

Diallel analysis of variance - covariance regression for spike length in six-row winter barley

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Abstract The choice of an efficient breeding procedure depends to a large extent on the knowledge of the genetic system controlling the character to be selected. The spike length holds great value for yield improvement in barley. High values of spike length cause a yield increase only if they are associated with high spike density. The present research were conducted to ascertain the nature of gene action involved in the determinism of spike length for a set of six doubled haploids lines of six-row winter barley.

The studied parental forms in terms of spike length submitted a higher proportion of dominant alleles and a nearly symmetrical distribution of positive and negative alleles. In both generations, the overdominance direction was associated with an increase in spike length. A high proportion of recessive and negative alleles have been reported in DH 19-1 line, respectively a large proportion of dominant and negative alleles submitted the DH 26-2 and DH 20-4 lines, while the other lines showed a relative instability during the two generations. Because the genetic system that controls the spike length four both generations is mainly additive, selection can play a great role in breeding method of that trait.

The main objective of barley breeding is to improve yield and related traits by selecting and improving yield components including spike length. This particular trait hold great value for plant breeders as it determines the yield of barley. High values of spike length cause a yield increase only if they are associated with high spike density.

The study of genetic conditions of different agricultural plants is one of the essential factors for the success of inbreeding plans. Therefore it is required that precise and comprehensive information of the genetic parameters controlling the components of yield is collected and used for making decisions on the selection of an appropriate breeding method [1]. Moreover, among all the mating designs, diallel mating, especially half diallel provided a simple and convenient method for estimating genetic parameters [2,8].

The diallel analysis advocated by Hayman [3] and Mather and Jinks [6] provides reliable method particularly in autogamous crops to review the genetic system and gene action involved in the expression of plant attributes, right in the F₁ generation. Diallel cross is used to study the genetic diversity and polygenic systems of quantitative traits. As the most important

Key words

six-row barley, spike length, diallel analysis

traits are inherited in a quantitative manner [10], therefore the results of such crosses are valuable for the improvement of the traits inside and among populations, as well as the production of cultivars [9, 11].

The present research were conducted to ascertain the nature of gene action involved in the determinism of spike length for a set of six doubled haploids lines of six-row winter barley.

Material and Method

The F₁ and F₂ progenies of a six-parent diallel cross (excluding reciprocals) were analyzed for spike length. The F₁ and F₂ s along with their parents were sown in the field in a randomized block design with four replications. The doubled haploid lines were obtained at INCDA Fundulea by the "bulbosum" method, modified for local conditions in field and greenhouse [7]. Spike length was measured from the base to the tip of the spike, excluding the awns. For this purpose main spikes from ten randomly selected plants were measured and average spike length/plot was obtained.

Genealogy of parental doubled haploid lines

No	Line	Genealogy
1.	DH 19-1	F 529/84
2.	DH 20-4	F 208/88
3.	DH 21-2	F 503/88
4.	DH 23-2	Miraj
5.	DH 26-2	Adi
6.	DH 33-2	F 549/88

The diallel analysis was carried out on the following assumptions: diploid segregation, no reciprocal effects, homozygous parents, no epistasis, no multiple allelism, and independent genes distribution among parents.

The data were subjected to regression covariance/variance (W_r/V_r) analysis and analysis of variance of W_r-V_r arrays, using diallel analyses technique [3,4]. Graphical analysis was supplemented with standard deviation graph of the parental values (y_r) and ($W_r + V_r$) sums, according to Johnson and Aksel [5]. This graph shows the relationship between dominance and positive and negative alleles

Results and Discussions

According to analysis of variance from F_1 hybrids it is noted that the (W_r-V_r) difference values are homogeneous and insignificant, so that the proposed model is properly for heredity study of this trait (Table 1). The significant values of the regression coefficient to zero and to unity, indicates the presence in the genetic determinism of this trait of both dominance and nonallelic interactions (Table 2).

Table 1.

Analysis of variance (W_r-V_r) for spike length in F_1 and F_2 six-row barley

Source of variation	F_1				F_2			
	SS	DF	MS	F Test	SS	DF	MS	F Test
Total	4,020	23			1.132	23		
Replications	1,110	3	0,37	2,46	0.013	3	0.004	0.66
Parents	0,610	5	0,12	0,80	0.130	5	0.026	0.39
Error	2,280	15	0,15		0.988	15	0.065	

Table 2.

Regression (W_r/V_r) coefficients values for spike length in F_1 and F_2 six-row barley

Regression coefficient	F_1			F_2			$t_{5\%}$
	Value	Significance to zero	Significance to unity	Value	Significance to zero	Significance to unity	
b	2,030	10,56*	5,35*	0.803	22.95*	5.62*	
s_b	0,192			0.034			

The heterogeneity test of ($W_r - V_r$) values for F_2 hybrids show that there are no important and significant deviations from the requirements of genetically adopted model. The significant values of the regression coefficient towards both criteria indicate just as for the F_1 generation, the presence in the genetic determinism of this trait of both dominance and nonallelic interactions.

For the analysis of F_1 generation, most of the parental genotypes are grouped close to the regression line (Fig. 1) confirming the presence of additive effects with major importance in genetic determinism of this trait. It means that due to the presence of additive

variance selection for this trait can be practiced in early generations. In case of DH 26-2 line, this character is under the influence of nonallelic interactions, thus explaining the significance of the regression coefficient to unity.

The average level of dominance, expressed by the distance between the point where the regression line intersects the covariances (W_r) axis and the point of origin ($a=-0.86$), revealed over dominant type of gene action for spike length (Fig. 1). It means that the genotypes are efficient for producing higher spikes in hybrid condition.

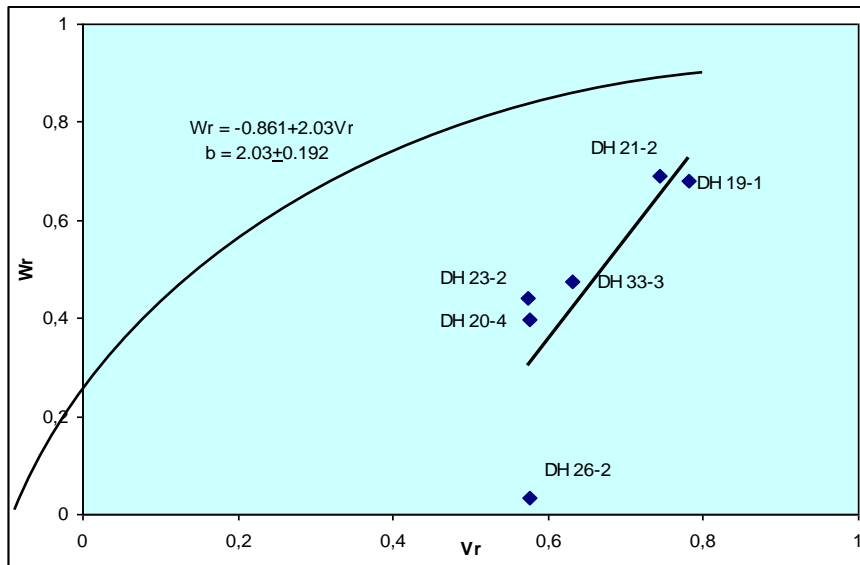


Fig. 1. W_r/V_r regression for spike length in F_1 hybrids of six-row barley

The distribution of parental genotypes (Fig. 1) shows that DH 21-2 and DH 19-1 lines had the highest proportion of recessive alleles while DH 26-2 line cumulates the most dominant genes. Relative size of

the area delimited by the parabola and the regression line as well the disposal of parental genotypes along the regression line, confirms the importance of additive effects in genetic determinism of this traits.

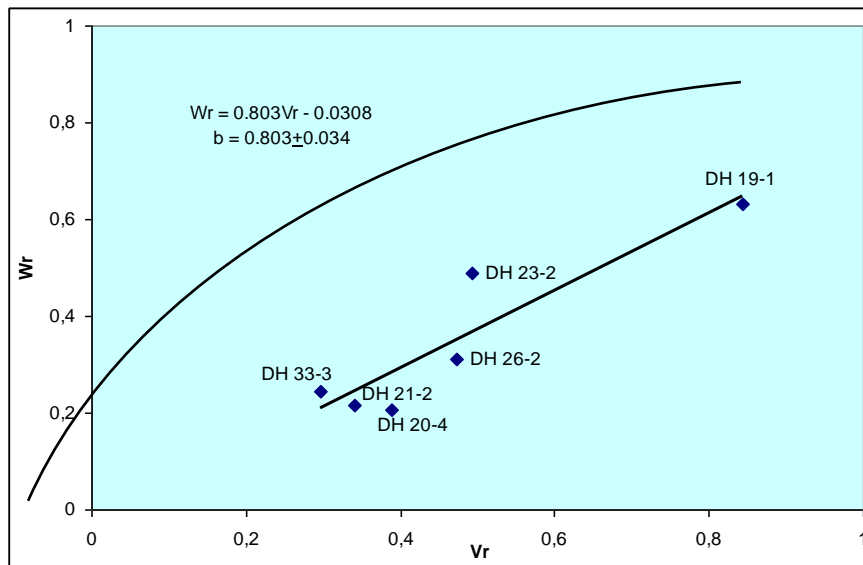


Fig. 2. W_r/V_r regression for spike length in F_2 hybrids of six-row barley

The figure 2. shows that most of the parental forms are closely clustered around the regression line, which proves that the genetic system that controls the spike length is mainly additive, just as in F_1 generation. Inferior position to origin for the intersection point between the regression line and W_r axis, indicates the presence of an over dominant type of gene action for spike length. Hence selection for spike length in the early segregating generation would be difficult.

Based on the position of parental forms along the regression line was found that DH 19-1 line possessed the most recessive genes being located farthest from the origin being closest to the origin, while at DH 33-3, DH 23-2 and DH 20-4 lines the dominant alleles prevailing. DH 26-2 and DH 23-2 lines have approximately equal proportions of the dominant and recessive alleles for this trait.

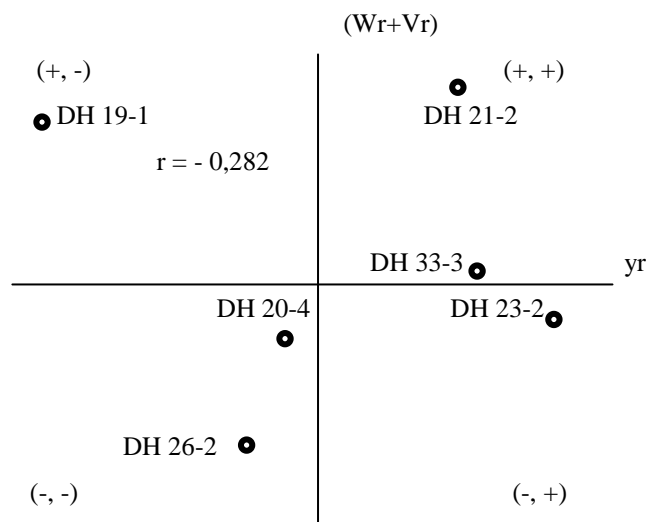


Fig. 3. Standardized deviations (W_r+V_r) and y_r for spike length in F_1 hybrids

The graph of ($W_r + V_r$) standard deviations and y_r (Fig. 3) shows a high differentiation of genotypes in terms of the relationship between the degree of dominance and positive or negative alleles. Therefore, at DH 21-2 and DH 33-3 lines recessiveness is associated with positive alleles, while at DH 1-1 line is associated with negative alleles. In addition the dominance is associated either with positive alleles in

DH 23-2 lines or with negative alleles at DH 26-2 and DH 20-4 lines.

This genotypes differentiation is also confirmed by the small and insignificant values of the correlation coefficient ($r = -0.282$) between the parental values (y_r) and order of dominance ($W_r + V_r$), which indicates that both positive and negative genes tend to equal dominance proportion.

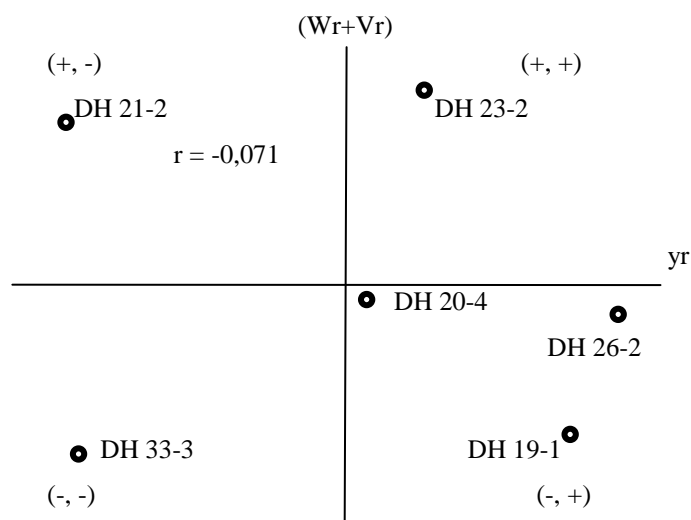


Fig. 4. Standardized deviations (W_r+V_r) and y_r for spike length in F_2 hybrids

The association of dominant or recessive allele with those positive or negative based on graph for y_r standard deviation and $W_r + V_r$ (Fig. 4), indicates that recessiveness is associated with positive allele at DH 23-2 line and with negative alleles at DH 19-1 line, just as in F_1 . However, the dominance is associated with positive alleles at DH 33-3 and DH 21-2 lines, and like in the first generation is associated with negative alleles at DH 26-2 and DH 20-4 lines.

Although the negative and insignificant values of the correlation coefficient ($r = -0.746$) between y_r and ($W_r + V_r$) suggests a trend of association of dominance with the reduction of spike length, both dominant and the recessive alleles can have different effects on this character.

Conclusions

1. Analysis of variance showed that the proposed model is properly for heredity study of this trait, and indicates the presence in the genetic determinism of this trait of both dominance and nonallelic interactions.
2. The studied parental forms in terms of spike length submitted a higher proportion of dominant alleles and a nearly symmetrical distribution of positive and negative alleles. In both generations, the overdominance direction was associated with an increase in spike length..
3. In terms of dominant or recessive alleles, positive or negative respectively, which they possess, the parental forms were highly differentiated. A high proportion of recessive and negative alleles have been reported in DH 19-1 line, respectively a large proportion of dominant and negative alleles submitted the DH 26-2 and DH 20-4 lines, while the other lines showed a relative instability during the two generations.
4. Because the genetic system that controls the spike length four both generations is mainly additive, selection can play a great role in breeding method of that trait.

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