ESTIMATING THE HEREDITY OF SOME QUANTITATIVE TRAITS OF TWO-ROW SPRINGBARLEY (*HORDEUM VULGARE var. distichum*)

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Abstract

Production is, perhaps, the most complex trait and, in comparison with other quantitative traits, itis the hardest to evaluate in the early generations of selection, which is primarily due to the highstate of heterozygosity and to the great number of major and minor genes implied in the heredityof this trait. The research undergone reached the conclusion that, in their turn, the elements of production possess a complex heredity. To estimate the effects of heredity gene involved in quantitative characters, yield component, it was used for genetic analysis model proposed by Hayman (1958) and applied by Gamble (1962). In this regard, the averages of the traits from the parental populations and from the geneticpopulations from the lineages were analysed, the following being estimated: additive geneticeffects (a), dominant (d) and the epistatic interactions of the type additive x additive (aa), additivex dominant (ad), dominant x dominant (dd), involved in the heredity of the analysed traits.

Key words: *Spring barley, Gamble, gene effects, dominance, traits cantitative, plant height, TKW*

INTRODUCTION

Accoding to [1], barley is used on a large scale as animal feed and inthe production of beer, but, lately, interest has been shown for the increasing of utilisation as foodfor people. The world barley production represents approximately 30% of that of corn, however, in comparison to the latter, barley contains more proteins, methionine, lysine, cysteine and tryptophan. In the feeding of ruminants, barley can also be found on the third place, from the point of view ofits degree of digestibility, after oat and wheat[5].
As it is known, in the heredity of quantitative trait (the elements of production and some morphological traits) a great number of genes is involved, with reduced and resemblant effects, acting, most of the times, additively in the determination of the respective trait. In the literature, these genes are known under the name of 'polygenes'. Besides the additive action of the polygenes in the heredity of quantitative traits, other types of interactions are implied, intra-allelic (dominance and recessiveness) and inter-allelic (epistasis), in the end all these determining a complex heredity of these traits. The implication of each polygene cannot be analysed singularly, but only as a unitary whole, at the level of the gene complex.

The main morphoproductive traits that were the object of this study were represented by: spike length,number of grains/spike, grain weight/spike and the TKW, the heredity of the plants' height was alsoanalysed, with the aim of improving the breeding programmes that focus on its reduction it. In this paper,only the genic effects for the plants' height and the number of grains/spike will be presented.
The analysis ofthese elements through quantitative genetics has a probabilistic character – it becomes precise only throughthe use of molecular markers in the analysis of these QTL.
At the basis of choosing the parental forms stoodthe homozygosity criteria, while the parents were differentiated more or less in regard to the traits analysed, a number of six hybrid combinations being performed. The cultivars chosen for this study were representedby two autochthonous varieties (JUBILEU – SCDA Turda; PRIMA – SCDA Suceava) and ten either older ornewer foreign varieties (THURINGIA, VICTORIANA, VIENNA – Saaten Union; ODISEY, CHRONICLE, SALOME – Limagrain; MAGNIF, ANABELLE – varieties of Czech origin.)

MATERIALS AND METHODS

In order to estimate the genic effects implied in the heredity of quantitative traits, production traits, the model of genetic analysis proposed by [1] and put into practice by [4] was used. In this regard, the averages of the traits from the parental populations and from the genetic population from the lineages were analysed, with additive genic effects (a), dominant (d) and the epistatic interactions of the type additive x additive (aa), additive x dominant (ad), dominant x dominant (dd) implicated in the heredity of the analysed characters being estimated. For every trait, a number of 50 plants were studied, with the mention that there were some combinations in which a smaller number of plants were analysed in the F1 generation. The height of the plants was determined with the help of a graduated ruler from ground level to the top of the aristae, while spike length was measured from the base of the spike to its top.

RESULTS AND DISCUSSIONS

The average performances of the parental populations and those of the segregant generations corresponding to each cross breeding for the plants' height are presented in table 1, the average of parental populations being between 87 and 112 cm. The average of the F1 generation has got values intermediate between the two parents at the majority of the combinations, but, in the F2 generation, most combinations registred values that were superior in comparison to the F1 generation. Looking at the backcrossing generations, it can be observed that there is a behaviour fairly in concordance with the value of the parent that participates in the respective backcross. In the case of combinations 2 and 3, the higher values of the plants' height from F2 as compared to those from F1 and of the tallest parent, indicate the presence of some transgressive segregants. In the case of combinations 5 and 6, the fact that the value of the plants' height in F2 is inferior to the shortest parent or only a bit higher (combination 6) is an indicator to the existence of some negative transgressive segregations. All these come to show the complex mechanism behind the transmission of plant height and the difficulties met in the improvement of this trait, which is why it is reccomended that the selection be made in successive generations, through the checking of lineages.

Table 1. The average plant height values (cm) of the parental populations in a spring barley crossbreeding system (Turda, 2016).

POPULATIONS						
COMBINATION	P1	P2	F1	F2	BCI	BCII
CB1 (Thuringia x Jubileu)	101	112	97	103	108	100
CB2 (Prima x Victoriana)	109	90	103	111	113	95
CB3 (Magnif x Odisey)	106	92	95	108	103	101
CB4 (VictorianaxAnabelle)	92	102	81	96	100	103
CB5 (Chronicle x Salome)	92	87	92	88	96	95
CB6 (Viena x Anabelle)	100	98	99	97	103	100

At the level of the F1 generation, in the majority of combinations, with the exeception of 1 and 4, the average of spike length is superior to the average of the best parent, which in these situations indicates a quite pronounced effect of heterosis, probably due to the effects of over dominance. In F2, for the four combinations still, a slight genetics depression can be observed; however, this is not significant and it points to the accumulation of additive genes in a heterotic state at the level of this generation. With respect to the retrocrossing generations, it can be said that in what the spike length is concerned, the behaviour in these generations corresponds to the performances of the parent from the respective cross, even if the differences are smaller. A deviation from this behaviour can be observed in the case of combination I, which confirms the probabilistic character of this method. From among the parents, in terms of spike length, the genotypes Jubileu and Anabelle stand out.

Table 2. The average spike length values (cm) for the parental populations in a two-row spring barley backcrossing system

POPULATION						
COMBINATION	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)	10,1	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

Estimation of genic effects
In o ur research, from the data presented in table 3, it can be observed the significant to very significant effects of the additivity genes in expressing plant height, with the exception of combinations 3 and 5. An absolutely superior value of additivity genes can be highlighted in the

case of combination 2, while the negative values of the additive effect in combination 4 are due tothe fact that the second parent's height was superior, an exception to this behaviour is made, again, by combination 1, for which the Jubileu cultivar is probably not homozygotous for the majority of the loci.

The high absolute values of the very significant dominance effects (only significant in combination 1) distinguish themselves, which confirms the important role dominance plays in the conditioning of this trait. For almost all the combinations, the values of the epistatic effects are superior to those of the additivity effects, which suggests a greater implication of the former in the heredity of plant height. Similar effects in what the implication of dominance genes in the heredity of plant height are concerned were also reported by [3]. On the other hand, [6] mention that, in plant height control, a high number of alleles intervenes, which usually act additively when they have a normal distribution.

Table 3. Estimation of gene effects on plant height in a set of six two-row barley hybrid combinations (Turda 2016)

GENE EFECTS						
COMBINATION	m	a	d	aa	ad	dd
CB1 (ThuringiaxJubile)	102,9 ***	8,1 ***	-3,9*	5 **	13,8 ***	-14,6 ***
CB2 (Prima x Victoriana)	110,5 ***	18 ***	-24,78 ***	-28,13 ***	8,45 **	19,03 ***
CB3 (Magnif x Odisey)	107,9 ***	2,55	-26,71 ***	-22,98 **	-4,18 **	2,73
CB4 (VictorianaxAnabelle)	96 ***	-3,3 *	6,25 ***	22,2 ***	1,5	-72,1 ***
CB5 (Chronicle x Salome)	87,88 ***	0,8	33,93 ***	31,68 ***	-1,85	-55,18 ***
CB6 (Viena x Anabelle)	97 ***	3,25 **	17,4 ***	18,1 ***	2,1	-23,8 ***

An estimated presentation of the role genes have in the control of spike length is displayed in table 4. From the reduced absolute values of additive genic effects, a reduced implication of additivity in the conditioning of this trait can be deduced. Regarding the dominance genes, their very significant contribution in the heredity of the spike length can be observed, this being eflected, as well, in the absolute superior values of the additity genic effects. Actually, in 5 of the6 combinations studied, the values of the dominance effects are also superior to ones epistatic of the type aa and ad. All these come to strenghten the major role of dominance effects in spike length conditioning.The major contribution of dominance effects in the expressing of spike length was also reported by [2], who show that the study of spike length heredity indicates, in the genetic

determinism of this trait, the presence of the phenomen of dominance and non allelic interactions.

Table 4. Estimation of gene effects on spike lenght in a set of six hybrid two-row barley combinations (Turda 2016)

GENE EFECTS						
COMBINATION	m	a	d	aa	ad	dd
CB1 (Thuringiax 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 (VictorianaxAnabelle)	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 ***

CONCLUSIONS

In barley production, a series of interdependant physiological processes are implied, which take place gradually in the course of the vegetation period, finding themselves under the influence ofthe environmental conditions a significant period of time (from sprouting to physiological maturity).

As it could be observed, all the agronomical elements of production have, in their turn, a complex heredity, which complicates selection works even more. The best breeding results were obtained when the selection criteria used were represented by the components of production with a heredity as simple as possible.

The role of additivity effects in plant height control is closely related to the differentiations between parental forms, so in the case CB2 (Prima x Victoriana), the values of the additivity effects are high and very significantly positive. The control of plant height is governed by dominant andepistatic additivity effects. The selection for plant height (evidently, for the forms resistant to fall) may begin in the earlier generations of selection, but the reduction of height has to be associated with high productivity, precisely because the plant height is directly and very significantly corellated with the number of grains/spike, the weight of the grains/spike and TKW. The superiority of the F1 generation to the parental forms in the case of spike length indicates thepresence of the phenomenon of heterozygosity in the case of this trait for four of the six combinations studied. In spike length conditioning, the greatest role can be attributed to the dominant, as well as to the epistatic effects of genes.

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