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Study of the inheritance of hull content in a six-parent half diallel cross of winter barley

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Abstract The hull content in barley is an important component of feed malt and quality of the grains. Also, the presence of hull influenced other attributes of barley grains like dormancy or sprouting resistance.
The present research aimed to evaluate the inheritance type, nature of gene action and the component of genetic variance for hull content in a six-parent half diallel cross of winter barley.
The dominance and recessiveness are both associated with positive and negative alleles. Worthy to be taken into account are the recessives alleles of Turul variety and the dominant alleles of Viktor variety that determine a reduction of grain hull content. For this set of varieties, the dominant alleles that control the hull content have a higher frequency than the recessive ones and also an asymmetry of positive and negative genes effects due to dominance is highlighted. The small value of narrow sense heritability indicates that a considerable part of the hull content variability is due to the dominance so that the response of this trait to selection will be low.

Key words

Winter barley, hull content, diallel, gene action.

The hull content in barley can reach 10-15% of grain weight, and the principal components of hull are the following: cellulose, hemi cellulose, pectin, lignin and a small amount of protein. The absence or removal of hull lead to the reduction of fiber content, thereby increasing the digestibility of grain administered to the animals. Adherence of hull to the grain is a trait genetically controlled by different recessive genes. Thus the non-adherent husk is determined by gene *n*, and the half-covered grain by *smn* and *sbn* genes [7].

The choice of an efficient breeding method depends to a large extent on the knowledge of the genetic system controlling the trait to be selected [1]. Moreover, among all the mating designs, diallel mating, especially half diallel provided a simple and convenient method for estimating genetic parameters [2;9]

Genetic analysis was made using the diallel technique as described by Hayman (1954) and Jinks (1954), which provides information on the inheritance mechanism in the early generations and helps the breeder to make effective selection. The diallel analysis 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 F_1 generation [3;8]. Diallel crosses are used to study the genetic diversity and polygenic systems of quantitative traits. As the most important traits are inherited in a quantitative manner [11], 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 [10;12].

The present research aimed to evaluate the inheritance type, nature of gene action and the component of genetic variance for hull content in a six-parent half diallel cross of winter barley.

Material and Method

The biological material comprised of 15 hybrids resulting from a diallel cross between six winter barley varieties (Metal, Orizont, Plaisant, Viktor, Turul, Lyric) with different ecological and genetic origin. The research was conducted based on a randomized complete block design with three replications.

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 analysis of covariance/variance (Wr/Vr) regression and analysis of variance of Wr-Vr arrays, using diallel analyses technique [3; 5]. Graphical analysis was supplemented with standard deviation graph of the parental values (yr) and (Wr +Vr) sums, according to Johnson and Aksel [6]. This graph shows the relationship between dominance and positive and negative alleles. Components of genetic variance have been calculated following the model of Jinks and Hayman (1953).

Results and Discussions

According to the Fig. 1 it is noted that the additives effects are involved in the determinism of this trait only in the case of "Lyric" and "Orizont" varieties, which are relatively grouped around the regression line. For other varieties, the alleles with epistatic or complementary effect significantly influenced by environmental conditions play an important role in the genetic control of hull content.

Table 1

Mean (Yr), variance (Vr), covariance (Wr) values, and proportion of dominant alleles for husk content of parents

Parents	Mean Yr	Variance Vr	Covariance Wr	Proportion of dominant alleles
Metal	12.20	4.350	-0.818	0.761
Orizont	11.86	0.563	0.255	0.893
Plaisant	14.86	2.971	1.600	0.710
Viktor	10.73	2.568	-1.260	0.869
Turul	7.93	4.587	1.766	0.623
Lyric	14.60	3.328	-0.287	0.785

The distribution of parents along the regression line (Figure 1) indicates that "Turul" (37.70 %) and "Plaisant" (29.00 %) varieties had the highest proportion of recessive allele, while "Orizont" (89.30%) and "Viktor" (86.90%) varieties cumulates the most dominant genes.

The average degree of dominance, expressed by the distance between the point where the regression line intersects the axis of covariance (Wr) and the origin, with a = -0.19 indicates the presence of over dominance effects. The relative size of the area delimited by parabola and regression line, as well as the position of parents along the regression line, confirms that the additives effects are less important for inheritance of hull content.

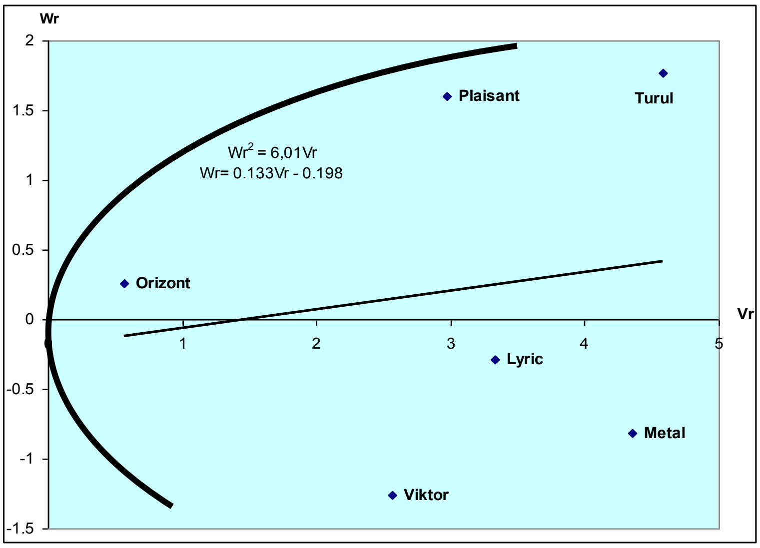

Fig. 1 Wr/Vr regression for husk content in F_1 barley hybrids

From the graph of standardized deviations (Wr+Vr) and yr (Figure 2) we can see that there is an association of positive and negative allele with both dominance and recessivity, in accordance with the low values of the correlation coefficient. Thus, recessiveness is associated with positive alleles in the case of "Plaisant" and "Metal" varieties, and with alleles that leads to a reduction of the grains hull content in Turul variety, respectively.

The largest proportion of the dominant negative allele is encountered in "Viktor" and "Orizont" varieties. At the opposite pole we found "Lyric" varieties that possess dominant alleles that determine an increase of the hull content.

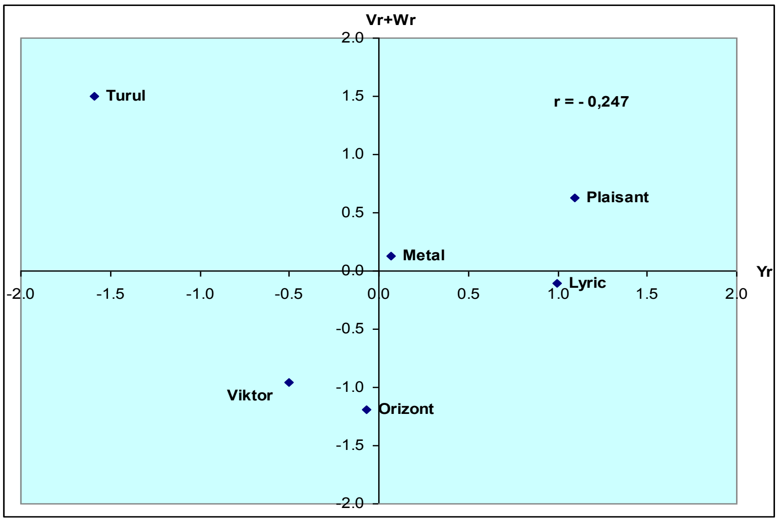

Fig.2 Standardized deviations (Wr+Vr) and yr for husk content

In the inheritance of hull content both additive (D), and dominance (H_1) effects are significantly involved, but the contribution of the dominant effect is prevailing. The dominant alleles that control the hull content (F) have a higher frequency than the recessive ones and also an asymmetry of positive and negative genes effects due to dominance (H_2) is highlighted.

Table 2

Components of genetic variance and some report for husk content in F_1 hybrids

Variance component / ratio	Estimate value
D- additive effects of genes	6.015*
H_1- dominance effects of genes	17.425***
H_2 – corrected dominance effects of genes	9.963***
F- covariance of additive and dominance effects	11.19***
h^2- cumulative dominance effects	0.133
E- environmental variance	0.619
$(H_1/D)^{1/2}$ – average level of dominance	1.702
kD/(kD+kR) – proportion of dominance genes	0.773
$\overline{F_1} - \overline{P}$ - average direction of dominance	0.255
D-H_1 – average direction of genes effects	-11.410
H_2/ 4H_1 – average frequency of positive and negative alleles	0.143
h^2/ H_2 – number of genes groups or effective factors	0.161
Hb – broad sense heritability	0.854
Hn – narrow sense heritability	0.269

$LSD_{5\%}$ = 4,66 $LSD_{1\%}$ = 6,24 $LSD_{0,1\%}$ = 8,22

The average degree of dominance assessed by the ratio $(H_1/D)^{1/2}$ with a value above unity (1.02) indicates the presence of over dominance in the inheritance of this trait, according with the graph of Wr/Vr regression**,** due to a higher proportion (77.30%) of dominant alleles indicated by the kD/(kD+kR) ratio. The average direction of dominance given by the positive value of $\overline{F_1} - \overline{P}$ shows the presence of over dominance for higher hull content in grains.

The dominant alleles with positive and negative effects in the determinism of this trait from parents do not have equal proportions according to the subunit value of H2 / 4H1 ratio.

The higher values of broad sense (85,40 %) and lower for narrow sense heritability (26,90 %) of this trait, indicate that a considerable part of the hull content variability is due to the dominance gene effects, taking into account also the insignificant influence of the environmental conditions.

Conclusions

In the case of “Lyric” and “Orizont” varieties the hull content is controlled mainly by the additives effects, while for “Plaisant”, “Turul”, “Viktor” and “Metal” the alleles with epistatic or complementary effect significantly influenced by environmental conditions play an important role in the genetic control of this trait.

The dominance and recessiveness are both associated with positive and negative alleles. Worthy to be taken into account are the recessives alleles of "Turul" variety and the dominant alleles of "Viktor" variety that determine a reduction of grain hull content.

For this set of varieties, the dominant alleles that control the hull content have a higher frequency than the recessive ones and also an asymmetry of positive and negative genes effects due to dominance is highlighted.

The small value of narrow sense heritability indicates that a considerable part of the hull content variability is due to the dominance so that the response of this trait to selection will be low.

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