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Diallel Analysis for Spike Length in Winter Wheat

^aNataša LJUBIČIĆ*, ^aSofija PETROVIĆ, ^aMiodrag DIMITRIJEVIĆ, ^bNikola HRISTOV, ^cMirjana VUKOSAVLJEV,
^aZorana SREČKOV

^aDepartment of Field and Vegetable Crops, Faculty of Agriculture, University of Novi Sad, Serbia

^bInstitut of Field and Vegetable Crops, Novi Sad, Serbia

^cPlant Breeding, Wageningen University, Wageningen, The Netherlands

*Corresponding author: ljubicic.natasa@gmail.com

Abstract

The mode of inheritance and gene effect for spike length of 5x5 full diallel crosses of wheat varieties was estimated in F₁ generation. The results indicated significant differences among the parents for general combining ability (GCA) and crosses for specific combining ability (SCA) for spike length. However, highly significant differences for the general (GCA) and specific (SCA) combining ability in the F₁ generation denoted that spike length had resulted from the genes with additive and non-additive, i.e. dominant impact. The absence of interallelic interaction between the genes determining the expression of spike length was concluded from the regression analysis. The regression line intercepts the W_r axis below the origin in F₁ indicating overdominance over an average of all arrays.

Keywords: Winter wheat, spike length, diallel, gene effects, combining ability, regression analysis

Introduction

Wheat is one of the most widespread, cultivated crops in the world and is an important factor in achieving food security of any country. Over the last 20 years, the global wheat acreage varied between 207 and 227 million hectares, which were on average 26% of the total harvested area (Denčić et al. 2009, USDA, 2013).

Increasing the genetic potential for grain yield of wheat is the main goal of breeding. Yield is a complex character and is the result of many quantitative traits which are controlled by numerous genes each having small effects. Improving direct and some other indirect components, grain yield can be improved (Zečević, 2005).

Spike length has an indirect effect on grain yield through the number of spikelet, number of fertile spikelet, number of grains per spike and number of grains per spike, which suggests that breeders should give great attention to this feature (Ijaz and Kashif, 2013). It is considered that the spike length and spike architecture provide an opportunity to further yield improvement.

The main objective of the present study was to identify the best combiners and their crosses on the basis of their general and specific combining ability for spike length. Using the method of

regression analysis in diallel crossing it was determined the gene system of inheritance of spike length.

Materials and Methods

Five varieties of hexaploid wheat (*Triticum aestivum* L.), namely, Pobeda, Renesansa, Sara, Partizanka and Pasma, were crossed in all possible combinations in a 5 x 5 diallel fashion and it was obtained F₁ generation of progenies.

The trial was set up on the trial field of the Institute of field and vegetable crops in Novi Sad, according to random block design with three replications, in three growing seasons (2009/2010, 2010/2011 and 2011/2012). The cultivars were sown in 2 m long rows with 20 cm of inter-row spacing and 10 cm spacing between plants in the row. We analyzed the spike length of plants at the stage of full maturity. The main sample consisted of 10 plants per replication. General combining ability (GCA) and specific combining ability (SCA) was made following the method 2 (parents and F₁ generation) mathematical model 1 of Griffing (1956). The regression analysis was conducted by the method of Mather and Jinks (1971).

Results

Based on the mean values of the parents and their progenies in the F₁ generation, the analysis of variance of the combining ability was made and presented in Table 1. The results of the analysis indicated highly significant differences for the general (GCA) and specific (SCA) combining

ability in the F₁ generation, meaning that spike length having resulted from the genes with additive and non-additive, i.e. dominant effects. However, the GCA/SCA ratio tilted in favour of GCA in this trait, which had amounted 1.7. This indicates the preponderance of additive gene effects in the genetic control of spike length.

Table 1. Analysis of variance for combining ability for the spike length in a 5 x 5 diallel cross of wheat

Source of variance	F _t					
	DF	SS	MS	F	0.05	0.01
GCA	4	1.94	0.48	8.37**	2.69	4.02
SCA	10	2.88	0.29	4.99**	2.16	2.98
E	28	4.86	0.06			
GCA/SCA				1.7		

*GCA: General Combining Ability, SCA: Specific Combining Ability, E: Error; DF: Degree of Freedom, SS: Sum of Squares, MS: Mean Square, F: Level of Significance by the F test; *Significant (P < 0.05), **Highly significant (P < 0.01)

Estimates of general combining ability were presented in Table 2. Estimates of combining ability revealed that positive GCA effects were maximum in genotype Partizanka followed by genotype Pema, which showed a similar tendency.

Genotype Sara was the poorest general combiner with maximum negative and significant GCA effects. Negative GCA effects were also observed in two genotypes: Pobeda and Renesansa.

Table 2. General combining ability values for spike length of wheat

Parents	LSD				
	GCA Values	Rank	SE	0.05	0.01
Pobeda	-0.132	4	0.129	0.26	0.35
Renesansa	-0.042	3			
Sara	-0.318*	5			
Partizanka	0.391**	1			
Pema	0.101	2			

GCA: General combining ability, SE: Standard Error; LSD: Least Significant Difference test; *Significant (P < 0.05), **Highly significant (P < 0.01)

Estimates of specific combining ability were presented in Table 3. Estimates of SCA effects showed the highest positive value for crosses Pobeda x Pema (0.749*) and Partizanka x Pema (0.692*), which values were significant. Tendency of higher values of SCA effects was also observed in

crosses Pobeda x Partizanka (0.559) and Renesansa x Sara (0.444). The highest negative value for estimates of SCA effects was shown by Renesansa x Pema (-0.408). Negative SCA effects was also observed in crosses Sara x Partizanka (-0.289) and Pobeda x Sara (-0.065).

Table 3. Specific combining ability values for spike length of wheat

Parents	LSD							
	Pobeda	Renesansa	Sara	Partizanka	Pema	SE	0.05	0.01
Pobeda		0.192	-0.065	0.559	0.749*	0.29	0.58	0.78
Renesansa			0.444	0.102	-0.408			
Sara				-0.289	0.068			
Partizanka					0.692*			

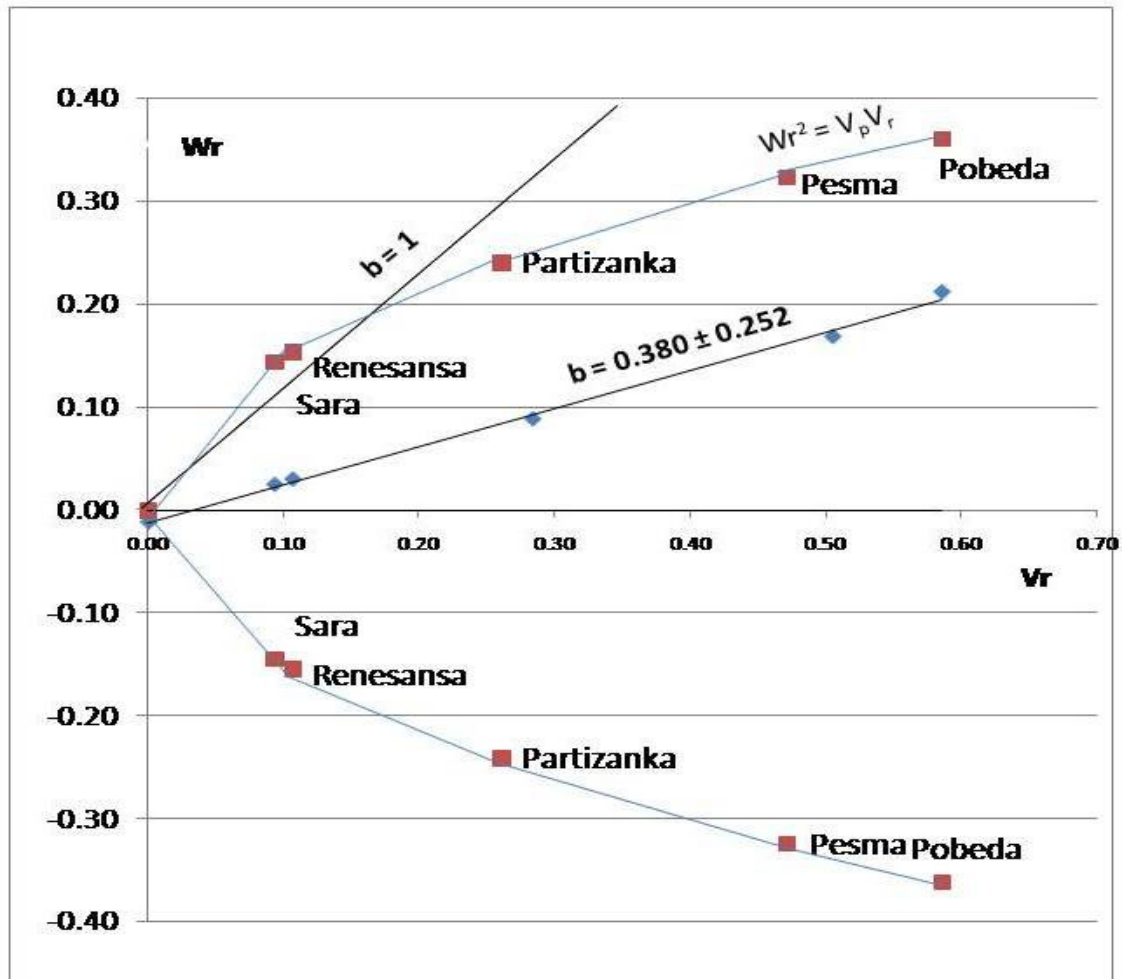
SCA: Specific combining ability, SE: Standard Error; LSD: Least Significant Difference test; *Significant (P < 0.05), **Highly significant (P < 0.01)

Figure 1 revealed that the regression analysis (V_r/W_r) indicated super dominance for spike length because regression line intersected the W_r axis below the origin. The estimated regression line wasn't deviated significantly from the unit slope,

(b=0.380±0.252), which suggests the absence of non allelic interaction. The arrays that correspond to parents were similarly distributed along the regression line and they indicate that the parents were genetically divergent for the analyzed trait.

The varieties Sara and Renesansa had higher dominant genes, but variety Pesma and Pobeda which is far away from the origin had higher

recessive genes for spike length in wheat. The genotype Partizanka had an equal proportion of both genes.



b: Coefficient of Regression, *Wr*: Covariance, *Vr*: Variance

Figure 1. Vr/Wr regression analysis for spike length of wheat

Discussion

The combining ability analyses revealed that both general and specific combining ability effects played an important role in the control of the spike length of the studied genotypes. General effects were being greater than the specific effects which suggests an important role for additive genetic effects, although the significance of specific combining ability effects indicates that dominance and epistasis were also involved in the expression of this trait. The present findings thus supported the results of Inamullah (2004), Maphara (2008) and Perišić et al. (2011), which also showed highly significant differences for the general and specific combining ability with similiar GCA/SCA ratio, tilted in favour of GCA. The highest positive GCA effects were shown by the genotypes Partizanka and

Pesma suggesting that these genotypes contain more genes with additive effects and could be a good parent for this trait. Findings of current study were similar to findings of Zečević et al. (1997), who also observed the best general combining ability for the spike length of genotype Partizanka, in previous research by crossings with other genotypes. The genotype Sara, Pobeda and Renesansa were poor general combiners.

In this study, crosses which were displaying high specific combining ability effects for spike length were obtained from parents with various types of general combining ability effects (high x high, high x low and low x low). High SCA values between different combinations of general combiners, was observed by Perišić et al. (2011). Estimates of SCA effects showed the highest positive value for crosses Pobeda x Pesma (low x

high) and Partizanka x Pasma (high x high), which values were significant. Tendency of higher values of SCA effects was also observed in crosses Pobeda x Partizanka (low x high) and Renesansa x Sara (low x low). In self-pollinated crops, as a wheat, the most important are greater SCA effects in crosses, which were involving both parents with high GCA, such as a combination crosses Partizanka/Pasma (high x high general combiner), because they contain an interaction additive x additive and can be used in future plant breeding. The importance of greater SCA effects in crosses which were involving both parents with high GCA in self-pollinated crops was pointed out by Joshi et al. (2004). Greater SCA effects obtained in crosses which were involving both parents with high GCA, such as a combination crosses Partizanka/Pasma, which is considered that contain an interaction additive x additive, indicated the possibility of genetic improvement for spike length through pedigree selection. This cross combination may be produce transgressive recombinants for spike length.

Greater SCA effects obtained in crosses Pobeda x Pasma (low x high), which were involving one parent with high GCA, indicated the involvement of additive x dominance gene interaction in expression of this trait.

Higher values of SCA effects observed in crosses Renesansa x Sara (low x low), which involving both parents with low general combiner, indicated the presence of epistasis (non-allelic interaction) at heterozygous loci. Interaction between the heterozygous loci is not fixed so it is suggested utilizing these crosses through single plant selection in the later generations (Hassan, 2004). According to Jinks and Jones (1958), in these parental lines (which involving both parents with low general combiner), compared with parents of high GCA, heterozygous were highly responsive to the environment due to non-additive effects such as dominance and epistasis. It's certainly, parents with high values of SCA are good combiners for F_1 generation, which uses dominant gene action, while for wheat are more important parents which show a high general combining ability and they used in cases where the selection is done in subsequent generations (Borojević, 1985).

The regression analysis for spike length revealed that regression line intercepts the W_r -axis on the negative side of the origin and thus indicates over dominance type of gene action. The regression line wasn't deviate significantly from unit slope which indicate the absence of non-allelic interactions or epistasis in the crosses of diallel set. Varieties Sara and Renesansa possessed maximum dominant genes which were being closest to the origin, whereas the parents Pobeda and Pasma had

maximum recessive genes which were being father from origin. The arrays that correspond to parents were similarly distributed along the regression line and they indicate that the parents were genetically divergent for the analyzed trait. The similar finding, which indicated overdominance type of gene action, was also obtained by Chowdhry et al. (2001), Hassan (2004), Akram et al. (2009) and Jadoon (2011).

Conclusion

Both additive and non-additive gene effect was responsible for the inheritance of spike length according to the analysis of variance for combining ability. General effects were being greater than the specific effects which suggest an important role for additive genetic effects, although the significance of specific combining ability effects indicates that dominance and epistasis were also involved in the expression of the spike length. To improve the spike length, the parent Partizanka is consider as the best for this task, because showed the highest positive and significant GCA for the spike length among all parental genotypes and had also the highest mean value of this trait. High specific combining ability effects for spike length were obtained from many parents with various types of general combining ability effects (high x high, high x low and low x low). Greater SCA effects obtained in crosses which were involving both parents with high GCA, such as a combination crosses Partizanka/Pasma, indicated the possibility of genetic improvement for spike length through pedigree selection.

The regression analysis in F_1 indicated overdominant inheritance of spike length. Regression coefficient in F_1 generation was not significantly different from unity which indicates the absence of interallelic interaction for spike length.

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