# Inheritability of grain weight per spike in spring barley hybrids

## Margarita Gocheva\*, Darina Valcheva

Agricultural Academy, Institute of Agriculture – Karnobat, Bulgaria \*E-mail: *m\_gocheva30@abv.bg* 

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#### Abstract

In the period 2009-2011 was conducted genetic research on parental forms of spring barley and their hybrids to obtain information about the type of inheritability of the trait grain weight per a spike. As parental components were used 6 accessions of spring barley. For three consecutive years in a hybridization nursery were carried out 30 diallel crosses. Additive-dominant relationships of the trait were analyzed by the ratio between parameters (d/a). Results from the study provide broad information about the genetic control of the trait grain weight per spike. It was established that variance in hybrid populations is determined by the additive-dominant genetic system. Dominant action outperforms the additive and has greater significance in inheriting the attribute.

Key words: spring barley; inheritability; genetical components; grain weight per spike

## INTRODUCTION

In combinatory, breeding a suitable method for studying genetic nature of main quantitative traits is diallel analysis (Ognyanova, 1972; Genchev et al., 1975). It had its beginning in the works of Yates (1947). Diallel crossing schemes are used to analyze the combinatory ability and to receive information regarding the genetic mechanism which controls yield and its structural elements (Mersikov, 1982; Molle, 1988; Dimova, 2015; Khan et al., 2007). This method allows crosses of source parental varieties in all possible combinations (Pesaraklu et al., 2016). In self-pollinated plants is mostly applied the traditional diallel analysis of Hayman (1954), and for analysis were used generations F1, F2, and in some cases F<sub>3</sub> (Simakov, 1990; Aleksandrov, 2005; Tsenov, 2005).

Knowledge of the genetic structure and way of inheritability helps to select the right breeding strategy for desirable source parental forms to create hybrids, which possess the traits wanted by the breeders (Eshghi & Akhundova, 2009; Ilker et al., 2010).

The diallel analysis can help determine the significance of each structural element of the yield and thus expand the possibilities to conduct a suitable, scientifically grounded selection of parental components for hybridization (Dehghani et al., 2006).

A number of studies on the genetic nature of the trait grain weight per spike established that the non-additive type of inheritability with dominant gene action towards high values of the trait is more frequent (Nikitenko & Todorov, 1979; Kamaluddin et al., 2007; Petrovic & Dimitrijevic, 2009). Zaazaa et al. (2012) and Ijaz & Kashif (2013) found that this trait is very important and directly related to the yield levels. They established that it is controlled by the additive-dominant genetic system with occurrences of epistasis.

The aim of this study was to clarify the genetic nature of the source material and to establish the inheritability type of the trait spike length of spring barley hybrids.

#### MATERIAL AND METHODS

The study was conducted in the period of 2009-2011 at the Institute of Agriculture in Karnobat, Bulgaria. In a hybridization nursery were carried out 30 diallel crosses. In the diallel cross took part 6 parental varieties of spring barley - Scarlett, Fink, Barke, Zernogradskij 73, Bitrana and 3717C-60. Parents and hybrids were sown by hand in three replications of 6 rows and nine seeds per row. Biometric measurements were taken annually from parents and hybrids to determine the trait values.

In accordance with Ognyanova's directions, in this specific diallel combination were determined two parameters which show the genetic difference effect on phenotype (Genchev et al., 1975). The additive dominant relations of the trait were analyzed by the ratio between the two parameters (d/a). In the statistical processing of data were applied analysis of variance and calculus of variations and was used software program JMP version 5.0 1a, 2002. The graphic analysis of the trait spike length was built and interpreted according to Mather (1949) and Jinks (1954).

Figures 1 and 2 show data on the average monthly temperatures and amount of rainfall by months for the three years of the study. It is clear in the graphics that compared to the multiannual values there were significant differences regarding rainfall and 2009 was characterized with severe and lasting soil drought in April, May, June; whereas 2010 - with more rainfall, especially in May, June and July.



Figure 1. Average amount of rainfall during the period



Figure 2. Average monthly temperatures during the period

### **RESULTS AND DISCUSSION**

Table 1 presents data on grain weight per spike from parents and hybrids in the three years of the study. Grain weight per spike average for the used parental forms ranged from 1.16 g in 2010 to 1.54 g in 2011. It belongs to the traits which vary from weak to medium under the influence of the environment (Mersinkov, 2000; Dimova, 2015). The results showed that in 2011 grain weight per spike was highest, average for the varieties, whereas in the other two years it was significantly lower. These values came as a result from the contrasting weather conditions during the period of study (Figures 1 and 2). The drought during the grain filling and ripening period in 2009 and the great amount of rainfall in 2010 caused reduction of grain weight.

In the diallel combination were included 6 parents of spring barley, which can be conditionally divided into three groups by the studied trait. In the first group fell variety Scarlett, which formed heavy spikes with weight ranging from 1.22 g to 1.68 g. In the second group were varieties Barke, Bitrana and 3717C-60. The average weight of their spikes in the

	Grain weight per spike								
Parents and hybrids	2009		2010		20	2011		Average for the period	
	g	d/a	g	d/a	g	d/a	g	d/a	
Scarlett	1.44		1.22		1.68		1.45		
Fink	1.18		1.12		1.45		1.25		
Barke	1.09		1.19		1.60		1.29		
Zernogradskij 73	1.14		1.22		1.46		1.27		
Bitrana	1.37		1.14		1.51		1.34		
3717C-60	1.33		1.05		1.52		1.30		
Average	1.26		1.16		1.54		1.32		
$P_{1X} P_2$	1.27	-0.34	1.19	0.34	1.54	-0.20	1.33	-0.17	
$P_{1X} P_{3}$	1.22	-0.24	1.19	-1.07	1.64	0	1.35	-0.25	
$P_{1X} P_4$	1.34	0.34	1.22	-0.33	1.52	-0.44	1.36	0	
$P_{1X} P_5$	1.33	-2.25	1.15	0.89	1.59	-0.04	1.36	-0.71	
$P_{1X} P_{6}$	1.37	-0.35	1.14	0.06	1.59	-0.11	1.37	-0.11	
$P_{2X}P_{3}$	1.17	0.69	1.14	-0.34	1.55	0.32	1.29	0.67	
$P_{2X}P_4$	1.16	-0.35	1.17	-0.04	1.46	1.00	1.26	-0.13	
$P_{2x} P_5$	1.24	-0.37	1.13	-0.57	1.51	1.10	1.29	-0.06	
$P_{2X} P_6$	1.19	-1.56	1.14	1.60	1.47	-0.37	1.27	-0.31	
$P_{3X}P_4$	1.14	0.88	1.20	-0.27	1.52	-0.13	1.29	0.30	
$P_{3x} P_5$	1.23	-0.01	1.16	-0.05	1.53	-0.53	1.31	-0.38	
$P_{3X}P_{6}$	1.25	0.33	1.10	-0.25	1.56	-0.17	1.30	1.22	
$P_{4x} P_5$	1.21	-0.45	1.15	-0.77	1.49	0.25	1.28	-0.74	
$P_{4X}P_{6}$	1.26	0.27	1.08	-0.71	1.49	-0.15	1.20	-0.86	
$P_{5X} P_6$	1.32	-1.25	1.06	0.84	1.51	-1.00	1.30	-1.21	
Average	1.25		1.15		1.53		1.31		
LSD	0.04		0.04		0.05				
Variation of parents and hybrids									
P min	1.09		1.05		1.45		1.25		
P max	1.44		1.22		1.68		1.45		
F <sub>1</sub> min	1.14		1.06		1.46		1.26		
F <sub>1</sub> max	1.37		1.22		1.64		1.37		

Table 1. Grain weight per spike from parents and F1 hybrids

studied period ranged from 1.29 g for variety Barke to 1.34 g for Bitrana. The varieties in the third group

– Fink and Zernogradskij 73 had low grain weight per spike, 1.25 g and 1.27 g, respectively.



Figure 3. Diallel diagram for grain weight per spike in 2009



Figure 4. Diallel diagram for grain weight per spike in 2010



Figure 5. Diallel diagram for grain weight per spike in 2011

Average for the group of hybrids, grain weight per spike was highest in 2011 (1.53 g), a year which was more favorable in terms of weather conditions. The variation of values from parents and hybrids was greatest in 2009 and weaker in 2010. Grain weight from parents varied within a wider range compared to hybrids. Average for the three years, the studied trait in parents ranged from 1.25 g to 1.45 g, and in hybrids its values were from 1.26 g to 1.37 g. In 2011,  $F_{max}$  in hybrids was 1.64 g, whereas  $P_{max}$  in parents reached up to 1.68 g (Table 1).

The d/a ratio showed that in the diallel combination for 9 of the hybrids in the three years of the study and average for the period, the inheritability of grain weight per spike was additive. Crosses  $P_1 \times P_5$ ,  $P_2 \times P_3$ ,  $P_4 \times P_5$  and  $P_4 \times P_6$  had incomplete dominance average for the period, and in different years changed the degree and direction of inheritability depending on the year conditions. Two of the crosses, which included parents of medium manifestation of the trait, showed that grain weight per spike is inherited dominantly. The inheritability of the trait strongly changed in hybrids  $P_1 \times P_5$  and  $P_2 \times P_6$ . There, in 2009, the inheritability was negative overdominance. In 2010, the cross  $P_1 \times P_5$  changed the direction of inheritability and the d/a value showed incomplete dominance. In  $P_2 \times P_6$  the inheritability was overdominant in direction to the parent with the higher value.

Positive overdominance, even though in only one of the years, can be a precondition for transgressive variability in  $F_2$  by grain weight per spike which would benefit the selection by this trait.

Whitehouse et al. (1958) considered that the graphic presentation of inheritability by the studied trait is sufficient to obtain information on its genetic basis. Figures 3, 4 and 5 show the diallel diagrams by the trait grain weight per spike by years for the period 2009-2011. In the three years, the regression line crossed the ordinate axis above the beginning of the coordinate system and showed manifestations of incomplete dominance of the trait. In the years, the points of the parents from the diallel combination changed their position as a result of the genotype-environment interaction. In 2009, on the lower end of the regression line were located varieties Fink and Barke, which shows that grain weight per spike is determined by the dominant genes in them.

All the other varieties are located near the center of the regression line which shows relative balance between dominant and recessive genes. Despite of this, varieties Scarlett and Zernogradskij 73 are a little further from the center and it can be suggested that the recessive genes were predominant in them. The results also correspond with the data in Table 2 regarding the order of the parental varieties by value of grain weight per spike and by presence of dominant genes.

The lack of proven correlation in 2009 shows the presence of dominant genes acting in a different direction.

It was observed in 2010 that the variety points shifted, which showed that when the environmental conditions changed, different genetic systems were activated, controlling the grain weight per spike. Such behavior of varieties was reported by the research scientists Savova & Valcheva (2017).

Other studies over the years did not report changes in the position of the parental varieties (Mersinkov, 2000). Variety Fink kept its position, which confirmed the effect of dominant genes. With variety Zernogradskij 73, which in this year was again in the upper end of the regression line, the recessive genes determined the occurrence of the trait. Prevailing recessive genes in this year were observed for variety Bitrana. With Scarlett and Barke, the correlation between dominant and recessive genes was approximately the same. The values of Wr+Vr, which correspond to the position of varieties towards the regression line, show that the varieties with low absolute values of the trait (3717C-60 and Fink) had most dominant genes (Table 2). These varieties combined with parents showing high values of grain weight per spike can produce hybrids with high values of the trait. This is made possible by the presence of dominant genes which determined its expression and the dominant nature of inheritability. In 2011, which was the most favorable in terms of weather conditions for barley development, the position of varieties along the regression line was different than the previous years. Varieties Zernogradskij 73 and Bitrana were found on the lower end of the regression line and showed prevalence of the dominant genes responsible for grain weight per spike. Unlike the previous two years, Scarlett and Barke had more recessive genes which determine the trait.

As both varieties in the year had the highest phenotype values and strong positive correlation

Mo	Variation	Grain weigh	Grain weight per spike		Dominant genes		
JNG	varieties	g	rank	$W_r + V_r$	rank	= <b>∓</b> ſ	
			$F_1 - 2009$				
1.	Scarlett	1.44	1	0.01471	5		
2.	Fink	1.18	4	0.00773	1		
3.	Barke	1.09	6	0.01156	2		
4.	Zernogradskij 73	1.14	5	0.01706	6		
5.	Bitrana	1.37	2	0.01314	4	+0.20	
6.	3717C-60	1.33	3	0.01209	3		
	Average for 2009	1.26		0.01272			
F <sub>1</sub> -2010							
1.	Scarlett	1.22	2	0.00347	3		
2.	Fink	1.12	5	0.00217	1		
3.	Barke	1.19	3	0.00393	4		
4.	Zernogradskij 73	1.22	1	0.00663	6		
5.	Bitrana	1.14	4	0.00655	5	+0.48	
6.	3717C-60	1.05	6	0.00274	2		
	Average for 2010	1.16		0.00425			
		F	– 2011 year				
1.	Scarlett	1.68	1	0.00962	6		
2.	Fink	1.45	6	0.00616	3		
3.	Barke	1.60	2	0.00786	5		
4.	Zernogradskij 73	1.46	5	0.00288	1		
5.	Bitrana	1.51	4	0.00440	2	+0.85	
6.	3717C-60	1.52	3	0.00644	4		
	Average for 2011	1.54		0.00623			
F <sub>1</sub> – Average for period 2009-2011							
1.	Scarlett	1.45	1	0.00927	6		
2.	Fink	1.25	6	0.00535	1		
3.	Barke	1.29	4	0.00778	3		
4.	Zernogradskij 73	1.27	5	0.00886	5		
5.	Bitrana	1.34	2	0.00803	4	+0.66	
6.	3717C-60	1.30	3	0.00709	2		
	Average for 2009-2011	1.32		0.00773			

<b>Table 2.</b> Grain weight per spike and	dominant genes ranking of the parents
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(r=+0.85) with high values of Wr+Vr, it can be said that they also had the most recessive genes and it is not advisable to use them as parents. Fink and 3717C-60 were in the center of the regression line and demonstrated equality of the dominant and recessive genes.

Table 3 presents data on the genetic components of grain weight per spike. The additive parameter D during the three years of the study and average for the period had relatively low values, which comes to show that the additive effect of the genes was less significant for the variability of the trait. The mean square deviation by years and average for the period had lower values and demonstrated weak dispersing around the mean arithmetic. The dominant action expressed with first dominant parameter  $H_1$ , superseded the additive and showed greater significance of the dominant variance in inheritability of grain weight per spike.  $H_1$  during the three years of the study was greater than  $H_2$ , which shows that the positive and negative alleles on the loci, which show dominance in the parents, were not proportionally distributed as  $H_1$  and  $H_2$ significantly distinguished and were proven values. This was also confirmed in the studies of Pal & Kumar (2012).

Constis components -		Average for the						
Genetic components -	2009	2009 2010 2011		period				
Parameters								
D	$0.0178 \pm 0.0015$	$0.0037 \pm 0.0005$	$0.0064 \pm 0.0010$	$0.0093 \pm 0.0010$				
F	$0.0050 \pm 0.0014$	$-0.0007 \pm 0.0012$	$-0.0007 \pm 0.0010$	$0.0012 \pm 0.0012$				
H <sub>1</sub>	$0.0255 \pm 0.0027$	$0.0081 \pm 0.0011$	$0.0095 \pm 0.0091$	$0.0144 \pm 0.0043$				
H <sub>2</sub>	$0.0101 \pm 0.0012$	$0.0075 \pm 0.0007$	$0.0088 \pm 0.0067$	$0.0088 \pm 0.0029$				
h <sup>2</sup>	$-0.0004 \pm 0.0005$	$0.0001 \pm 0.0005$	$-0.0010\pm0.0020$	$-0.0014 \pm 0.0010$				
Traits								
H <sub>1</sub> /D	1.430	2.215	1.498	1.714				
$\sqrt{H_1/D}$	1.196	1.488	1.224	1.303				
F <sub>1</sub> -P	-0.0132	-0.0124	-0.0051	-0.0307				
$H_{2}/4H_{1}$	0.10	0.23	0.23	0.19				
K	0.069	0.083	1.458	0.537				
h <sup>2</sup> /H <sub>2</sub>	-0.041	0.008	-0.115	-0.148				
K <sub>d</sub> /K <sub>r</sub>	1.268	0.872	0.914	1.018				
$H_1$ - $H_2$	0.015	0.001	0.001	0.006				
$F^2/\sqrt{4D}(H_1-H_2)$	0.0007	0.0002	0.0001	0.0003				
Inheritability H <sup>2</sup>	89.26	88.52	75.30	84.36				
Inheritability h <sup>2</sup>	75.76	46.66	48.23	56.88				

Table 3. Genetic components of grain weight per spike

Parameter F in two of the years had a negative value, which suggests certain predominance of the recessive over dominant alleles. In the first year of the study and average for the period the parameter had a positive value and we see prevalence of the dominant alleles. The diversity observed by years for F can be explained with the readjustment of genetic formulas for the trait in terms of change of environmental conditions. At the same time its values were very low and tended to zero and it should be accepted that the positive and negative alleles had the same relative frequency.

The average degree of dominance in the whole cross expressed by means of ratio  $H_1/D$  was 1.71, mean for the period, and showed that in the inheritability of this trait decisive role was played by the overdominance effect. The average degree of dominance in every locus was expressed by the square root of the same ratio and its high positive value in this study shows the role of the overdominance effect.

The average degree of the dominance direction  $(F_1-P)$ , expressed by the difference between the mean values of the crosses minus the mean values of the parents was a negative number and pointed that the dominance was in the direction of reducing the trait.

Index  $H_2/4H_1$ , which indicated the nature of distribution of the dominant and recessive alleles in

the parental forms, was 0.19 mean for the period. Its value was lower than 0.25 and consequently there was asymmetry in the distribution of dominant and recessive alleles in the parents.

Analyzing the values of ratio Kd/Kr also proved the uneven distribution of the dominant and recessive alleles and average for the period the dominant prevailed (Kd/Kr=1.018). The prevalence of the dominant alleles in the parents by years was reported in 2009 (Kd/Kr=1.268), whereas in the other two years of the study the recessive prevailed (in 2010 -Kd/Kr=0.872 and in 2011 - Kd/Kr=0.914).

The contrasting environmental conditions during the years of the study led to readjustment of the genetic formula of grain weight per spike. An indicator for distinguishing variability depending on the expression of genes, caused by readjustment of the genetic trait control was the change in parameter  $h^2$  and index  $h^2/H_2$ . In 2009 and 2011,  $h^2$  had a negative value and in 2010 it was positive. Index  $h^2/H^2$  did not express the exact number of genes, as there was genetic effect in opposing directions. The values of  $\kappa$  showed that one gene or a group of genes were responsible for the manifestation of the trait grain weight per spike. Index F2/ $\sqrt{4D(H_1-H_2)}$  average for the period and by years had a value of zero, which showed strongly variable dominance by locus. The inheritability coefficients established over the years of the study in the broad sense ( $H^2$ ) varied from 75.30% to 89.26%, which points that it was inherited and therefore breeding by the trait of grain weight per spike can be successful. Inheritability in the narrow sense ( $h^2$ ), average for the period, was 56.88%, whereas in two of the years it was under 50.00%. These lower than the average values show that the effective breeding selection by the trait grain weight by spike can be directed in later segregating generations.

## CONCLUSIONS

The trait of grain weight per spike is controlled by an additive-dominant genetic system where the dominant effect of genes surpasses the additive. In hybrid populations it is determined by the same gene or the same group of genes with opposing effect. Breeding by grain weight per spike should be conducted in later segregating generations.

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