F_1-2004 where we observe slight overdominance. The mean degree of dominance in the loci expressed with the $H_1/D^{1/2}$ parameter was respectively incomplete dominance and overdominance. It is seen from $M_{L1}–M_{L0}$ that average for the two diallel combinations, the dominance was directed to slight increase of fiber length.

The ratio $H_2/4H_1$ expresses uneven distribution of the dominant and recessive alleles in the parental forms. The ratio K_D/K_R also shows certain unevenness of dominant and recessive alleles. The average value of the F parameter is negative but it is not significant and it may be accepted that the dominant and recessive alleles in the populations were about equal. The null value of the $F^2/4D(H_1\text{-}H_2)^{1/2}$ parameter shows that there was a strongly variable dominance in the crosses by loci.

The correlation between the mean values of the parental forms and the sum of covariance-variance values varies from high negative ($r_{xp}(w_r+v_r)$ = -0.7939) to medium high positive ($r_{xp}(w_r+v_r)$ = 0.6568). Slight and positive correlation at F_1-1993 - 1995 indicates that it is difficult to assess the nature of the dominant determination of the studied character in the diallel crosses. The higher values of W_R+V_R at F_1-2004 are in positive correlation with the parental values, while with F_1-2005 – in negative one. It means that the parents with the highest indexes for fiber length (T-073, Millenium and Fantom) had the most recessive genes in the first year and had the most dominant in the second. The values of κ for the number of efficient factors appoint one group of genes.

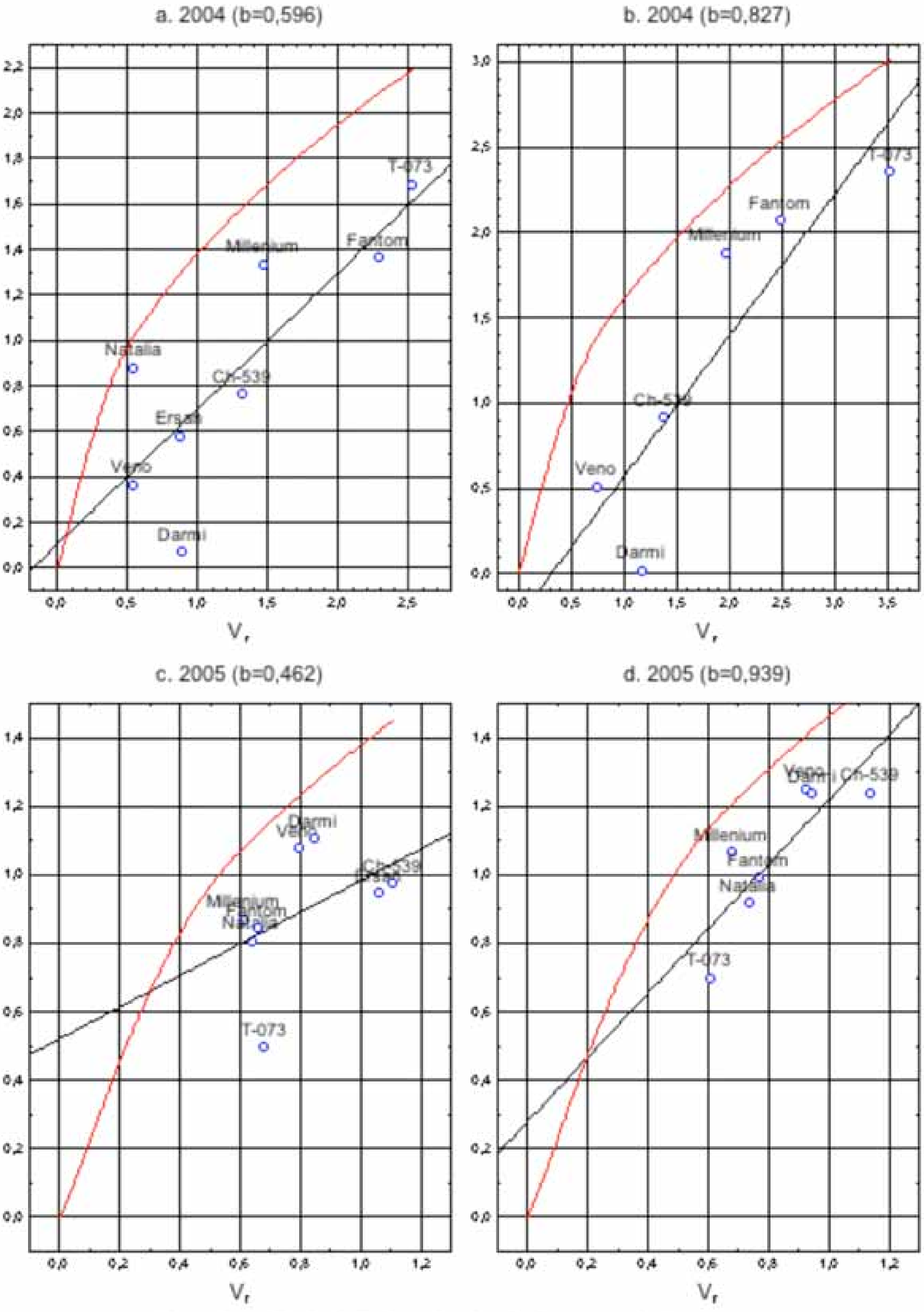

Fig. 2. Graphical Diallel Analysis of Fibre Length (2004-2005)

Table 2. Genetic components of the fiber length inheritance

Genetic parameters	F_1 – 1993	F_1 – 1994		F_1 – 1995	F_1 – 2004		F_1 - 2005	
	Removed 27, 41, 147, 65, T-073, C-9070	Complete set of parents	Removed 68 and 268	Complete set of parents	Complete set of parents	Removed Ersan and Natalia	Complete set of parents	Removed Ersan
Parameters								
D	1.95±0.11	1.12±0.06	1.15±0.05	2.13±0.07	1.68±0.23	2.36±0.25	1.69±0.10	1.92±0.06
F	-0.33±0.25	-0.27±0.14	-0.22±0.12	-0.09±0.15	-0.041±0.55	-0.30±0.61	-0.06±0.24	-0.26±0.14
H_1	0.88±0.25	0.59±0.12	0.54±0.10	0.95±0.13	2.99±0.53	4.34±0.63	0.98±0.24	0.62±0.14
H_2	0.77±0.22	0.47±0.10	0.40±0.87	1.01±0.11	2.50±0.46	3.31±0.57	0.80±0.21	0.57±0.13
h^2	0.34±0.04	-0.03±0.02	-0.06±0.01	-0.13±0.02	0.04±0.31	0.15±0.38	1.06±0.14	0.55±0.08
E	0.42±0.14	0.26±0.06	0.251±0.06	0.54±0.07	0.21±0.07	0.21±0.09	0.20±0.03	0.22±0.02
Indexes								
H_1/D	0.4510	0.5267	0.4696	0.4460	1.7723	1.8406	0.5772	0.3265
$H_1/D^{1/2}$	0.6717	0.7251	0.6866	0.6669	1.3313	1.3567	0.7597	0.5714
$H_2/4H_1$	0.2201	0.2010	0.1845	0.2662	0.2094	0.1903	0.2064	0.2295
$(M_{L1}-M_{L0})^2$	0.1314	0.0108	0.0042	0.0037	0.0327	0.0687	0.2878	0.1655
$F^2/4D(H_1-H_2)/^{1/2}$	0.10	0.15			0.0010	0.0293	0.0040	0.1096
K (h^2/H_2)	0.4415	-0.0638	-0.1500	-0.1287	0.0160	0.0453	1.3250	0.9649
K_D/K_R	0.7786	0.7122	0.7513	0.9384	0.9810	0.9095	0.9505	0.7864
$Yr_{ij(WR+VR)}$	0.2448	0.0681	0.2883	0.0601	0.5055	0.6568	-0.7939	-0.7749
Inheritance, %								
H^2	0.767	0.771	0.774	0.712	0.947	0.926	0.853	0.851
h^2	0.660	0.667	0.684	0.577	0.794	0.640	0.706	0.745
Forecast for most dominant/recessive parent								
Y_D	25.790	28.051		27.404	28.285	27.676	33.728	33.341
Y_R	28.373	28.700		28.235	31.197	31.613	22.335	23.527

The coefficients of heritability in a broad sense (H^2) were high and indicate that the variability was due to genetic reasons. The coefficients of heritability in narrow sense (h^2) were also high and an efficient selection by fiber length may be carried out in the early hybrid generations ($F_2 – F_3$).

Conclusion

The inheritance of fiber length in the investigated diallel crosses was controlled by an additive-dominant genetic system with superiority of additive effects mainly. Complementary epistasis was possible in dependence with the environmental conditions.

A change in the environmental conditions may lead to predetermination of the genetic formulas controlling the character.

The genetic variability was high and reveals an opportunity for efficient breeding in the early hybrid generations.

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It provides very useful information about genetic components of inheritance for a fixed set of parents and their combining and specific ability, on the basis of one hybrid generation only.

The aim of this study was by diallel analysis of fiber length in F_1 cotton hybrids to establish some genetic parameters and indexes necessary for specifying the breeding strategy by this character and breeding value of parental forms.

MATERIAL AND METHODS

In the period 1993-1995 14 cotton varieties and lines of various origin (*G. hirsutum L.* and *G. hirsutum L. x G. barbadebse L.*), differing in fiber length, were included in a half diallel cross.

In 2004-2005 another diallel cross was made between eight other varieties.

The diallel schemes included one set of F_1's and parents. The trials were set in three replications and 30 "butterflies" were measured from 10 plants of each replication.

The data was processed by application of diallel analysis appropriate for the diallel scheme (Mather, Jinks, 1971).

RESULTS AND DISCUSSION

Table 1. Testing the validity of the null hypothesis for the fiber length character

Diallel cross year	Removed parents	$b_{Wr/Vr}$±b	0>b>0	1>b>1	$t_{(Wr-Vr)}$
F_1 - 1993	-	0.38±0.10	3.67^{++}	5.90^{+++}	3.99^{++}
	27, 41, 147, 65, T-073, C-9070	0.78±0.22	3.49^{+}	0.95	0.20
F_1 - 1994	-	0.65±0.15	4.43^{+++}	2.41^{+}	1.28
	68, 268	0.73±0.13	5.73^{+++}	2.11	1.37
F_1 - 1995	-	0.90±0.11	7.84^{+++}	0.86	0.15
F_1 - 2004	-	0.60±0.17	3.53^{+++}	2.39^{+}	1.62
	Ersan, Natalia	0.83±0.21	3.90^{+++}	0.81	0.37
F_1 - 2005	-	0.46±0.36	1.29	1.51	0.04
	Ersan	0.94±0.26	3.62^{+++}	0.21	0.52

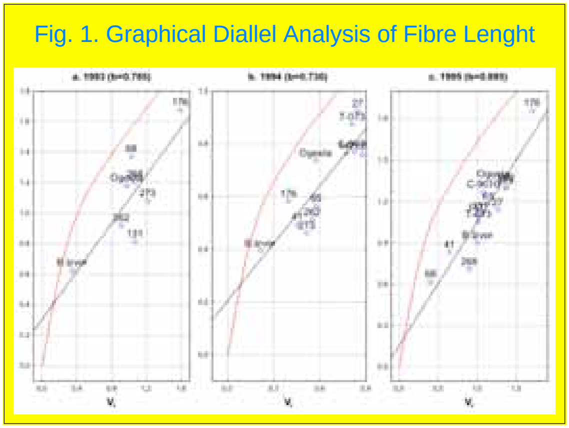


Fig. 1. Graphical Diallel Analysis of Fibre Lenght

a. 1993 (b=0.785) b. 1994 (b=0.730) c. 1995 (b=0.885)

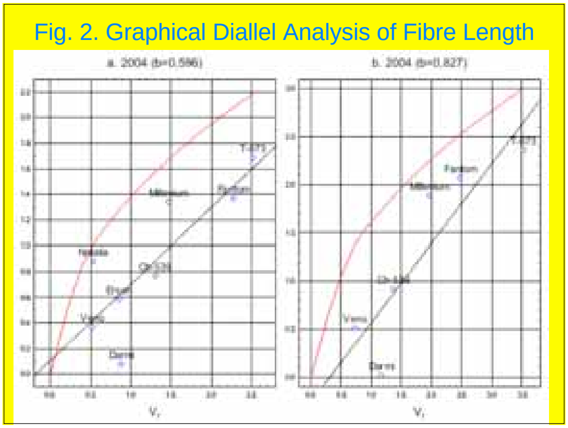


Fig. 2. Graphical Diallel Analysis of Fibre Length

a. 2004 (b=0.586) b. 2004 (b=0.827)

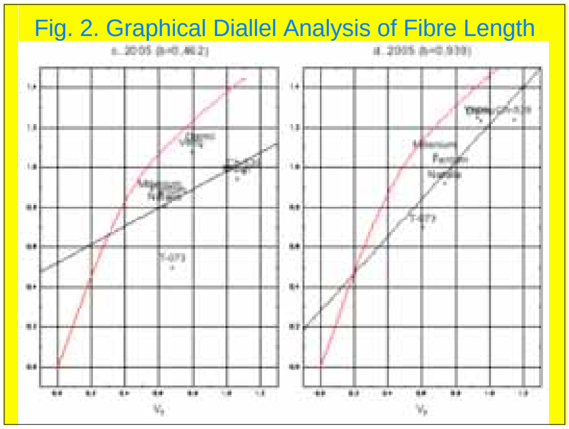


Fig. 2. Graphical Diallel Analysis of Fibre Length

c. 2005 (b=0.462) d. 2005 (b=0.939)

The results analysis led to conclude that the variety T-073 had different dominance during the years of research.

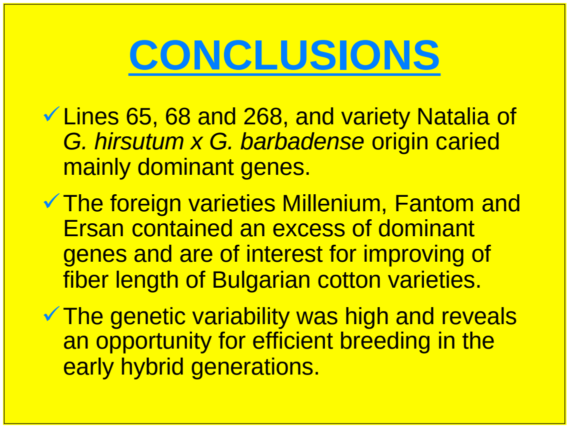
The other varieties had also different ratio of dominant and recessive alleles during the two years which could be explained with the changes in the genes spectrum which determines the fiber length under influence of the environmental conditions (years).

Table 2. Genetic components of the fiber length inheritance

Genetic parameters	F_1 1993	F_1 1994	F_1 1995	F_1 2004		F_1 2005
D	1.95^{+++}	1.15^{+++}	2.13^{+++}	1.68^{+++}	2.36^{+++}	1.92^{+++}
F	-0.33	-0.22	-0.09	-0.04	-0.30	-0.26
H_1	0.88^{+++}	0.54^{+++}	0.95^{+++}	2.99^{+++}	4.34^{+++}	0.62^{+++}
H_1/D	0.45	0.47	0.45	1.77	1.84	0.33
$H_1/D^{1/2}$	0.67	0.69	0.67	1.33	1.36	0.57
$H_2/4H_1$	0.22	0.18	0.27	0.21	0.19	0.23
$(M_{L_1} - M_{L_0})^2$	0.13	0.01	0.01	0.03	0.07	0.17
K_D / K_R	0.78	0.75	0.94	0.98	0.91	0.79
$Y_{r_{ij}(W_R+V_R)}$	0.24	0.29	0.06	0.51	0.66	-0.77
h^2	0.66	0.68	0.58	0.79	0.64	0.74

CONCLUSIONS

- ✓ The inheritance of fiber length in the investigated diallel crosses was incompletely dominant and overdominant. Complementary epistasis was possible.
- ✓ A change in the environmental conditions may lead to predetermination of the genetic formulas controlling the character.



CONCLUSIONS

✓ Lines 65, 68 and 268, and variety Natalia of *G. hirsutum x G. barbadense* origin caried mainly dominant genes.

✓ The foreign varieties Millenium, Fantom and Ersan contained an excess of dominant genes and are of interest for improving of fiber length of Bulgarian cotton varieties.

✓ The genetic variability was high and reveals an opportunity for efficient breeding in the early hybrid generations.