

**THE ANALYSIS OF GENE EFFECT IN THE INHERITANCE OF
KERNEL NUMBER PER SPIKE IN BARLEY HYBRID**

Milomirka MADIĆ¹, Aleksandar PAUNOVIĆ¹, Dragan ĐUROVIĆ¹, Marija
KRALJEVIĆ-BALALIĆ², and Desimir KNEŽEVIĆ³

¹Faculty of Agronomy, Cara Dušana 34, 32000 Čačak,

²Faculty of Agriculture, 21000 Novi Sad,

³Center for Small Grains Kragujevac, Serbia and Montenegro

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In diallel crossing, excluding reciprocal ones, five divergent genotypes of barley (Vada, Đerdap, NS-293, Jagodinac and Sladoran) were included with the mode of inheritance and gene effect studied using the regression analysis of variance and co-variance for the number of kernels per spike. The absence of inter-allele interaction established using the regression analysis $VrWr$ and WrW' resulted from the use of the mode selected. In the inheritance of the number of kernels per spike, the regression pointed at dominant gene effect as well as at the unevenly distributed dominant and recessive genes in the genotypes selected. While Jagodinac, Vada and NS-293 had the highest number of dominant, Đerdap and Sladoran had the highest one of the recessive genes for the number of kernels per spike. Therefore, in the two-rowed genotypes, the higher number of dominant genes was, the higher number of kernels per spike was, and conversely, the higher number of the recessive genes was, the lower number of kernels per spike was.

Key words: barley, the number of kernels, gene effect, inheritance, heritability

Corresponding author: Milomirka Madić, Faculty of Agronomy, Cara Dušana 34, 32000
Čačak, Serbia and Montenegro
Phone: +381 32 303 400; fax: +381 32 345 264; e-mail: mmadic@tfc.kg.ac.yu

INTRODUCTION

Grain yield implies a complex trait of an outstanding economic importance dependent on several hereditarily exerted traits as well as on the environmental conditions plants are growing under. Hence, the researches in genetics and plant breeding contributing to a better knowledge of yield and its components not only in barley, but also in a range of other plants grown for grains are countless.

The number of kernels per spike is referred to as the direct component of yield dependent on the spike density and length as well as on the number of kernel rows per spike. CHOO *et al.* (1980), PRŽULJ and MOMČILOVIĆ (1995), pointed to the number of kernels as the most important component of yield. SINHA *et al.* (1985) suggested that barley be selected more strictly in the earlier generations on a higher number of kernels per spike and a longer spike for ensuring a higher mass of 1000 kernels as well as the mass of kernels per spike in the next level of selection.

HESSELBACH (1985) denoted that, over recent years, kernel yield of barley had mainly increased as the result of a higher number of kernels per spike, with the number of spikes per unit area remaining unaltered and kernel mass now and then reduced.

As the number of kernels per spike is considered a direct component of yield, the inheritance mode, gene effect and the components of genetic variance ought to be determined using the analysis of diallel crossing so as to enable the selection in later generations with more safety.

MATERIALS AND METHOD

The mode of inheritance and the components of genetic variance of the number of kernels per spike were studied using the genotypes Vada, Đerdap, NS-293, Jagodinac and Sladoran.

Diallel crossings, excluding reciprocal ones, proceeded over 1999, with six hybrid combinations of the F₁ and F₂ generation obtained. In the same year, hybrid material and parents were sown in the trial plot of the Centre of Small Grains in Kragujevac, using a random split-block-design with three replications. Sowing was performed using a thin sowing pattern, with 1 m long, 20 cm inter-spaced rows and 10 cm inter-spaced plants within the row, thereby providing invariable growing conditions for all the plants of the generations observed.

The test of significance of the mean values of generations related to the parental average was used for the inheritance mode determinations (KRALJEVIĆ-BALALIĆ *et al.*, 1991) with the components of genetic variance from diallel crossings calculated using the method of MATHER and JINKS (1971).

RESULTS AND DISCUSSION

The mean values and inheritance of the number of kernels per spike.

– Analysing the mean values of kernel number per spike, Đerdap, NS-293 and Jagodinac did not significantly differ from each other, whereas the remaining parents did.

Therefore, the highest mean value for the number of kernels per spike was recorded in Vada (33.4), and the lowest one in Sladoran (28). The cross combinations of Vada x Jagodinac (34.4) and Vada x Sladoran (34.3) had the highest number of kernels in the F₁ generation whereas Đerdap x NS-293 had the lowest one (29.9).

The mean values of kernel number in the F₁ generation were lower in most combinations than being in the F₁ generation. Thus, the combination Vada x Đerdap had the highest and Đerdap x Sladoran the lowest number of kernels per spike.

The highest variability of such a trait was observed in the cultivar Đerdap (11.75%) and the lowest one in Sladoran (7.03%). The F₁ hybrids indicated a lower variability than the parents did with the exceptions to the cross combination of Vada x NS-293, the variability coefficient of which amounted to 13.29%.

As manifested by standard deviations and variability coefficients, higher variability of the trait under consideration in the F₂ generation was in the main present in those combinations in which some of the genotypes, showing higher variability themselves, were included as parents. Thus, the highest coefficient of variability in the F₂ generation was recorded in the combination Đerdap x NS-293 (15.8%) and the lowest one in that of NS-293 x Sladoran (8.97%) (Table 1).

Considering that the number of kernels resulted from the number of spikes and flowers per spike on the one hand, and from the efficiency with which kernels were fertilised and set in the flowers, on the other, it appeared to be a highly variable trait. While ZECEVIC (1996) revealed high values of the coefficient of variability, KOVAČEVIĆ (1980; 1987) got somewhat lower ones, which was in agreement with the currently obtained results, the coefficient of variability ranging from 6.74% to 15.8%.

The inheritance of the number of kernels per spike in the F₁ and F₂ generation varied depending on the cross combination. Thus, in the combinations in which parents did not significantly vary in the number of kernels per spike, a full dominance or super-dominance inclining to a higher number of kernels per spike was revealed. In the crossings in which the parents notably varied in the number of kernels, partial dominance in the inheritance of the trait under consideration occurred. So obtained results were in agreement with those of KOVAČEVIĆ (1980), LALIĆ *et al.*, (1984), and ORE (1991) whereas, in the diallel crossing of two- and many-rowed barley, the partial dominance in the inheritance of the number of kernels per spike was observed by MADIĆ (1995).

Therefore, the values obtained for heritability were found to range from low (8.79%) in the cross combination NS-293 x Sladoran to high (52.68%) in that of Jagodinac x Sladoran (Table 1).

Tab.1. Statistical parameters and the inheritance of kernel number per spike in barley

Cross	Generation	No. of. Plants	$\bar{X} \pm s_{\bar{x}}$	S	V (%)	h^2
K-1	P ₁	30	33.4±0.60	3.27	9.79	
Vada	F ₁	30	33.8±.41 <i>od</i>	2.28	6.74	
x	F ₂	90	33.3±.33 <i>od</i>	3.28	10.21	26.27
Đerdap	P ₂	30	30.8±.66	3.62	11.75	
K-2	P ₁	30	33.4±0.60	3.27	9.79	
Vada	F ₁	30	31.2±0.75 <i>pd</i>	4.12	13.29	
x	F ₂	90	30.7±0.39- <i>d</i>	3.72	12.12	13.36
NS-293	P ₃	30	30.3±0.53	2.90	9.43	
K-3	P ₁	30	33.4±0.60	3.27	9.79	
Vada	F ₁	30	34.5±0.61 <i>od</i>	3.33	9.79	
X	F ₂	90	31.0±0.35 <i>d</i>	3.39	12.87	42.12
Jagodina	P ₄	30	31.5±0.40	2.22	7.03	
K-4	P ₁	30	33.4±0.60	3.27	9.79	
Vada	F ₁	30	34.3±0.59 <i>od</i>	3.28	10.90	
x	F ₂	90	31.2±0.37 <i>pd</i>	3.49	11.11	21.57
Sladoran	P ₅	30	28.0±0.49	2.70	9.64	
K-5	P ₂	30	30.8±0.66	3.62	11.75	
Đerdap	F ₁	30	29.9±0.63	3.50	11.70	
x	F ₂	90	30.0±0.49	4.74	15.80	49.44
NS-293	P ₃	30	30.3±0.53	2.90	9.43	
K-6	P ₂	30	30.8±0.66	3.62	11.75	
Đerdap	F ₁	30	31.7±0.57	3.15	10.16	
x	F ₂	90	30.3±0.40	3.71	12.24	35.75
Jagodina	P ₄	30	31.5±0.40	2.22	7.03	
K-7	P ₂	30	30.8±0.66	3.62	11.75	
Đerdap	F ₁	30	30.0±0.34 <i>d</i>	2.76	9.20	
x	F ₂	90	29.0±0.33 <i>pd</i>	3.22	10.92	10.18
Sladoran	P ₅	30	28.0±0.49	2.70	9.64	
K-8	P ₃	30	30.3±0.53	2.90	9.43	
NS-293	F ₁	30	32.0±0.64 <i>od</i>	3.56	11.12	
x	F ₂	90	31.9±0.34 <i>od</i>	3.25	10.19	21.09
Jagodina	P ₄	30	31.5±0.40	2.22	7.03	
K-9	P ₃	30	30.3±0.53	2.90	9.43	
NS-293	F ₁	30	30.5±0.36 <i>d</i>	2.04	6.68	
x	F ₂	90	30.2±0.28 <i>d</i>	2.71	8.97	8.79
Sladoran	P ₅	30	28.0±0.49	2.70	9.64	
K-10	P ₄	30	31.5±0.40	2.22	7.03	
Jagodina	F ₁	30	30.7±0.33 <i>pd</i>	2.11	6.87	
x	F ₂	90	30.8±0.33 <i>pd</i>	3.15	10.22	52.68
Sladoran	P ₅	30	28.0±0.49	2.70	9.64	

F1 (LSD - 0.05 = 1.45; 0.01 = 1.96); F2 (LSD - 0.05 = 1.39; 0.01 = 1.87); *od* - overdominance; *d* - dominance; *pd* - partial dominance

The components of genetic variance and graphic analysis. - Analysing the components of genetic variance, the value of additive gene effect was found to

be lower than that of non-additive one in all the generations together with all the combinations. The positive value F in the F_1 and in F_2 generation denoted that in the phenotypic expression of such a trait, the dominant genes prevailed over the recessive ones. The ratio $H_2/4H_1$ indicated a slight asymmetry of the dominant and recessive genes in the parents. Thus, the average level of the dominance was higher than 1 in the F_1 and in F_2 generation, pointing to the super-dominance in the inheritance of the number of kernels per spike. The ratio between the total number of dominant and recessive alleles K_D/K_R in both generations sought was higher than 1, thereby showing a prevalence of the dominant over the recessive alleles in all the parents (Table 2).

Table 2. The components of genetic variance for the number of kernels per spike

Variance Components	Values	
	F_1	F_2
D	1.786	1.967
H_1	3.176	11.395
H_2	3.010	10.756
F	0.795	2.635
E	0.251	0.213
$H_2/4H_1$	0.237	0.234
u	0.615	0.626
v	0.385	0.374
$\sqrt{H_1/D}$	1.334	2.407
K_D/K_R	1.401	1.771
Heritability (%)		45.2

The regression $VrWr$ -analysis for the number of kernels per spike in the F_1 (Fig. 1 and 2) and F_2 (Fig. 3 and 4) generation did not significantly deviate from one, suggesting the absence of inter-allele interaction. The cross-section of the regression line expected with Wr axis ($a = -$) was below the co-ordinate origin suggesting super-dominance in the inheritance of the trait concerned.

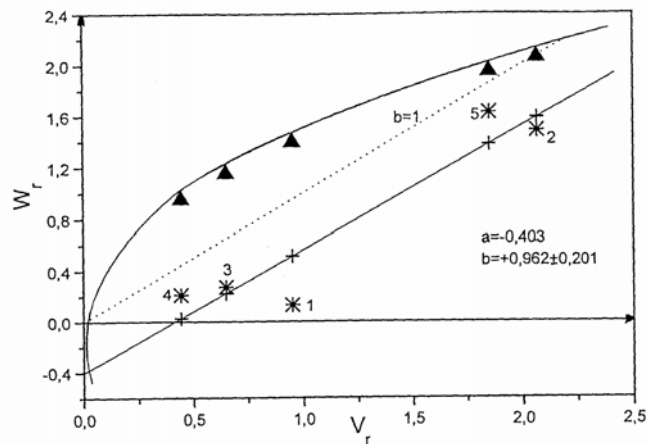


Fig. 1. V_r/W_r regression analysis of the number of kernels per spike (P and F_1)

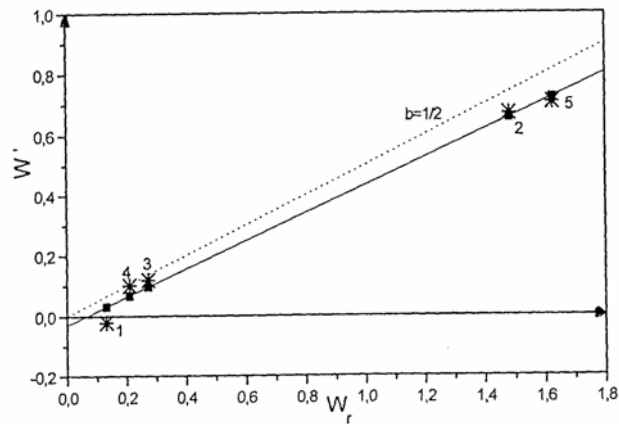


Fig. 2. $W_r W'$ regression analysis of the number of kernels per spike (P and F_1)

The distribution of the points in the distribution diagram suggested genetic divergence of the parents, hence the genotypes Jagodinac (4), Vada (1) and NS-293 (3) had mainly the highest number of dominant genes with points distributed in the lower part of the regression line very much near the co-ordinate origin. However, Sladoran (5) and Đerdap (2) had the highest number of recessive genes for the number of kernels per spike since they were the farthest way from the co-ordinate origin in the F_1 and F_2 generation (Figs. 1 and 3).

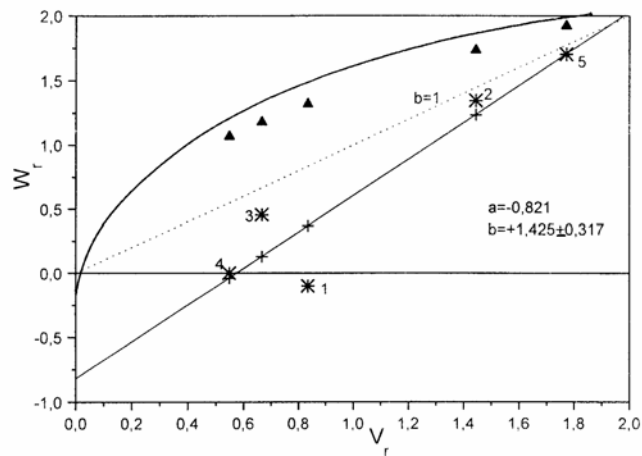


Fig.3. Vr/Wr regression analysis of the number of kernels per spike (P and F₂)

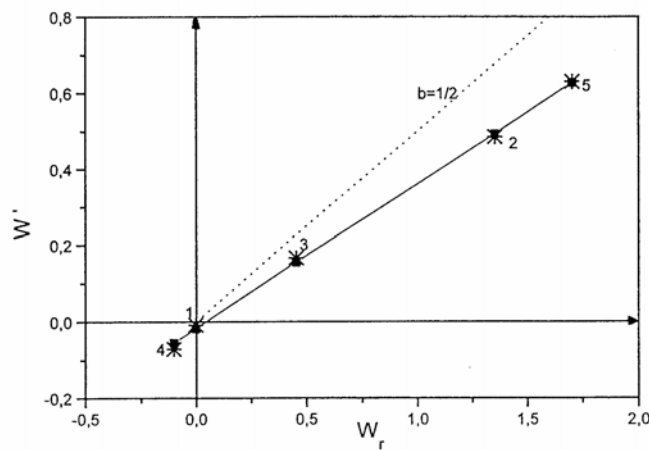


Fig.4. Wr/W' regression analysis of the number of kernels per spike (P and F₂)

CONCLUSION

In the diallel crossing, excluding reciprocal ones, the mode of inheritance, gene effect and the components of genetic variance for the number of kernels per spike were studied.

Sladoran was reported to have the lowest and Vada the highest number of kernels per spike.

As the cross combination might have been, the mode of inheritance was intermediary, dominant or superdominant.

The regression $VrWr$ and WrW' analysis helped establish the absence of inter-allele interaction so justifying the application of the model chosen. In the inheritance of the number of kernels per spike, the regression pointed at the dominant effect of genes as well as at the unevenly distributed dominant and recessive genes in the genotypes picked out. The highest number of dominant genes for the number of kernels per spike was revealed in Jagodinac, Vada and NS-293 and the highest one of the recessive genes in Đerdap and Sladoran.

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**ANALIZA EFEKTA GENA U NASLEĐIVANJU BROJA ZRNA PO KLASU
KOD HIBRIDA JEČMA**

Milomirka MADIĆ¹, Aleksandar PAUNOVIĆ¹, Dragan ĐUROVIĆ¹, Marija
KRALJEVIĆ-BALALIĆ² i Desimir KNEŽEVIĆ³

¹ Agronomski fakultet, Čačak,

² Poljoprivredni fakultet, Novi Sad,

³ Centar za strna žita, Kragujevac, Srbija i Crna Gora

Izvod

U dialelnom ukrštanju, bez recipročnih pet divergentnih genotipova ječma (Vada, Đerdap, NS-293, Jagodinac i Sladoran) regresionom analizom varijanse i kovarijanse proučavan je način nasleđivanja i efekat gena za broj zrna po klasu. Regresionom VrWr i WrW' analizom utvrđeno je odsustvo interalelne interakcije, što opravdava primenu odabranog modela. U nasleđivanju broja zrna po klasu regresija je ukazala na dominantan efekat gena, kao i na nejednak raspored dominantnih i recesivnih gena kod odabranih genotipova. Najveći broj dominantnih gena za broj zrna po klasu imaju genotipovi Jagodinac, Vada i NS-293, dok recesivnih Đerdap i Sladoran. Dobijeni rezultati ukazuju da kod dvorednih genotipova ječma veći broj dominantnih gena dovodi do povećanja broja zrna po klasu, a povećan sadržaj recesivnih gena ima suprotan efekat.

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