ESTIMATION OF THE VARIABILITY AND INHERITANCE OF SOME QUANTITATIVE TRAITS IN TWO ROWS SPRING BARLEY IN THE CONDITIONS OF ARDS TURDA

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ABSTRACT

From the spring barley collection of ARDS Turda, a number of 60 genotypes were chosen and analysed in terms of variability parameters (the mean, minimum and maximum, coefficient of genetic, phenotypic and environmental variation and the heritability coefficient in broad sense). The morpho-productive characters analysed were: the number of grains/ear, ear length, grain weight/ear, TKW and harvest index.

To estimate gene effects involved in the inheritance of quantitative traits, such as yield components, the genetic analysis model proposed by Hayman (1958) and applied by Gamble (1962) was used. The study was conducted to evaluate a number of six hybrid combinations. The parental forms were chosen on the basis of homozygosity and phenotypic differences in yield between parents c. To estimate additive gene effects, dominance and epistatic interaction of additive x additive (aa), additive x dominance (ad) and dominance x dominance (dd) types, involved in the heritability of a trait, we established the mean of: parental population, of F1, F2 and backcross (BCI and BCII). genetic populations.

Keywords: spring barley, coefficient of variation, heritability, gene effects, morpho-productive traits.

INTRODUCTION

Physiological features (precocity and intense rhythm of photosynthesis) have made barley a cereal that can be grown under different environmental conditions, where other cereals don't find favourable development conditions. According to Tianu and Bude (1985) barley supremacy in agriculture was maintained until the Bronze Age (1700-1000 b.c), when the importance of wheat and its spreading began to grow.

The success of breeding is closely related with the existing variability at species level, which is often very diverse, so that it is not necessary to preserve the entire genetic diversity of species at the level of a single breeding program, this being often impossible. Therefore the main purpose of the work collection from ARDS Turda is to use as efficiently as possible the useful portion of this variability, to obtain new cultivars with high yield and a good yield stability from year to year.

Information on the nature and extent of variability and heritability and identifying genotypes with the desired traits are important prerequisites for the success of breeding programs (Dudly and Moll, 1969, quoted by Dyulgerova and Valcheva, 2014). In this regard, the knowledge of the heritability and variability of agronomic traits is of significant or even decisive importance in improving crop yields.

Falconer (1967) emphasized that the most important role of heritability in studying metric characters is that of prevention or anticipation, which expresses the certainty of the breeding value. The success in modifying certain traits within the population can only be predicted by knowing the correlation between the phenotypic and breeding values. High genetic advantage, accompanied by high heritability, are prerequisites for streamlining selection work.

As it is known, in the inheritance of quantitative traits a large number of genes known as *polygenes,* with lower and similar effects acting additively in determining the trait, is involved. Besides the additive action of polygenes, other types of intra-allelic (dominance and recessivity) and inter-allelic

interactions (epistasis) are also involved in the inheritance of the quantitative traits, all of which ultimately determine their complex heritability. The implication of each polygene cannot be analysed singly, but only generically.

In order to estimate the gene effects involved in the inheritance of quantitative traits, like production components in spring barley, the genetic analysis model proposed by Hayman (1958) and applied by Gamble (1961) was used. In this regard, the mean of the traits of parental population and of genetic population from descendants were analysed, being estimated the additive gene effects (*a*), dominance (*a*) and epistatic interaction of additive x additive (*aa*), additive x dominance (*ad*) and dominance x dominance (*dd*) type involved in the hereditability of the analysed traits.

MATERIAL AND METHODS

The barley germplasm collection of ARDS Turda contains around 550 genotypes represented by a large number of foreign and indigenous varieties as well as lines in an advanced selection cycle.

Sowing was done manually and for each genotype five rows of 1 meter length were designed. All these genotypes were phenotypically compared with a control sample represented by the genotype Romaniţa, placed from 20 to 20 variants. Of all genotypes in the collection, a number of 185 genotypes, including the newest entries after they have completed a 2 year adaptation period, were analysed for morpho-productive traits.

The biometric work was done in the field for plant height, while the rest of the agronomic traits were analysed in the laboratory on a number of nine plants in three repetitions.

To estimate the mean effects of the genes, 12 cultivars were chosen, the criteria of homozygosity being the basis for choosing the parental forms. The parents were more or less differentiated with respect to the analysed characters. Therefore, six hybrid combinations were carried out involving two native varieties (Jubileu – ARDS Turda;

Prima – ARDS Suceava) and ten foreign varieties (Thuringia, Victoriana, Viena – Saaten Union; Odisey, Chronicle, Salome – Limagrain; Magnif, Anabelle – varieties of Czech origin). For each trait, a number of 25 plants were analysed in F1 generation, noting that there were some combinations where a smaller number of plants were available.

For the statistical interpretation of data, the following relationships were used:

- arithmetic mean $X = \dfrac{\sum x}{n}$;

- standard deviation of the average:

$$s = \sqrt{\dfrac{\sum (x - \bar{x})^2}{n-1}} = \sqrt{s^2}$$

- coefficient of variability (s%; CV):

$$s\% = \dfrac{s}{\bar{x}} \times 100$$

The variance assessment was made using the Polifact program for a total of 60 collection genotypes, respectively 20 lines. To estimate genetic ($\sigma^2 g$), phenotypic ($\sigma^2 p$) and environmental or residual variation ($\sigma^2 r$) the following relationships were used (Muhammad et al., 2014):

$$\sigma^2 g = \frac{s^2 g - s^2 r}{R} = \frac{Genetic\ variance - residual\ variance}{number\ of\ repetition}$$

where:

$\sigma^2 r = s^2 r$ = residual variance;

$\sigma^2 p = \sigma^2 g + \sigma^2 r/R$ = phenotypic variance = genetic variance + residual variance / number of repetitions;

Genetic variation coefficient (CVG%), phenotypic (CVP%) (Singh and Chaudhury (1985) used formula of Falconer, quoted by Dyulgerova and Valcheva, 2014) and residual (CVR%) (Muhammad et al., 2014):

CVG % = $\sqrt{\sigma^2 g}$ / $\overline{X}$ * 100; CVP % = $\sqrt{\sigma^2 p}$ / $\overline{X}$ * 100; CVR % = $\sqrt{\sigma^2 r}$ / $\overline{X}$ * 100

In order to calculate the genetic advance (AG) and the genetic advance over the mean expressed as a percentage % (AG%) the relationships proposed by Falconer (1989) and quoted by Muhammad et al., (2014) were used, and for the estimation of heritability

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coefficient in broad sense H^2 we applied the formula proposed by Falconer (1967).

AG = i * phenotipyc standard deviation $(\sqrt{\sigma^2 p}) * H^2$
where:
   i = 1.4 at 20% selection intensity for trait;
   H² = broad sense heritability of the trait.

$$AG \% = \frac{AG}{\overline{X}} * 100 \qquad H^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

For calculated coefficient of heritability in a broad sense the following formulas have also been used:
   - formula according to Burton (1951):

$$H^2 = \sigma^2 F_2 - \sigma^2 F_1 / \sigma^2 F_2$$

   - formula according to Mahmoud and Kramer (1951):

$$H^2 = \sigma^2 F_2 - \sqrt{\sigma^2 P1 + \sigma^2 P2} / \sigma^2 F_2$$

For estimation of heritability coefficient in narrow sense (h^2) we used the formula according Warner (1952):

$$h^2 = 2\sigma^2 F_2 - (\sigma^2 BC_1 - \sigma^2 BC_2) / \sigma^2 F_2$$

RESULTS AND DISCUSSION

The main indicators of the range of variation for eight morpho-productive traits are presented in Table 1. The variability analysis for one of the most important morphological traits with major implications for resistance to lodging reflects a small to moderate variability (s% = 7%), but the differences between the minimum and the maximum suggests a significant variation in plant height values. The average value of 101 cm, as well as the maximum of 116 cm, shows that tall genotypes predominate in the collection, but the minimum values, as well as the variation amplitude, indicates that among these genotypes some minus-variants, which could constitute future genitors for breeding work in order to reduce the height, could be identified.

Tamm (2003), following a study made on 57 spring barley cultivars carried out in European countries for four years, showed that this trait has a moderate variability between 6-8%. In a study done on 106 spring barley cultivars, the Serbian breeder Perovic obtained the following values for plant size (the mean = 77 cm, minimum = 56 cm, maximum = 94 cm) (Perovic et al., 2003).

Table 1. Parameters of variability for morpho-productive traits in 185 genotypes
of spring barley collection (Turda, 2016)

Traits*	Count	Mean	Minimum	Maximum	Sample variance	s (%)
PH (cm)	481	101 (77*)	78 (56*)	116 (94*)	49.66	7
Sfl (cm²)	185	7.51	2.4	12.45	3.22	23.89
Ngr/ear	185	26 (28.8*)	20 (7*)	31 (86*)	4.29	8
Gw/ear (g)	185	1.18 (1.23*)	0.78 (0.55*)	2.15 (2.58*)	0.02	12.41
Le (cm)	185	8.87	7.10	10.80	0.41	7.22
TKW (g)	185	44.19	35.8	51.2	6.76	5.9
Gw/pl. (g)	185	2.22	1.29	3.24	0.09	13.73
HI (%)	185	41	30	54	0.001	8.9

*plant height (PH), the foliar surface of the flag leaf (Sfl), number of grains/ear (Ngr), grain weight/ear (Gw), ear length (Le), grain weight/plant (Gw), harvest index (HI), variability coefficient (s%).
The values in brackets are for comparison (from the study by Perovic et al., 2003).

Most studies indicated that the flag leaves in cereal grains are important for harvest formation and carbohydrate accumulation. Therefore, the importance of the flag leaf in determining the grain yield has been analysed

for barley by several researchers (Tungland et al., 1987; Zheng 1999; Yang and Lu, 1991). The mean foliage surface value of 7.51 cm^2 shows that at the level of the 185 varieties analysed, the genotypes with a medium to

large foliage surface predominate. The important differences between the minimum and the maximum, as well as the value of the variability coefficient (≈ 24%) indicate a large variation of genotypes for this trait.

Among the agronomic traits related to yield, the highest values of the variation coefficient were found for the grain weight/plant and ear, indicating a moderate variability of genotypes for these traits. The wide range between the minimum and maximum values of the two yield components confirms that between the analysed variants both plus-variants and minus-variants can be identified. The mean value of grain weight/ear of 1.18 g (quite close to what the Serbian breeder Perovic obtained - 1.23 g), but also the maximum value indicates the presence of superior genotypes from this point of view.

The number of grains, another yield component, presented a small to moderate variability, this being suggested by the variation coefficients of only 8%.

Considering the mean value of 26 of the number of grains and the minimum and maximum values (20 and 31), we can say that genotypes with a large number of grains/ear can be identified in the germplasm collection.

The differences between the minimum and maximum values, as well as the value of the coefficient of variation for the ear length, shows that there is quite a significant variability in the studied genotypes regarding this quantitative trait.

An important direct indicator for the size and weight of the grains and indirect for quality is the TKW. The mean value of TKW shows that in the barley collection the genotypes with a high TKW are predominant and the value of the variability coefficient of ≈ 6% reflects a small to moderate variability. The wide range of minimum and maximum values (35.8-51.2) suggests a significant variation in TKW values, which could be effective and usable for obtaining some possible favourable transgressions in future breeding programs.

The harvest index is an important selection criterion that is often used to assess the productive potential of a large number of genotypes such as germplasm collections. The range of values between the minimum and maximum, as well as the variation coefficient of about 9% shows a quite significant variability of this synthetic indicator in the analysed collection. Starting from the negative correlation between plant height and the harvest index, it is important to remember that this selection criterion favours the short-height genotypes, therefore, it should also be seen in terms of the grain weight/plant.

A relatively large number of genotypes, namely 60, were analysed in terms of the genotypic, phenotypic and environmental or residual variability coefficients. For the most important agronomic characteristics of yield, the coefficient of heritability in broad sense, the genetic advance as well as the genetic advance over the average were calculated in these genotypes. For all the elements of the studied yield components we can see in Table 2 a very significant influence of the genotype, highlighting the presence of important differences between the 60 genotypes that can be used in future breeding programs. In the same table the performances of these traits regarding the minimum, maximum and the mean value are presented.

Looking at the data in Table 2, we can state that the studied genotypes showed a fairly wide range of variability for all traits and an important spectrum of variation between the minimum and maximum values. A significant variation can be observed in the case of grain weight/ear and harvest index (0.9-1.46 g, respectively 34% and 52%). Similar values for the number of grains/ear (minimum 26.6 and maximum 30.5) and for TKW (minimum 39.6 g and maximum 46.1 g) were also reported by Pržulj and Mihajlović (2012). Also, Dyulgerova and Valcheva (2014) presented values quite similar to those obtained in this study for the grain weight/ear (1.31 g – the mean, 1.13 – minimum and 1.57 – maximum) and for the ear length (8.94, 7.58 and 10.59).

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Table 2. Variability of some yield components at 60 genotypes of the spring barley collection
from ARDS Turda

Traits	GL	s^2	Minimum	Maximum	Mean
Gw/ear (g)	59	0.05***	0.90	1.46	1.16
Error	118	0.02			
Gw/pl. (g)	59	0.21***	1.63	2.65	2.11
Error	118	0.08			
Ngr/sp.	59	15.62***	21	32	26
Error	118	4.84			
Le (cm)	59	1.31***	7	10	8.71
Error	118	0.38			
TKW (g)	59	21.66***	37.66	49.33	43.87
Error	118	1.46			
HI (%)	59	0.0040***	34	52	42
Error	118	0.0012			

*** $p = 0.1\%$

In Table 3, the genotypic, phenotypic and environmental (residual) variation, the coefficients of genotypic (CVG), phenotypic (CVP) and residual variation (CVR), the broad-sense heritability index, and genetic advance are given for the six quantitative traits. Establishing these parameters provides some important information on the expected response of these traits to the selection work and for recommending the most appropriate methods of breeding. The highest values of genotypic and phenotypic variance can be attributed to TKW ($\sigma^2 g$ – 6.73 and $\sigma^2 p$ – 7.22) and the lowest for grain weight/ear ($\sigma^2 g$ – 0.01 and $\sigma^2 p$ – 0.017). As expected, the highest values of CVG and CVP were recorded by the grain weight/plant (9.48%; 12.18%), followed by the grain weight/ear (8.62%; 11.24%) and the number of grains/ear (7.29%; 8.77%). The greatest differences between CVG and CVP are also noteworthy for grain weight/ear and /plant, which suggests the important influence of the environment on the formation of these two important quantitative components of production. Obviously for all 60 genotypes analysed CVP values are higher than those of CVG and follow their trend. Following a study conducted in Bulgaria on 23 dihaploid lines Dyulgerova and Valcheva (2014) showed close values of CVG and CVP for ear length (7.46 and 8.27), number of grains/ear (4.96 and 5.63), grain weight/ear (8.04 and 9.08) and TKW (7.21 and 7.98).

The values of heritability in broad sense were between 0.59 and 0.93 for the six properties analysed. If we take into acount the heritability coefficient classification made by Addisu and Shumet (2015), TKW recorded the highest heritability, with a superior value over 0.9 (namely 0.93), followed by the ear length (0.70), the number of grains/ear and the harvest index (0.69) which are considered traits with moderate heritability ($H^2 = 0.6$-0.75). The lowest values of H^2 are for the grain weight/ear and /plant indicating a low heritability ($H^2 = < 0.59$). The highest values of H^2 reflect a reduced influence of the environment on these traits formation. Dyulgerova and Valcheva (2014) also presented the highest values of H^2 for TKW and the length of the ear.

Ali et al. (2002), quoted by Dyulgerova and Valcheva (2014), argued that a high heritability is not always associated with a high genetic advance and the two parameters must be seen generically in order to predict the selection effect on superior varieties. Addisu and Shumet (2015) also emphasized that the superiority of the genetic advance expressed as a percentage must be associated with a high heritability in order to predict the effects of selection. These two researchers claimed that the genetic advance expressed as percentage of the mean, gives more accurate results compared to the genetic advance. Highest values of genetic advance were found for TKW followed by the number of grains/ear and its length, these being also

associated with the highest values of heritability.

Panse (1957), quoted by Dyulgerova and Valcheva (2014), stated that a high heritability associated with a high genetic advance indicates the additive effects of the genes, while a high heritability accompanied with a small genetic advance indicates the non-additive effects of genes controlling the trait.

This study shows that TKW and the number of grains/ear have a high heritability and an important genetic advance, these being two criteria to be considered when carrying out the selection work and breeding for spring barley. Following a study on various wheat varieties, Mandea et al. (2016) also stated that TKW is a trait which can bring a significant contribution to increasing genetic progress in breeding.

Table 3. Estimation of genotypic, phenotypic and residual variance, coefficients of variation, heritability in broad sense, genetic advance and % genetic advance over the mean of six quantitative traits in 60 spring barley genotypes (Turda, 2016)

Traits	$\sigma^2 g$	CVG%	$\sigma^2 p$	CVP%	$\sigma^2 r$	CVR%	H^2	AG	AG% over the mean
Gw/ear(g)	0.01	*8.62*	0.017	11.24	0.02	11.24	0.59	0.11	9.48
Gw/pl (g)	0.04	*9.48*	0.066	12.18	0.08	13.4	0.61	0.22	10.43
Ngr/sp	3.59	7.29	5.20	8.77	4.84	8.46	0.69	2.20	8.46
Le (cm)	0.31	6.39	0.44	7.62	0.38	7.08	0.70	0.65	7.46
TKW (g)	6.73	5.91	7.22	6.12	1.46	2.75	0.93	3.50	7.97
HI	0.0009	7.14	0.0013	8.58	0.0012	8.25	0.69	0.028	6.66

$\sigma^2 g$, $\sigma^2 p$, $\sigma^2 r$ – genotypic, phenotypic and residual variance, CVG%, CVP%, CVR% – coefficient of genotypic, phenotypic and residual variance; H^2 – heritability coefficient in broad sense, AG – genetic advance, AG% – genetic advance over the mean.

Because the quantitative characters are governed by the action of several minor genes (polygenes), it is difficult to appreciate the effect of a single gene on the analysed trait. Also, the important influence of the environment on gene expression and on the quantitative traits is well known. Nevertheless, there are several models for estimating the gene effects involved in controlling quantitative traits and in this study, the so-called Gamble model was used. The main morpho-productive traits that were the subject of this study were represented by: ear length, number of grains/ear, grain weight/ear and TKW. Quantitative analysis of these elements has a probabilistic character, becoming more accurate only by using molecular markers in the analysis of these QTLs.

Table 4 shows the performances of parents and segregating generations for the ear length, parents recording values between

8.60 and 10.90 cm. The genotypes Jubileu and Anabelle had the highest values.

In the F1 generation in most combinations, with the exception of combinations 1 and 4, the mean value of ear length was superior to the mean value of the best parent, indicating a high effect of heterosis, which is probably due to the effects of over-dominance. In the same four combinations in F2 we can notice a slight depression, but which was not significant and indicated somewhat the accumulation of heterogeneous additive genes in this generation. Regarding the backcross generations we can say that in terms of ear length the behaviour corresponded to the performance of the recurrent parent even if the differences are smaller. A deviation from this behaviour can be seen in combination I, which confirms the probabilistic character of this method. Among the parents, the genotypes Jubileu and Anabelle are noticed in terms of ear length.

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Table 4. The mean values of ear length (cm) for parental populations, F1, F2, BCI and BCII
in a system of spring barley backcrosses (Turda, 2016)

Combination	Population					
	P1	P2	F1	F2	BCI	BCII
CB1 (Thuringia x Jubileu)	9.60	10.80	8.80	11.50	10.40	8.00
CB2 (Prima x Victoriana)	10.10	9.60	10.50	9.50	11.00	10.70
CB3 (Magnif x Odisey)	9.70	10.40	10.80	10.20	11.00	11.60
CB4 (Victoriana x Anabelle)	9.80	10.90	10.40	10.80	12.00	11.60
CB5 (Chronicle x Salome)	8.60	9.20	9.40	8.60	9.20	10.10
CB6 (Viena x Anabelle)	9.20	9.70	10.00	8.90	10.40	10.00

The mean values for the number of grains/ear of the six populations studied are presented in Table 5. From the analysis of this table we can deduce lower heterosis intensity for this trait, so that in all combinations the mean of F1 generation had intermediate values between the two parents, except for combination five, where F1's average is over the mean of the best parent. Even though in the backcross generations there were no significant differences compared to parental forms, the influence of the best parent can be seen in almost all combinations (except for combination 1).

The performance of one of the most important components of production, namely the grain weight/ear, is shown in Table 6, where parents recorded values between 0.99 and 1.45 g/ear. As can be seen from the data presented in this table, in the backcross generations the grain weight had superior values compared to F1, F2 and parental populations, with the exception of the first combination. F2 generation superiority compared to F1 in three of the six combinations indicated the presence of transgressions for this trait. The BCI of the combination (Prima x Victoriana) x Prima is remarkable, having the highest mean value for the grain weight/ear.

Table 5. The mean values of the number of grains/ear for parental populations, F1, F2, BCI, BCII
in a system of spring barley backcrosses at Turda (2016)

Combination	Populations					
	P1	P2	F1	F2	BCI	BCII
CB1 (Thuringia x Jubileu)	25	30	26	29	28	27
CB2 (Prima x Victoriana)	31	25	28	27	32	27
CB3 (Magnif x Odisey)	28	27	27	30	31	31
CB4 (Victoriana x Anabelle)	28	31	27	26	29	31
CB5 (Chronicle x Salome)	25	25	28	27	28	30
CB6 (Viena x Anabelle)	28	30	29	27	30	28

Table 6. The mean values of the grain weight/ear for parental populations, F1, F2, BCI, BCII
in a system of spring barley backcrossing at Turda (2016)

Combination	Populations					
	P1	P2	F1	F2	BCI	BCII
CB1 (Thuringia x Jubileu)	1.03	1.45	1.04	1.31	1.37	1.22
CB2 (Prima x Victoriana)	1.34	1.27	1.37	1.37	1.71	1.53
CB3 (Magnif x Odisey)	1.20	1.19	1.12	1.35	1.59	1.53
CB4 (Victoriana x Anabelle)	1.29	1.42	1.27	1.21	1.52	1.69
CB5 (Chronicle x Salome)	0.99	1.10	1.23	0.93	1.28	1.49
CB6 (Viena x Anabelle)	1.29	1.03	1.46	1.20	1.42	1.30

Estimation of genetic effects

An estimation of the role of the genes in controlling ear length is shown in Table 7. From the lower absolute values of additive genetic effects we can deduce the lower involvement of additivity in controlling this trait. Regarding the dominant genes, we can notice a very significant contribution in the heritability of ear length trait. In fact, in five of the six combinations studied, the values of the dominance effects are superior to those

of epistatic type *aa* and *ad*. All these come to strengthen the major role of the dominance effects in controlling the ear length.

The major contribution of the dominance effects in the expression of ear length was also reported by Ciulcă et al. (2012), who showed that the study of the ear length heritability indicated the presence of dominance phenomena and of non-allelic interactions in the genetic determinism of the trait.

Table 7. Estimation of gene effects on ear length in a set of six hybrid combinations of barley (Turda, 2016)

Combination	Gene effects					
	M	*a*	*d*	*aa*	*ad*	*Dd*
CB1 (Thuringia x Jubileu)	11.54***	2.42***	-10.57***	-9.23***	3.01***	10.32***
CB2 (Prima x Victoriana)	9.53***	0.3	5.66***	5.07***	0.03	-7.65***
CB3 (Magnif x Odisey)	10.22***	-0.58*	4.94***	4.17***	22.9***	-7.59***
CB4 (Victoriana x Anabelle)	10.18***	0.32	6.53***	6.43***	0.88***	-12.8***
CB5 (Chronicle x Salome)	8.58***	-0.9***	4.55***	4.08***	-0.59**	-5.82***
CB6 (Viena x Anabelle)	8.92***	0.4	5.63***	5.12***	0.64*	-7.14***

Sharief et al. (2011) stated that the number of grains/ear as well as the number of ears/ m^2, are the most important components of grain yield, contributing with approximately 91% to its formation. The relatively low values of the additivity effects (Table 8), reflects its reduced involvement in controlling the number of grains. In only one combination (CB2) the additive genetic effects are very significant, while in the combinations 5 and 6, the additive genetic effects are only distinctly significant or significant, and in the case of combinations 1, 3 and 4 no significance of additive effects was recorded. A much greater involvement in controlling this trait can be attributed to dominant genes, this being evidenced by the absolute superior values and by the significance attributed to

these effects. The genetic epistasis of type *aa, ad, dd* also had an important role to play in controlling this trait.

Similar results were also presented by Reza et al. (2009), in a system of backcrosses. They emphasized the importance of dominance and epistasis phenomena in the inheritance of the number of grains/ear. On the contrary, Eshghi et al. (2010), in a system of diallel crosses found that the additive genetic effects controlling this trait are higher compared to dominance effects. The same author stated that under drought conditions, the dominance effects are higher in controlling this trait. From these statements we can see the heritability complexity of the number of grains/ear.

Table 8. Estimation of the mean effects of genes on the number of grains in a set of six hybrid combinations of barley (Turda, 2016)

Combination	Gene effects					
	M	*a*	*d*	*aa*	*ad*	*dd*
CB1 (Thuringia x Jubileu)	29***	1	-7.50***	-6***	3.50***	3***
CB2 (Prima x Victoriana)	27***	5***	10***	10***	2*	-16***
CB3 (Magnif x Odisey)	30***	0.15	3.26***	3.22***	-0.27	-16.54***
CB4 (Victoriana x Anabelle)	26.40***	-1.7	10.48***	13.20***	-0.58	-19.75***
CB5 (Chronicle x Salome)	26.52***	-1.9**	11.57***	8.32***	-2**	-15.82***
CB6 (Viena x Anabelle)	27.32***	1.35*	5.95***	6.02***	2.03**	-6.17***

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Most researches showed that grain weight/ear had a rather complex inheritance, recommending that the selection for this trait, but also for TKW to be made in later generations. For the grain weight/ear the differences between additivity and dominance effects are lower, but a very significant contribution of the dominance effects in controlling this trait can still be seen in Table 9.

A very significant action of the additive genetic effects can be seen in CB 1, 2 and 5, but with absolute subunit values. With respect to the epistasis effects of type *aa* and *ad*, some lower values can be observed compared to the dominance ones. Nevertheless, aa type effects had a very significant influence on most combinations, except on CB 1.

Very significant effects in this trait genetics are found at the level of epistasis effects of type *dd*. Sherwan Esmail Tofiq et al. (2015) also affirmed that the nonadditive genetic effects had a greater contribution in controlling this trait compared to the additive ones.

Table 9. Estimation of the mean effects of genes on the grain weight in a set of six hybrid combinations of barley (Turda, 2016)

Combination	Gene effects					
	M	*a*	*m*	*aa*	*ad*	*dd*
CB1 (Thuringia x Jubileu)	1.31***	0.15***	-0.26***	-0.06*	0.36***	-0.55***
CB2 (Prima x Victoriana)	1.37***	0.18***	1.07***	1***	0.15***	-2.13***
CB3 (Magnif x Odisey)	1.35***	0.06	0.78***	0.85***	-0.37	-32.29***
CB4 (Victoriana x Anabelle)	1.21***	-0.16*	1.49***	1.57***	-0.1	-2.74***
CB5 (Chronicle x Salome)	0.93***	-0.21***	2.01***	1.82***	-0.15**	-2.80***
CB6 (Viena x Anabelle)	1.20***	0.12**	0.92***	0.63***	0.01	-0.82***

In order to identify the best breeding strategy by using these traits as selection criteria for higher yield potential in barley, we tried to estimate some derived genetic parameters, namely: the degree of dominance, heritability index in broad sense and in narrow sense.

The degree of dominance expressed as a ratio between the F1 generation mean and the best parent's mean, expressed as a percentage, showed partial to complete dominance for ear length, number of grains and grain weight. In Table 10 only the mean values of dominance for the four traits are presented, but in some combinations, the dominance registered higher values, indicating a complete dominance, as is the case of the following combinations: Magnif x Odyssey (D = 104), Chronicle x Sallome (D = 102), Vienna x Anabelle (D = 103) for ear length. For grain weight in Chronicle x Sallome and Vienna x Anabelle combinations, the dominance values of 112 and 113 indicated an over-dominance tendency.

Viewed as a simple parameter, the heritability coefficient is not of great importance in the appreciation of some traits, but with the selection pressure and the existing variability, it can provide information on the gene transmission probability to be obtained in new cultivars.

To determine the heritability coefficient in broad sense two calculation methods proposed by Burton (1951) and Mahmoud and Kramer (1951) were used. From the data presented in Table 10 one can observe that there are quite a lot of differences between the two calculation methods, which is probably due to the fact that the F1 populations registered a large variability inside combination. This is why, many authors prefer the model proposed by Mahmoud and Kramer (1951) which does not include F_1 generation, only the F2 generation and parental population variation.

Regarding the mean values of heritability in narrow sense (h^2), it can be said that the grain weight/ear had a medium to high heritability of 0.56, and ear length and

number of grains/ear had a low heritability of 0.36 and 0.42 (Table 10). In a study made on local populations of Ethiopian barley, Addisu et al. (2015) reported the following values of the heritability coefficient in a narrow sense: for ear length 0.14 and for the number of grains 0.91. Compared with the

results from this study, those presented by Addisu et al. (2015) are superior, except h^2 of ear length. Eshghi and Akhundova (2009), analysing two hybrid combinations in a system of diallel crosses, also stated that the number of grains/ ear had a low heritability of 0.2, respectively 0.4.

Table 10. The mean values of genetic parameters estimated for some agronomic characters in spring barley

Trait	Dominance $\dfrac{F1}{HP} * 100$	Coefficient of heritability in a broad sense (H²)		Coefficient of heritability in a narrow sense (h^2) (Warner, 1952)
		according to Burton (1951)	according to Mahmoud and Kramer (1951)	
Ear length	98.33	0.37	0.19	0.36
Number of grains	95.5	0.53	0.81	0.42
Grain weight	97	0.48	0.65	0.56

CONCLUSIONS

The highest values of genetic advance were observed for TKW followed by the number of grains/ear, these being also associated with the highest values of heritability in broad sense. Therefore TKW and the number of grains/ear can be considered two criteria in performing selection work and breeding for spring barley, because of the high heritability and the important genetic advance.

The F1 generation superiority compared with the parental forms for the ear length indicated the presence of heterosis in four of the six combinations studied. In controlling the ear length, the highest role can be attributed to the dominance effects of genes, but also to the epistasis ones. Low values of heritability index in a narrow sense for the ear length identified in this paper, as well as in other studies, indicated a low heritability for this trait and a higher influence of environmental conditions.

For the number of grains/ear, the high dominance effect involved in this trait expression indicated that selection may be effective in later generations. However, from the gene effects analysis, the important role of additivity can be observed in some combinations, which would recommend the selection in early generations. Therefore, it is recommended to continue selection for the number of grains/ear associated with yield

"*per se*". The importance of different types of genetic actions which control the number of grains/ear, is different depending on the hybrid combination, being therefore dependent on genotype.

From the analysis of genetic effects which control grain weight, the important role of dominance and epistatic effects can be observed. The additivity effects had lower values and are acting differently depending on the combination, but in almost all cases they had very significant or significant values. Therefore, it would be advisable to apply selection in later generations for grain weight/ ear.

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