

## INHERITANCE AND COMBINING ABILITY FOR FIBER LENGTH IN F<sub>1</sub> DIALLELCOTTON CROSSES (*Gossypium hirsutum* L.)

Valentina DIMITROVA, Minka KOLEVA

Agricultural Academy, Field Crops Institute, 2 G. Dimitrov Blvd, Chirpan, Bulgaria

Corresponding author email: m\_koleva2006@abv.bg

### Abstract

*The aim of this study was by means of diallel analysis of fiber length of F<sub>1</sub> cotton hybrids to establish some genetic parameters and inheritance indexes necessary for specifying the breeding strategy by this character and breeding value of parental forms. The hybrid populations of two diallel combinations, each involving 6 parental components, were studied. A half diallel crossing scheme was used including the parents and one set of F<sub>1</sub> hybrids from direct crosses. Each diallel combination was tested in replicated trials in two consecutive years. It was found that additive and non-additive gene effects participated in the genetic control of fiber length. The main component of genetic variance was of non-additive type (dominance and epistasis). The varieties Darmi, Mytra and Dorina, from the 1<sup>st</sup> diallel combination, and Natalia, from the 2<sup>nd</sup> diallel combination, were identified as good general combiners for this trait.*

**Key words:** cotton, *G. hirsutum* L., diallel analysis, fiber length, genetic variances, combining ability.

### INTRODUCTION

Bulgarian cotton production is based exclusively on Bulgarian varieties, foreign varieties late in maturing and do not realize their productive potential and fiber properties. In our country cotton is grown under non-irrigated conditions with very limited temperatures and rainfall for this crop. In cotton selection the greatest attention is paid to earliness, productivity and fiber quality, especially its length. At this stage cotton selection is mainly aimed at improving the productivity and quality of the fiber, while preserving earliness.

In Europe cotton is grown in Spain, Greece, more limited in Portugal and Bulgaria. In Spain and Greece cotton is grown under irrigated conditions and yields are much higher. Varieties grown in these countries have a longer growing season, higher productivity and a better quality fiber.

In recent years as a result of selection many new cotton varieties have been created: Sirius (Valkova, 2017), Tsvetelina (Koleva & Valkova, 2019), Aida, Anabel, Tiara and Melani (Dimitrova, 2022a; 2022b; 2022c). All these varieties are early ripening and high yielding, Anabel and Melani have improved fiber quality characteristics. Selection results in terms of productivity and fiber quality of the European countries and a number of other cotton-

producing countries are much higher and set higher criteria in front of our selection. In cotton breeding the genetic plasm exchange is very limited, and in addition, genetically modified cotton is grown in the countries outside of Europe.

From the specialized literature it can be seen that various selection methods and techniques are used for genetic improvement of traits and genotypes. Gene action and genetic variation are some of the most important criteria for any breeding program. Additivity, epistasis, dominance, overdominance, heterosis, heterobeltiosis, heritability, general combining ability (GCA) and specific combining ability (SCA) are some of the most important statistical approaches for choosing a selection strategy (Sajjad, 2015). GCA is a criterion for selection of parental forms, while hybrids are selected based mainly on SCA effects. Additive gene action in control of fiber quality properties was reported by Akiskan & Gencher (2014), Carvalho et al. (2018). However, other researchers (Bölek et al., 2014; Khan et al., 2017) found a non-additive type of gene action. An additive type of gene action with partial dominance for fineness, staple length and strength was reported by Rasheed et al. (2014). In the studies of Nasimi et al. (2016) additive action with partial dominance and absence of non-allelic interactions determined the

inheritance of fiber length, strength and fineness under normal and drought conditions. In the studies of Khokhar et al. (2018) non-additive gene effects were essential for fiber length and strength.

In the selection of cotton in our country the genetic control of traits has been insufficiently studied both in intra- and inter-species crossing. The gene action controlling the fiber quality properties has been insufficiently studied. There is limited information on the selection value of modern varieties of Bulgarian and foreign selection as parental components for crossing, on the genes they contain and their effects on the expression of traits. The genetic potential of hybrid populations obtained through intra- and inter-specific crosses is insufficiently appreciated.

Quantitative traits are largely influenced by environmental conditions and modification of their genetic parameters is also insufficiently studied. The use of diallel analysis will help to obtain the necessary information for selection programs and to expand the theoretical basis of cotton selection in our country.

The aim of this study was by means of diallel analysis of fiber length of F<sub>1</sub> 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.

## MATERIALS AND METHODS

The hybrid populations of two diallel crosses were studied. First one included six (four Bulgarian and two foreign) upland cotton varieties: Beli Iskar - P<sub>1</sub>; Barut 2005 (Turkish) - P<sub>2</sub>; Darmi - P<sub>3</sub>; Mytra (Greek) - P<sub>4</sub>; Helius - P<sub>5</sub> and Dorina - P<sub>6</sub>. Second diallel cross included varieties: Chirpan-539 - P<sub>1</sub>; Helius - P<sub>2</sub>; Rumi - P<sub>3</sub>; Boyana - P<sub>4</sub>; Natalia - P<sub>5</sub> and Nelina - P<sub>6</sub> (Bulgarian selection).

A half diallel crossing scheme was used including the parents and one set of F<sub>1</sub> hybrids from direct crosses. The study was carried out at the Field Crops Institute in Chirpan and each diallel combination was tested in two consecutive years, in three replicates. The parents and their F<sub>1</sub> hybrids were sown in 2 rows of 2.4 m in a 60×20×1 sowing scheme. Ten plants from each replicate were accounted.

Dispersion and diallel analyses adequate of diallel scheme were applied to the data processing (Mather & Jinks, 1982). Adequacy of data for diallel analysis was assessed by the regression coefficient  $b$  and  $t$  ( $Wr - Vr$ ) (Mather & Jinks, 1982).

The following components of genotypic variation along with their standard errors were calculated:  $D$  - additive variance;  $H_1$  and  $H_2$  - dominance variances;  $F$  - shows the ratio of dominant to recessive genes in parents;  $E$  - variability due to the influence of environmental conditions.

Based on the above components the following indicators were calculated:  $(H_1/D)^{1/2}$  - average degree of dominance in each locus;  $H_2/4H_1$  - ratio of the positive and negative alleles in the loci showing dominance in the parents;  $K_D/DR$  [ $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ ] - the ratio of dominant to recessive genes in parents;  $K=(h^2/H_2)$  - number of effective factors;  $H^2$  and  $h^2$  - coefficients of heritability in a broad and in a narrow sense, calculated by Mather & Jinks (1982).

## RESULTS AND DISCUSSIONS

Fiber length is a genetically stable characteristic, but it is also influenced by environmental conditions (the years). Due to their specific response to the years conditions, parents changed their order by years, but parents with high and low values of this trait generally maintained their positions.

The preliminary analysis of variance of this trait showed significant differences between crosses from the two diallel combinations (data are not given here).

The statistical analysis to verify the main hypotheses for the representativeness of the results of the diallel analysis (Table 1) reveals that in three of the four experimental studies - 1<sup>st</sup> DC - 2<sup>nd</sup> year, 2<sup>nd</sup> DC - 1<sup>st</sup> year and 2<sup>nd</sup> year, the regression coefficient  $b$  was significantly less than 1 and indicated the presence of complementary epistasis. Only in 1<sup>st</sup> DC - 1<sup>st</sup> year the regression coefficient  $b$  did not significantly differ from 1, which indicates that a regression line can be constructed that reliably reflects the genetic dependencies in the diallel combination.

Table 1. Additive-dominant model test of fiber length in two diallel combinations carried out in two consecutive years  
1<sup>st</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years and 2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years

Diallel cross, Year	Excluded parent	$b_{Wr/Vr} \pm b$	$0 > b > 0$ $b \neq 0$	$1 > b > 1$ $b \neq 1$	$t_{(Wr - Vr)}$
1 <sup>st</sup> DC - 1 <sup>st</sup> year	-	0.815 ± 0.127	6.420 <sup>++</sup>	1.469	1.245
	P <sub>4</sub>	0.876 ± 0.245	3.581 <sup>+</sup>	0.505	0.123
	P <sub>5</sub>	0.881 ± 0.184	4.778 <sup>+</sup>	0.646	0.382
1 <sup>st</sup> DC - 2 <sup>nd</sup> year	-	0.656 ± 0.127	5.172 <sup>++</sup>	2.697	2.287
	P <sub>1</sub>	0.840 ± 0.091	9.215 <sup>++</sup>	1.797	1.748
2 <sup>nd</sup> DC - 1 <sup>st</sup> year	-	0.710 ± 0.239	2.965 <sup>+</sup>	1.217	0.649
	P <sub>1</sub>	0.852 ± 0.371	2.287 <sup>ns</sup>	0.407	0.209
	P <sub>5</sub>	0.829 ± 0.247	3.364 <sup>+</sup>	0.690	0.301
2 <sup>nd</sup> DC - 2 <sup>nd</sup> year	-	0.399 ± 0.465	0.857	1.292	0.237
	P <sub>5</sub>	1.134 ± 0.263	4.316 <sup>+</sup>	-0.509	0.930

The diallel scheme (1<sup>st</sup> DC - 1<sup>st</sup> year) from which one of the parents - P<sub>4</sub> (Mytra variety) or P<sub>5</sub> (Helius variety) was excluded, provided more constant values of the  $Wr - Vr$  differences. There was an insignificant but considerably variation of the parental rows according to the  $Wr - Vr$  parameter for 1<sup>st</sup> DC - 2<sup>nd</sup> year, which can be assumed to be due to the influence of non-allelic interactions. The diallel scheme, from which P<sub>1</sub> (Beli Iskar variety) was excluded, provided more constant values of  $Wr - Vr$  differences and, therefore, a better fit of the additive-dominant model. Variation of parental rows according to the  $Wr - Vr$  criterion for 2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years was statistically insignificant and did not indicate the presence of non-allelic interactions. However, the regression coefficients were low, especially for 2<sup>nd</sup> DC - 2<sup>nd</sup> year, and were not significantly different from 0, and it was considered that the regression lines in the diallel graphs did not adequately represent the relationship between the covariances ( $Wr$ ) and variances ( $Vr$ ) of the diallel combinations. After excluding P<sub>1</sub> (Chirpan-539 variety) or P<sub>5</sub> (Natalia variety) from the diallel scheme of 2<sup>nd</sup> DC - 1<sup>st</sup> year, and P<sub>5</sub> (Natalia variety) from the diallel scheme of 2<sup>nd</sup> DC - 2<sup>nd</sup> year, the resulting set of parents satisfied the requirements for diallel analysis.

Ali et al. (2010) noted that staple fiber length data were unsuitable for further diallel analysis. In our study the fiber length data showed partial or incomplete compliance for genetic interpretation. According to Jinks (1954), Rood & Major (1981) in some situations the exclusion of one or more of the parents of the diallel scheme can improve the fit of the data to the additive-dominant model.

In Figure 1, A-C and Figure 2, A-B the data from the analysis for 1<sup>st</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years were graphically presented. From the graphs of the parental forms of the F<sub>1</sub> populations the following characteristics can be made: the inheritance of the studied trait in the populations was overdominant, the regression line crossed the ordinate below the zero point; there was a displacement of the points when the environmental conditions changed; after excluding parents considered to be carriers of non-allelic interactions from the diallel analysis the remaining parents retained their location. After excluding some parents (P<sub>5</sub> - Helius variety from 1<sup>st</sup> DC - 1<sup>st</sup> year) the others noticeably moved to the more dominant part of the diallel graph, which means inclusion of more dominant genes in the trait expression (fig 1, C). Darmi variety (P<sub>3</sub>) having longer fiber (1<sup>st</sup> DC) had high dominance possessing the most dominant genes for fiber length during the first year and moderately high dominance during the second year (Figure 2, A and Figure 2, B) Cultivar Mytra (P<sub>4</sub>) had high to medium high dominance during the first year and high recessiveness with the most recessive genes during the second year. Beli Iskar variety (1<sup>st</sup> DC) with most recessive genes (during the first year) and with most dominant genes (during the second year) has shown inconsistent dominance/recessiveness during the two years of the study. Helius variety, having the shortest fiber, was of constant medium-high dominance for fiber length in both years of the study. Dorina variety, having the longest fiber, had relatively high dominance (during the first year) and moderately high dominance (during the second year).

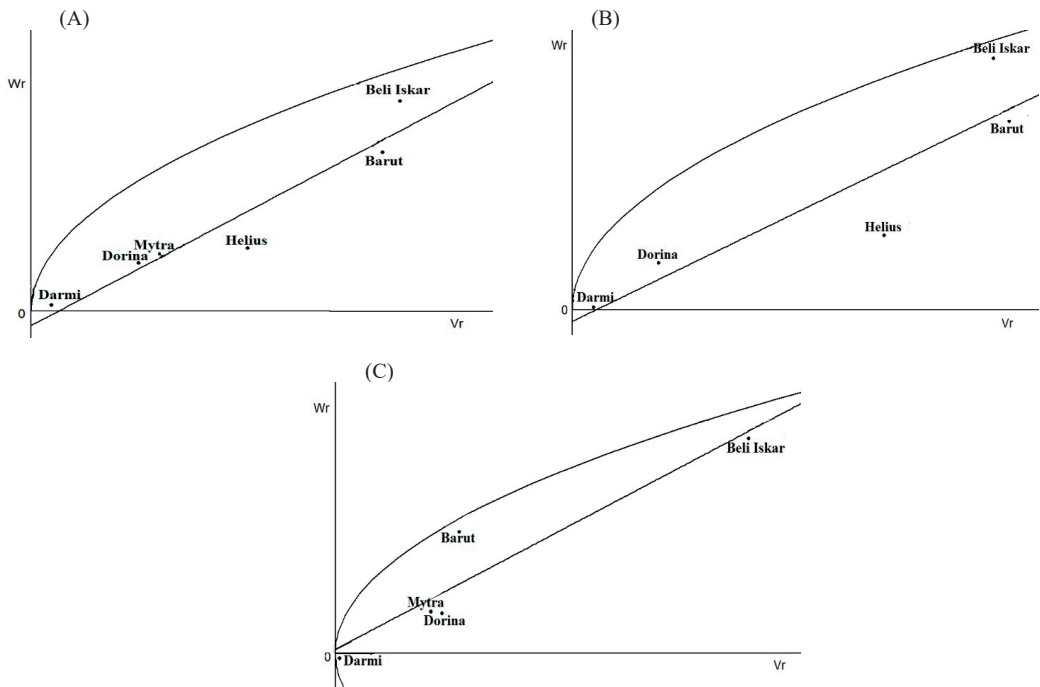


Figure 1. Graphical diallel analysis of fiber length for the first diallel combination tested for first year (1<sup>st</sup> DC - 1<sup>st</sup> year). (A) - all parents; (B) - excluded P<sub>4</sub> - Mytra variety; (C) - excluded P<sub>5</sub> - Helius variety

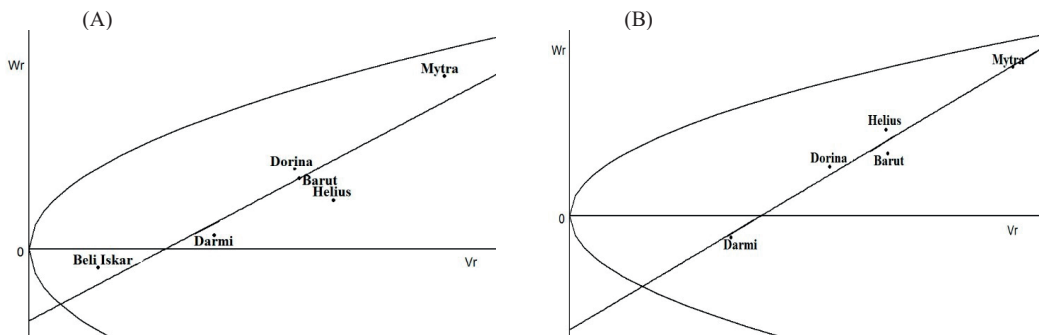


Figure 2. Graphical diallel analysis of fiber length for the first diallel combination tested for second year (1<sup>st</sup> DC - 2<sup>nd</sup> year). (A) - all parents; (B) - excluded P<sub>1</sub>- Beli Iskar variety

In Figure 3, A the diallel graph of 2<sup>nd</sup> DC - 1<sup>st</sup> year without exclusion of parents was constructed, and in Figure 3, B - with excluded P<sub>1</sub> - cultivar Chirpan-539. From the graph with the full set of parents it can be seen that the regression line crossed the ordinate below the zero point and expressed overdominance. Helius

variety (having short fiber) had high dominance possessing most dominant genes, while Nelina variety (having the longest fiber) was with most recessive genes. The remaining varieties were located in the dominant part of the diallel graph, which means a preponderance of dominant alleles over recessive ones.

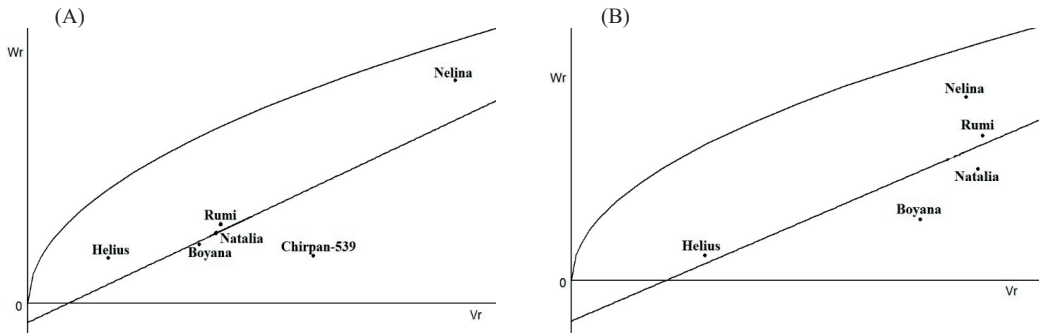


Figure 3. Graphical diallel analysis of fiber length for the second diallel combination tested for first year (2<sup>nd</sup> DC - 1<sup>st</sup> year). (A) - all parents; (B) - excluded P<sub>1</sub>- Chirpan-539 variety

Compared to 2<sup>nd</sup> DC - 1<sup>st</sup> year, in 2<sup>nd</sup> DC - 2<sup>nd</sup> year (Figure 4, A) there was a slight movement of parents under the influence of the year conditions. Rumi, Boyana and Chirpan-539 varieties retained their high dominance, while Helius and Natalia varieties with high dominance in the 1<sup>st</sup> year had medium high

dominance in the 2<sup>nd</sup> year, their points were shifted towards the middle of the regression line. There was a noticeable reshuffling of the parental forms after exclusion of P<sub>5</sub> (Natalia variety) (Figure 4, B), which was likely due to intraparental interactions.

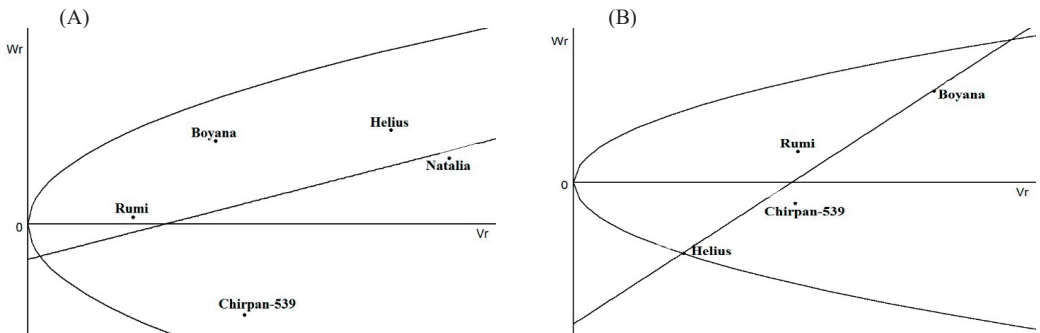


Figure 4. Graphical diallel analysis of fiber length for the second diallel combination tested for second year (2<sup>nd</sup> DC - 2<sup>nd</sup> year). (A) - all parents; (B) - excluded P<sub>5</sub> - Natalia variety

Inheritance in 2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years was overdominant with manifestations of complementary epistasis. The regression lines deviated significantly from the normal line and intersected the ordinate below zero. The genetic components from the performed diallel analysis are presented in Table 2. The additive parameter *D* and the dominant parameters *H*<sub>1</sub> and *H*<sub>2</sub> were statistically significant. In 1<sup>st</sup> DC - 1<sup>st</sup> year the dominant gene action slightly exceeded the additive (*D*) or both variance components had equal participation - with P<sub>5</sub> - Helius variety excluded, while in 1<sup>st</sup> DC - 2<sup>nd</sup> year and 2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years the dominant gene action was much more pronounced than the additive one showing the great importance of the dominant variance in the trait variation.

The *H*<sub>1</sub>/*D* ratio was consistent with the significance of both variances showing overdominance, with the exception of 1<sup>st</sup> DC - 1<sup>st</sup> year after excluding P<sub>5</sub> - Helius variety, where complete dominance was observed. Mean dominance in loci expressed as *H*<sub>1</sub>/*D*<sup>1/2</sup> was overdominance and complete dominance, respectively. The *M*<sub>L1</sub> - *M*<sub>L0</sub> indicator showed that the dominance was in the direction of increasing fiber length in both diallelic combinations. The two dominant parameters - *H*<sub>1</sub> and *H*<sub>2</sub> in most cases had close values, but the ratio *H*<sub>2</sub>/*H*<sub>1</sub> showed an unequal distribution of positive and negative alleles showing dominance, with the exception of 1<sup>st</sup> DC - 2<sup>nd</sup> year with full set of parents.

The zero value of the parameter  $F^2/4D(H_1 - H_2)^{1/2}$  indicated the presence of highly varying dominance by loci in the crosses. The average value of the parameter  $F$  in most cases had a positive sign and it can be assumed that dominant alleles prevailed over recessive ones. The growing importance of the dominant alleles was confirmed by the positive and significant values of the parameter  $h^2$  with the exception of 1<sup>st</sup> DC - 1<sup>st</sup> year without P<sub>4</sub> - Mytra variety (data are not given).

The parameter  $F$  had a negative sign for 1<sup>st</sup> DC - 2<sup>nd</sup> year, but it was insignificant for the complete set of parents and it can be assumed that the dominant and recessive alleles in the population had the same frequency. The ratio  $K_D/K_R$  reflected superiority of recessive alleles, while for all other experimental settings (1<sup>st</sup> DC - 1<sup>st</sup> year and 2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years) it showed superiority of the dominant alleles.

Ali et al. (2009) found that dominant genes outperformed recessive ones, while Igbal et al. (2011) noted a predominance of recessive alleles.

The correlation between the mean values of the parental forms and the total covariance-variance values was negative and high for 1<sup>st</sup> DC - 1<sup>st</sup> year, which means that dominant genes having unidirectional, trait-enhancing effect, were acting in the population. For 1<sup>st</sup> DC-2<sup>nd</sup> year, this relationship was very weakly negative to weakly positive indicating that genes with multidirectional action were acting in the populations. With such a relationship, it is difficult to assess the nature of the dominant determination of the studied trait in the diallel crosses.

The high and positive correlation in 2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years was an indication that the parents with maximum recessive genes were responsible for increasing fiber length. The high  $W_R+V_R$  values for 2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years were in a positive correlation with the parental values, and for 1<sup>st</sup> DC - 1<sup>st</sup> year - in a negative correlation. This means that in 2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years parents with high fiber length indices had most recessive genes, while in 1<sup>st</sup> DC - 1<sup>st</sup> year parents with a longer fiber had most

dominant genes acting to increase the trait. The values of  $k$  - number of effective factors indicated a group of genes that were responsible for the trait manifestation.

Heritability coefficients in the broad sense ( $H^2$ ) in most cases were high, in the narrow sense ( $h^2$ ) they were low to moderately high and effective selection for fiber length should be conducted in the later hybrid generations F<sub>3</sub>-F<sub>4</sub>.

Aziz et al. (2014), Srinivas et al. (2014), Ahsan et al. (2015), Wagar et al. (2016), Nizamani et al. (2017), Khan et al. (2017) reported moderate to high heritability, which revealed that this trait was influenced by additive gene effects.

The parents were ranked by mean value and by presence of dominant/recessive genes expressed by the sum of covariances and variances ( $W_r + V_r$ ) (data are not given here).

As for 1<sup>st</sup> DC - 1<sup>st</sup> year, parental forms with high mean values for fiber length (Dorina, Darmi, Mytra) had low  $W_r+V_r$  values, i. e. they had high dominance (data are not given here). Their high dominance makes them very valuable for the selection of a longer fiber with them the dominant genes acted in a positive direction to increase the trait values. For 2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years, Nelina and Natalia varieties, with high average values for fiber length, had high  $W_r + V_r$  values, i. e. these had high recessiveness (data are not given here). The remaining varieties, which had a shorter fiber (Helius, Chirpan-539, Rumi and Boyana) had low  $W_r + V_r$  values and had high dominance, but in these the dominant genes acted to reduce the fiber length. The  $rxp(W_r + V_r)$  values were positive and medium high to very high for 2<sup>nd</sup> DC - 1<sup>st</sup> year without P<sub>1</sub> - cultivar Chirpan-539 carrier of dominant genes for shorter fiber.

The assessment of the degree of dominance of the parental varieties from the graphic analysis was supplemented by the data in the Tables 3 and 4. In 1<sup>st</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years constant dominance in different ecological environments was found for Barut 2005 variety. Unstable dominance was found for the varieties Beli Iskar (very high in the first year and low in the second year), Mytra, Helius, Darmi and Dorina (low in the first year and high in the second year).

Table 2. Genetic components and indicators of inheritance of fiber length in the first and second diallel combinations, first and second years (1<sup>st</sup> DC – 1<sup>st</sup> and 2<sup>nd</sup> years and 2<sup>nd</sup> DC – 1<sup>st</sup> and 2<sup>nd</sup> years)

Genetic components	1 <sup>st</sup> DC F <sub>1</sub> - 1 <sup>st</sup> year		1 <sup>st</sup> DC F <sub>1</sub> - 2 <sup>nd</sup> year		2 <sup>nd</sup> DC F <sub>1</sub> - 1 <sup>st</sup> year		2 <sup>nd</sup> DC F <sub>1</sub> - 2 <sup>nd</sup> year	
	All parents b = 0.815	Excluded P <sub>3</sub> - Helius b = 0.881	All parents b = 0.656	Excluded P <sub>1</sub> - B. Iskar b = 0.840	Full set of parents b = 0.710	Excluded P <sub>1</sub> Chirpan-539 b = 0.852	Full set of parents b = 0.399	Excluded P <sub>1</sub> Chirpan-539 b = 1.134
D	1.272±0.087	1.538±0.118	0.242±0.088	0.192±0.040	1.231±0.135	1.052±0.094	0.434±0.184	0.155±0.034
F	0.562±0.212	0.926±0.295	-0.352±0.214	-0.630±0.099	0.581±0.329	0.385±0.234	0.427±0.460	0.301±0.087
H <sub>1</sub>	1.925±0.220	1.506±0.319	2.135±0.223	2.577±0.108	2.412±0.342	1.990±0.253	2.481±0.497	1.418±0.099
H <sub>2</sub>	1.349±0.197	1.180±0.289	2.144 ±0.199	2.471±0.977	1.992±0.305	1.797±0.230	2.327±0.451	0.938±0.091
h <sup>2</sup>	0.275±0.133	0.834±0.195	0.131±0.134	0.158±0.066	0.306±0.206	0.433±0.155	0.147±0.304	-0.004±0.062
E	0.130±0.033	0.132±0.048	0.245 ±0.033	0.272±0.016	0.141±0.051	0.133±0.038	0.068±0.075	0.070±0.015
Indicators								
H <sub>1</sub> /D	1.513	0.979	8.822	13.422	1.959	1.892	5.716	9.148
H <sub>1</sub> /D <sup>1/2</sup>	1.230	0.990	2.970	3.664	1.400	1.375	2.391	3.025
M <sub>L1</sub> - M <sub>L0</sub>	0.087	0.010	0.067	0.083	0.096	0.130	0.048	0.020
F <sup>2</sup> /4D.(H <sub>1</sub> -H <sub>2</sub> ) <sup>1/2</sup>	0.184	0.606	0.00	0.415	0.235	0.165	0.267	0.212
H <sub>2</sub> /4H <sub>1</sub>	0.175	0.193	0.251	0.230	0.207	0.226	0.234	0.165
K <sub>D</sub> /K <sub>R</sub>	1.438	1.568	0.606	0.381	1.406	1.307	1.518	1.946
r xp (W <sub>T</sub> +V <sub>r</sub> )	-0.710	-0.738	0.486	-0.048	0.619	0.960	0.503	0.752
k	0.204	0.707	0.061	0.064	0.154	0.241	0.063	-0.004
Heritability, %								
H <sup>2</sup>	0.883	0.853	0.773	0.799	0.800	0.869	0.907	0.825
h <sup>2</sup>	0.579	0.523	0.273	0.343	0.455	0.425	0.110	0.354
Prediction of the most dominant/recessive parent								
YD	29.11	29.12	26.67	27.50	24.0	22.82	26.66	26.58
YR	25.94	25.65	27.91	27.38	27.6	29.69	28.20	27.81



In 2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years Chirpan-539, Boyana, Helius and Natalia varieties had non-permanent dominance.

In the 1<sup>st</sup> diallel combination (1<sup>st</sup> DC) 4 crosses showed constant and positive heterosis

manifestations conditioned by positive overdominance during the two studied years (data are not given here).

Table 3. Mean values of the Fr parameter for each parental row for fiber length in the first diallel combination during the first and the second years (1<sup>st</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years)

Parents	1 <sup>st</sup> DC - 1 <sup>st</sup> year						1 <sup>st</sup> DC - 2 <sup>nd</sup> years					
	Complete set of parents b = 0.815		Excluded P <sub>4</sub> - Mytra variety b = 0.876		Excluded P <sub>5</sub> - Helius variety b = 0.881		Parents	Complete set of parents b = 0.656		Excluded P <sub>1</sub> - B. Iskar variety b = 0.840		
	Fr	R	Fr	R	Fr	R		Fr	R	Fr	R	
P <sub>1</sub> -B. Iskar	-2.057	6	-1.751	5	-3.046	5	P <sub>1</sub> -B. Iskar	1.494	1	-	-	
P <sub>2</sub> -Barut	-1.345	5	-1.156	4	0.593	4	P <sub>2</sub> -Barut	-0.548	3	-0.728	3	
P <sub>3</sub> -Darmi	2.846	1	3.444	1	3.305	1	P <sub>3</sub> -Darmi	0.470	2	1.133	1	
P <sub>4</sub> -Mytra	1.463	3	-	-	1.925	2	P <sub>4</sub> -Mitra	-2.330	6	-2.399	5	
P <sub>5</sub> -Helius	0.747	4	0.873	3	-	-	P <sub>5</sub> -Helius	-0.595	4	-0.945	4	
P <sub>6</sub> -Dorina	1.719	2	2.558	2	1.852	3	P <sub>6</sub> -Dorina	-0.606	5	-0.213	2	

Table 4. Mean values of the Fr parameter for each parental row for fiber length in the second diallel combination during the first and the second years (2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years)

Parents	2 <sup>nd</sup> DC - 1 <sup>st</sup> year						2 <sup>nd</sup> DC - 2 <sup>nd</sup> year					
	Complete set of parents b=0.710		Excluded P <sub>1</sub> - Chirpan-539 b=0.852		Excluded P <sub>5</sub> - Natalia b=0.829		Parents	Complete set of parents b=0.399		Excluded P <sub>5</sub> - Natalia b=1.136		
	Fr	R	Fr	R	Fr	R		Fr	R	Fr	R	
P <sub>1</sub> -Chirpan-539	0.575	5	-	-	1.750	4	P <sub>1</sub> -Chirpan-539	1.604	1	0.481	2	
P <sub>2</sub> - Helius	2.140	1	1.987	1	2.147	2	P <sub>2</sub> -Helius	-0.597	4	1.110	1	
P <sub>3</sub> - Rumi	0.911	4	-0.275	4	2.092	3	P <sub>3</sub> -Rumi	1.409	2	0.189	3	
P <sub>4</sub> - Boyana	1.304	2	0.725	2	2.539	1	P <sub>4</sub> -Boyana	0.391	3	-0.574	4	
P <sub>5</sub> -Natalia	1.041	3	0.031	3	-	-	P <sub>5</sub> -Natalia	-0.671	5	-	-	
P <sub>6</sub> -Nelina	-2.482	6	-0.542	5	-3.620	5						

The heterosis effect was the highest in the Beli Iskar × Helius cross - 3.2%, with a fiber length of 27.6 mm. In this cross, both parents had short fiber. The longest fibers were found for the crosses Mytra × Dorina (29.5 mm), Darmi × Mytra (28.8 mm) and Barut × Darmi (28.7 mm) with overdominant inheritance in both years and heterobeltiosis 2.1-2.7%. In these crosses both parental forms had longer fiber than the other parents (data are not given here).

Overdominant inheritance of this trait has been found by many other researchers (Karademir et al., 2010; Patel et al., 2014). Usharani et al. (2015) noted maximum values - 34.82% relative heterosis and 27.41% heterobeltiosis.

In the second diallel combination (2<sup>nd</sup> DC) positive overdominance for fiber length was found for two crosses during the first year and for three crosses during the second year. Crosses showed negative overdominance (26.6% in the

first year and 33.3% in the second year) and incomplete dominance of the parent with the lower value predominated confirming the results of diallel analysis that the dominance was in direction of reducing the trait meanings.

From the data in Table 5 it can be seen that there were significant differences between the tested crosses in terms of GCA and SCA. In the first diallel combination (1<sup>st</sup> DC) GCA effects were significant in the first year and insignificant in the second year showing that for the fiber length inheritance under the conditions of second year non-additive gene effects were mainly important. The SCA effects were significant in both years (1<sup>st</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years). In the second diallel combination the variances of the general (GCA) and specific (SCA) combining ability were highly significant indicating that additive and non-additive gene effects were important for the inheritance of studied trait. The



ratio of variances GCA/SCA was in favor of GCA, but tested with the F-criterion to SCA was

insignificant, which did not confirm a greater importance of additive gene effects.

Table 5. Analysis of GCA and SCA variances for fiber length in the first and second diallel combinations, each one tested two years (1<sup>st</sup> DC – 1<sup>st</sup> and 2<sup>nd</sup> years and 2<sup>nd</sup> DC – 1<sup>st</sup> and 2<sup>nd</sup> years)

Diallel combination, year	Source of variation	Degrees of freedom	Mean squares	F-exp.
1 <sup>st</sup> DC - 1 <sup>st</sup> year	Crosses	20	2.999	7.77 <sup>++</sup>
	GCA	5	7.596	19.68 <sup>++</sup> /5.18 <sup>++</sup> *
	SCA	15	1.466	3.80 <sup>++</sup>
	Errors	40	0.386	
1 <sup>st</sup> DC - 2 <sup>nd</sup> year	Crosses	20	2.440	3.69 <sup>++</sup>
	GCA	5	3.561	5.39 <sup>ns</sup> /1.72 <sup>ns</sup> *
	SCA	15	2.066	3.13 <sup>++</sup>
	Errors	40	0.661	
2 <sup>nd</sup> DC – 1 <sup>st</sup> year	Crosses	20	2.903	6.60 <sup>++</sup>
	GCA	5	5.582	12.69 <sup>+</sup> /2.78 <sup>ns</sup> *
	SCA	15	2.010	4.57 <sup>++</sup>
	Errors	40	0.440	
2 <sup>nd</sup> DC – 2 <sup>nd</sup> year	Crosses	14	1.759	8.84 <sup>++</sup>
	GCA	4	1.254	6.30 <sup>++</sup> /0.64 <sup>ns</sup> *
	SCA	10	1.962	9.86 <sup>++</sup>
	Errors	28	0.199	

\*tested with the F-criterion to SCA

The effects of GCA are indicated in Tables 6 and 7. Varieties Darmi, Mytra, Dorina, from the 1<sup>st</sup> diallel combination, and Natalia, from the 2<sup>nd</sup> diallel combination, showed a positive and high GCA in different environments (in both years of the study). Since GCA is determined by additively acting genes, it can be considered that

these cultivars possessed the largest number of additive genes.

Zhang et al. (2016) reported that GCA effects were closely related to parental values for yield and fiber quality, which was confirmed in our study. Parents having longer fiber had higher GCA values.

Table 6. Mean values in mm (x) and GCA of the parents for fiber length in first diallel combination tested two years (1<sup>st</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years)

Parent	1 <sup>st</sup> DC - 1 <sup>st</sup> year		1 <sup>st</sup> DC - 2 <sup>nd</sup> year		Average	
	x	GCA	x	GCA	x	GCA
P <sub>1</sub> - B. Iskar	26.0	-0.489	26.6	-0.410	26.3	-0.449
P <sub>2</sub> - Barut 2005	27.9	-0.360	26.9	-0.297	27.4	-0.328
P <sub>3</sub> - Darmi	28.2	0.124	27.6	0.436	27.9	0.280
P <sub>4</sub> - Mytra	28.2	0.453	27.9	0.303	28.1	0.378
P <sub>5</sub> - Helius	27.3	-0.555	26.5	-0.335	26.9	-0.445
P <sub>6</sub> - Dorina	29.6	0.828	28.2	0.303	28.9	0.565
Standard error	1.01	0.179	1.34	0.235	1.18	

Table 7. Mean values in mm (x) and GCA of the parents for fiber length in second diallel combination tested two years (2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years)

Parent	2 <sup>nd</sup> DC – 1 <sup>st</sup> year		2 <sup>nd</sup> DC – 2 <sup>nd</sup> year		Average	
	x	GCA	x	GCA	x	GCA
P <sub>1</sub> - Chirpan-539	24.1	-0.514	26.9	-0.139	25.5	-0.326
P <sub>2</sub> - Helius	24.0	-0.639	26.9	-0.205	25.5	-0.422
P <sub>3</sub> - Rumi	25.9	0.211	27.0	-0.961	26.5	-0.375
P <sub>4</sub> - Boyana	25.4	0.194	27.0	0.032	26.2	0.113
P <sub>5</sub> - Natalia	26.4	0.628	27.4	0.408	26.9	0.518
P <sub>6</sub> - Nelina	26.8	-0.119	-	-	-	-
GD 5 %	1.09		0.68			
Standard error		0.191		0.138		

SCA data varied more strongly depending on environmental conditions. There were 5 out of 15 crosses from the 1<sup>st</sup> diallel combination and 2 crosses from the 2<sup>nd</sup> diallel combination with significant positive SCA in both years (data are not given hier). These crosses have a high

selection value. It is believed that they exhibit dominant and epistatic interactions, causing transgressive variability in the next F<sub>2</sub> generation. Estimates of the variance components for the GCA and SCA are presented in Table 8.

Table 8. Variance components for fiber length in the first and second diallel combinations tested in replicated trials in two years (1<sup>st</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years and 2<sup>nd</sup> DC - 1<sup>st</sup> and 2<sup>nd</sup> years)

Sources of variation	Variance ± standard error			
	1 <sup>st</sup> DC - 1 <sup>st</sup> year	1 <sup>st</sup> DC - 2 <sup>nd</sup> year	2 <sup>nd</sup> DC - 1 <sup>st</sup> year	2 <sup>nd</sup> DC - 2 <sup>nd</sup> year
Crosses	0.871 <sup>++</sup> ±0.317	0.593 <sup>±</sup> ±0.261	0.821 <sup>++</sup> ±0.308	0.520 <sup>±</sup> ±0.222
GCA	0.255± 0.201ns	0.062± 0.099 ns	0.148±0.150 ns	0.034±0.059 ns
SCA	0.360 <sup>±</sup> ±0.181	0.468± 0.256	0.523 <sup>±</sup> ±0.246	0.587 <sup>±</sup> ±0.293
Errors	0.386 <sup>+++</sup> ±0.086	0.661 <sup>+++</sup> ±0.147	0.440 <sup>+++</sup> ±0.117	0.198±0.053 <sup>+++</sup>

Their values confirmed the results of the diallel analysis that the non-additive (for the 1<sup>st</sup> and 2<sup>nd</sup> diallel combinations) gene effects were important for inheritance. The results obtained were consistent with those reported by other authors (Hussain et al., 2010; Singh et al., 2010; Bölek et al., 2014; Khan et al., 2017) that non-additive gene effects were more important for fiber length. Akiskan & Gencer (2014), Ekinci & Basbag (2018), Carvalho et al. (2018) noted a predominance of additive gene effects. Nasimi et al. (2016) found an additive type of gene action with partial dominance in the inheritance of this trait.

From the research results it can be concluded that additive and non-additive gene effects participated in the inheritance of fiber length. Non-additive gene action predominated over additive and reveals that fiber length was more strongly influenced by genes with non-additive action. The varieties Dorina, Mytra, Darmi (1<sup>st</sup> diallel combination) and Natalia (2<sup>nd</sup> diallel combination) exhibited the longest fibers and the highest GCA appeared to be the best general combiners and can be used in future breeding programs to enhance this trait. The low to medium-high heritability coefficients in the narrow sense and the high contribution of non-additive genetic variation reveal that effective selection should be conducted in the later hybrid generations - F<sub>3</sub>-F<sub>4</sub>.

## CONCLUSIONS

Additive and non-additive gene effects were important for the inheritance of fiber length. In both diallel crosses the non-additive gene action

predominated and selection by this trait should be conducted in the later hybrid generations - F<sub>3</sub>-F<sub>4</sub>.

Cultivars having longer fibers possessed dominant genes that acted to increase fiber length, while in cultivars having short fiber dominant genes acted to decrease this trait.

The varieties Darmi, Mytra, Dorina, from the 1<sup>st</sup> diallel combination, and Nataliya, from the 2<sup>nd</sup> diallel combination, were identified as good general combiners for this trait. These varieties had longer fiber and high GCA effects in different environments.

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