GENETIC ANALYSIS OF SPIKE TRAITS IN TWO- AND MULTI-ROWED BARLEY CROSSES

Milomirka MADIĆ[1], Desimir KNEŽEVIĆ[2], Aleksandar PAUNOVIĆ[1], Dragan ĐUROVIĆ[1]

[1]University of Kragujevac, Faculty of Agronomy, Čačak, Serbia
[2]University of Priština, Faculty of Agriculture, Lešak, Serbia

Madić M., D. Knežević, A. Paunović and D. Đurović (2012): *Genetic analysis of spike traits in two- and multi-rowed barley crosses* - Genetika, Vol. 44, No3, 475-482.

Mode of inheritance and genetic variance components for spike length, grain number per spike and grain weight per spike were evaluated in four parental genotypes and their F_1 and F_2 hybrids obtained through incomplete diallel crossing. Multi-rowed barley genotypes HVW-247 and Partizan and two-rowed barley genotypes KG-15 and NS-293 were selected for the crossing based on the trait concept with the parents being divergent for spike length, grain number per spike and grain weight per spike.

The average values for spike length in F_1 and F_2 generations were intermediate or close to those of the parent having longer spikes, with the mode of inheritance being partial dominance, dominance or overdominance, depending on the crossing combination. The six-rowed x six-rowed and

_____

Corresponding author: Milomirka Madić, University of Kragujevac, Faculty of Agronomy, Cara Dušana 34, 3200 Čačak Phone +38132 303 410;
e-mail: mmadic@tfc.kg.ac.rs

two-rowed x two-rowed crossing combinations showed dominance of increased grain number per spike and increased grain weight per spike in the inheritance of grain number per spike and grain weight per spike, respectively, whereas the six-rowed x two-rowed cross was predominated by partial dominance.

Key words: barley, diallel analysis, gene effect, spike traits

INTRODUCTION

Breeding institutions are creating new genotypes using different methods of analysis of the inheritance of major grain yield components and other traits in search of adequate genotypes that will transfer their good traits to their progeny through crossings.

Crossing multi- and two-rowed barley cultivars is sometimes a desirable approach to incorporating good traits of two-rowed cultivars, primarily large uniform grain and higher number of spikelets per spike, into multi-rowed cultivars that are generally suited for livestock feed (STOJANOVIĆ *et al.*, 1998; MADIĆ *et al.,* 2004).

An increase in spike length both in wheat and multi- and two-rowed barley is among the most promising approaches to breeding for increased yield (STOJANOVIĆ *et al*., 1998; DODIG, 2000). Spike productivity is a cultivar-specific characteristic associated with the vegetative mass production potential (PAUNOVIĆ *et al*., 2008).

Transgressive segregation in barley has been observed in a number of quantitative traits such as grain yield and its components, plant height, days to heading, malting quality, etc. (KUCZYNSKA *et al.*, 2007a).The regression analysis performed by KUCZYNSKA *et al.* (2007b) suggests the importance of genetic distances between parents for the occurrence of transgression effects in plant height, spike length, grain weight per spike and grain yield per unit area. Moreover, phenotypic differences between parents are also significant for the frequency of transgressive lines.

In their analysis of interactions between grain yield and yield components in two-rowed barley, BARCZAK and MAJCHERCZAK (2009) found the highest interaction between grain yield and spike number per m^{-2}, and between grain yield and grain number per spike.

Genetic differences between parents and estimates of the mode of inheritance of major yield components and mode of gene action can help identify combinations in the hybrid material that will form the basis for selecting desirable genotypes or genes determining desirable traits.

Since spike length, grain number per spike and grain weight per spike are important barley yield components, it is necessary to explore the underlying modes of inheritance, gene effect and genetic variance components in F_1 and F_2 generations in multi- and two-rowed barley crosses. Another important reason to study spike trait inheritance is the presence of negative correlations between the traits.

MATERIALS AND METHODS

Mode of inheritance and genetic variance components for spike traits were evaluated in four parental genotypes and their F_1 and F_2 hybrids obtained through

incomplete diallel crossing. Multi-rowed barley genotypes HVW-247 and Partizan and two-rowed KG-15 and NS-293 were selected for the crossing based on the trait concept with the parents being divergent for spike length, grain number per spike and grain weight per spike.

A field experiment was set up at the Small Grains Research Center in Kragujevac in a randomized block design in three replications. F_1 and F_2 generation parents were sown in the same year in 1 m long rows at a row spacing of 20 cm and plant spacing of 10 cm.

At full maturity, a random sample of plants was taken from each generation, and included:
- a total of 30 plants for all parents and F_1 combinations (3x10),
- a total of 150 plants for all F_2 combinations (3x50).

Modes of inheritance of spike length, grain number per spike and grain weight per spike were evaluated using the test of significance of generation means in relation to the parental mean. Genetic variance components from diallel crosses were calculated by MATHER and JINKS method (1971).

RESULTS AND DISCUSSION

Analysis of variance for primary spike length showed differences in the test genotypes. Spike length was lowest in KG-15 (8.2 cm) and highest in NS-293 (11.7 cm), (Table 1). Significant differences were also observed between parents and F_1 hybrids as well as among F_2 progenies, indicating the presence of diversity in the material (SHARMA *et al*., 2002). SINGH *et al*. (2007) and KAKANI and SHARMA (2010) also reported that significant differences among parents suggested their high genetic variability. KAKANI and SHARMA (2010) further observed that significant differences between parents and F_1 and those between parents and F_2 for most yield components under diverse environments suggested the presence of heterosis.

There was an increase in primary spike length in F_1 generation, the values ranging from 9.1 cm in the Partizan x KG-15 cross to 11.9 cm in HVW-247 x NS-293. Mean values for primary spike length in F_2 generation were lower in most combinations as compared to F_1 generation.

Different modes of inheritance of spike length in F_1 and F_2 generations were observed. Crosses where parents significantly differed showed intermediate inheritance or partial dominance of parents having longer spikes, whereas dominance or overdominance of parents having longer or shorter spikes, respectively, was the predominating mode of inheritance in the other combinations. Intermediate inheritance or dominance of parents having longer spikes was the predominant inheritance pattern for spike length in F_2 generation (Table 1).

Grain number per spike and grain weight per spike are direct yield components dependent upon spike length, spike density and number of rows of grains per spike. Different modes of inheritance of grain number per spike and grain weight per spike were identified, depending on the parental cultivars used in the crossing. Six-rowed x six-rowed and two-rowed x two-rowed crosses revealed dominance or overdominance of an increased grain number per spike, whereas six-rowed x two-rowed combinations were mostly marked by dominance or partial

dominance of parents having a low grain number per spike. Grain weight per spike also follows different patterns of inheritance, ranging from partial dominance of low grain weight to dominance to overdominance of increased grain weight per spike (Table 1).

Table 1. Mean values for parents of F_1 and F_2 generation for spike length, grain number per spike and grain weight per spike in barley

Parents and their hybrids	Spike length		Grain number per spike		Grain weight per spike	
	F_1	F_2	F_1	F_2	F_1	F_2
HVW-247	9.2		61.2		2.8	
HVW-247 x PARTIZAN	10.6 ^{d}	10.5 ^{d}	69.2 ^{d}	71 ^{d}	4.01 ^{sd}	3.6 ^{sd}
HVW-247 x KG-15	9.3 ^{d}	9.0 ^{d}	31.2 ^{d}	43.3 ^{pd}	2.5 ^{pd}	2.2 ^{pd}
HVW-247x NS-293	11.9 ^{sd}	11.2 ^{sd}	37.8 ^{d}	42.3 ^{pd}	2.6 ^{d}	2.4 ^{i}
PARTIZAN	10.4		69.2		3.4	
PARTIZAN x KG-15	9.1 ^{i}	9.2 ^{i}	32.2 ^{d}	43.3 ^{pd}	2.2 ^{pd}	2.5 ^{i}
PARTIZAN x NS-293	10.5 ^{d}	11.7 ^{d}	37.4 ^{sd}	44.8 ^{pd}	2.9 ^{i}	2.7 ^{pd}
KG-15	8.2		27.2		1.8	
KG-15 x NS-293	10.1 ^{i}	10.2 ^{i}	30.3 ^{d}	29.6	2.3 ^{d}	2.2 ^{d}
NS-293	11.7		30		2.2	
LSD 0.05	0.65	0.56	4.81	5.44	0.33	0.26
0.01	0.90	0.77	6.59	7.46	0.46	0.36

Pd – partial dominance, **d** - dominance, **i** – intermediate inheritance and **sd** – overdominance

The analysis of the genetic variance components for spike length in F_1 generation revealed a higher value of the additive component; most of the genetic variance in the inheritance of spike length is due to additive gene action if all crossing combinations are considered. In F_2, the dominant component increases, with almost no differences being observed between additive and dominant components (Table 2). The average degree of dominance in F_1 generation is less than unity, indicating partial dominance in the inheritance of spike length, whereas that in F_2 is close to unity (1.18), suggesting dominance and overdominance. This conforms to the results on individual crosses which were mostly governed by dominance. The high variability in F_2 generation for spike length implies that, to a large extent, progeny will have traits of parental cultivars. Partial dominance of increased primary spike length was also reported by STOJANOVIĆ *et al.* (1998) and MADIĆ *et al.* (2010). KAKANI and SHARMA (2010) also suggested the importance of both additive and non-additive gene effects in governing yield components with preponderance of non-additive gene action for spike length and grain number per spike.

The analysis of the genetic variance components for grain number per spike and grain weight per spike revealed that additive components for grain number per spike in both generations and grain weight per spike in F_1 generation were greater than dominance components, as opposed to F_2 generation where a shift occurred in genetic components for grain weight per spike, with dominance components

becoming greater than additive components. The F value for grain number per spike and grain weight per spike was negative in both generations, suggesting a higher effect of recessive genes. Partial dominance for grain number per spike and grain weight per spike was also confirmed by the average degree of dominance, which was less than unity (Table 2).

Table 2. Genetic variance components for spike length, grain number per spike and grain weight per spike in barley

Variance Components	Spike length		Grain number per spike		Grain weight per spike	
	F_1	F_2	F_1	F_2	F_1	F_2
D	2.25	2.20	482.0	481.2	0.73	0.75
H_1	0.85	2.02	37.7	174.2	0.30	1.01
H_2	0.82	2.18	28.7	146.7	0.28	0.76
F	0.52	2.16	-10.3	-104.4	-0.60	-0.33
E	0.05	0.48	2.6	3.4	0.02	0.01
$H_2/4H_1$	0.24	0.25	0.19	0.21	0.23	0.19
u	0.59	0.54	0.74	0.70	0.63	0.75
v	0.41	0.46	0.26	0.30	0.37	0.25
$(H1/D)^{1/2}$	0.61	1.18	0.28	0.60	0.69	0.42
K_D/K_R	1.67	0.97	0.93	0.70	0.87	1.10
Heritability	0.63		0.89		0.76	

Using the results of regression analysis of a diallel mating of 9 barley genotypes under 4 diverse environments, KAKANI and SHARMA (2010) found that the additive dominance model was fitted for F_1 and F_2 generations for spike length and grain number per spike in most environments. The authors also suggested that both additive (D) and dominance (H1 – the dominant effect and H2 - the dominance ratio due to positive and negative gene effects) components were significant for spike length and grain number per spike, which indicated the existence of both additive and dominant gene action in controlling the inheritance of these traits. The H1 component was greater than D for both yield components, indicating the preponderance of dominant gene action in the parents. The estimate obtained for H1 is in agreement with the positive significant estimate for dominant gene action, as reported by PRAKESH and VERMA (2006), VERMA *et al.* (2007), SHARMA and SHARMA (2008) and KAKANI and SHARMA (2010).

The ratio of the total number of dominant to recessive genes in all parents is governed by potential genetic advance. If recessive alleles predominate in a certain population, the genetic gain acquired through selection would be controlled by dominant gene action. Therefore, the degree of genetic advance is limited if dominant alleles are present in a certain population. Accordingly, estimates of the ratio of dominant to recessive genes in a population are vital for the selection of superior genotypes.

The high values of heritability for grain number per spike and grain weight per spike suggest significant differences in the genetic constitution between the parents and imply that their progeny will have most of the parental traits. FREGEAU-REID *et al.* (1998) reported high heritability estimates (71% - 93 %) for grain number per spike in crosses between multi-rowed barley types. Mean heritability values for grain weight per spike were obtained by BOUZERZOUR and DJAKOUNE (1998). Different heritability estimates for different barley traits were also reported by BHANTAGAR *et al.* (2001) and SHARMA and SHARMA (2008).

If both additive and non-additive genetic variance components are involved in the genetic determination of yield components, the use of additive genetic variance while retaining heterozygosity would be the most acceptable breeding procedure. Therefore, certain types of recurrent selection, such as diallel selective mating or biparental mating in early segregating generations, might prove to be an effective alternative approach to improving yield components in barley through assimilation of desirable additive genes while exploiting dominance variance.

CONCLUSION

Significant differences in primary spike length, grain number per spike and grain weight per spike were observed between barley genotypes and their progenies. The average values for spike length in F_1 and F_2 generations were intermediate or close to those of the parent having longer spikes, with the mode of inheritance being partial dominance, dominance or overdominance of parents having longer spikes, depending on the parental combination used. Both the analysis of genetic variance components and the average degree of dominance suggested a significant impact of additive and dominant gene effects in governing the inheritance of primary spike length

The six-rowed x six-rowed and two-rowed x two-rowed crossing combinations showed dominance of an increased grain number/weight per spike in the inheritance of grain number/weight per spike whereas the six-rowed x two-rowed cross exhibited partial dominance of parents having a low/high grain number/weight per spike.

ACKNOWLEDGEMENTS

REFERENCES

BARCZAK, B., E. MAJCHERCZAK *(2009):* Effect of varied fertilization with sulfur on selected spring barley yield structure components. Journal of Central European Agriculture, *9(4): 777-784.*

BHANTAGAR, V.K., S.N. SHARMA and E.V. SASTRY (2001): Genetics of quantitative characters in six rowed barley over environments. Indian J. Genet., *61:* 358-359.

BOUZERZOUR, H., A. DJAKONE (1998): Inheritance of grain yield and grain yield components in barley. Rachis. *16*: 9-16.

DODIG, D. (2000): Morphological and productive traits in F$_4$ and F$_5$ generation hybrids in two-rowed *(H. distichum)* and six-rowed *(H. hexastichum)* barley crosses. M. SC. thesis. Faculty of Agriculture, Belgrade – Zemun. (in Serbian)

FREGEAU-REID, J., T.M. CHOO, P. JUI, K.M. HO (1998): Inheritance of kernel size and shape of barley. SABRAO J. *28*: 47-55.

KAKANI, R.K., Y. SHARMA (2010): Genetic component analysis for yield and yield contributing traits under diverse environments in barley. SABRAO Journal of Breeding and Genetics, *42*(1): 9-20.

KUCZYŃSKA, A., M. SURMA, T. ADAMSKI (2007a): Methods to predict transgressive segregation in barley and other self-pollinated crops. Journal of Applied Genetics, *48*(4): 321-328.

KUCZYŃSKA, A., M. SURMA, Z. KACZMAREK, T. ADAMSKI (2007b): Relationship between phenotypic and genetic diversity of parental genotypes and the frequency of transgression effects in barley (*Hordeum vulgare* L.). Plant Breeding *126*(4): 361-368.

MADIĆ, M., D. ĐUROVIĆ, A. PAUNOVIĆ (2004): Genetic analysis of yield components in the crossings of two-and six-rowed barleys. Acta Agriculturae Serbica, *17*: 157-164.

MADIĆ, M., D. KNEŽEVIĆ A. PAUNOVIĆ, D. ĐUROVIĆ (2010): Inheritance of stem height and primary spike length in barley hybrids. 45th Croatian and 5th International Symposium on Agriculture, Faculty of Agriculture, University of Josip Juraj Strossmayer in Osijek, Proceedings, Opatija, Croatia, 456-460.

MATHER, K. and J.L. JINKS (1971): Biometrical Genetics. Sec. En. Champan and Half., London, England.

PAUNOVIĆ, A., M. MADIĆ, D. KNEŽEVIĆ, M. BIBERČIĆ (2008): Nitrogen and seed density effects on spike length and grain weight per spike in barley. Cereal Research Communications, *36*(I): 75-78.

PRAKESH, V., R.P. S. VERMA (2006): Inheritance of grain yield and some quantitative traits in six rowed barley *(Hordeum vulgare* L.*)*. Indian J. Genet. *66:*39-40.

SHARMA, Y., S.N.SHARMA, P. JOSHI, R.S. SAIN (2002): Combining ability analysis for yield and yield contributing characters in six-rowed barley. SABRAO Journal of Breeding and Genetics, *34*(2): 55-63.

SHARMA YOGENDRA, S.N. SHARMA (2008): Effect of sowing dates on genetic components in six-rowed barley. Acta Agronomica Hungarica, *56:*349-356.

SINGH, S., G. S. DHINDSA, A. SHARMA, P. SINGH (2007): Combining ability for grain yield and its components in barley (*Hordeum vulgare* L). Crop Improvement, *34*(2): 128-132.

STOJANOVIĆ, Ž., D. DODIG, S. STANKOVIĆ, R. PETROVIĆ (1998): Importance of six-rowed spike for increases in genetic fertility potential of barley. Breeding of Small Grains. Proceedings. Kragujevac, 209-215.

VERMA, A.K., S.R VISHWAKARMA and P.K. SINGH (2007): Genetic Architecture for Yield and Quality Component Traits over Two Environments in Barley (*Hordeum vulgare* L.). Barley Genetics Newsletter *37:* 24–38.

GENETIČKA ANALIZA OSOBINA KLASA U UKRŠTANJU DVOREDOG I VIŠEREDOG JEČMA

Milomirka MADIĆ[1], Desimir KNEŽEVIĆ[2], Aleksandar PAUNOVIĆ[1], Dragan ĐUROVIĆ[1]

[1]Univerzitet u Kragujevcu, Agronomski fakultet, Čačak
[2]Univerzitet u Prištini (Kosovska Mitrovica), Poljoprivredni fakultet, Lešak

Za ispitivanje, načina nasleđivanja i komponenti genetičke varijanse dužine klasa, broja i mase zrna po klasu analiziran je materijal četiri roditeljska genotipa i njihovi hibridi F_1 i F_2 generacije dobijeni nepotpunim dialelnim ukrštanjem. Za ukrštanja odabrani su genotipovi višeredog ječma HVW-247, Partizan i dvoredog KG-15 i NS-293 na bazi koncepta svojstva pri čemu su roditelji bili divergentni za dužinu klasa, broj i masu zrna po klasu.

Srednje vrednosti dužine klasa u F_1 i F_2 generaciji su intermedijarne ili se približavaju roditelju sa većom dužinom klasa, a način nasleđivanja je parcijalna dominacija, dominacija ili superdominacija, zavisno od kombinacije ukrštanja. U ukrštanju šestoredi x šestoredi i dvoredi x dvoredi u nasleđivanju broja i mase zrna po klasu preovladava dominacija većeg broja zrna po klasu, odnosno veće mase zrna po klasu, a u ukrštanju šestoredi x dvoredi parcijalna dominacija.