UDC 633.16:631.523.11

Genetic weight control of 1000 grains at modern grades of spring barley

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The purpose. To determine selection-genetic features of modern grades of spring barley by mass of 1000 grains in Central Forest-steppe of Ukraine and to secrete genetic sources of increased combining ability for use in hybridization. **Methods.** Modern grades of domestic and foreign selections are used in crossings by full double-allele scheme (7x7). Analysis of results and interpretation of genetic parameters are carried out according to practical standards (M.A. Fedin, etc., 1980). **Results.** High values are determined of quotients of heritability both in wide (H2=0,98 – 0,99) and narrow (h2=0,73 – 0,82) comprehension. That testifies to the big contribution of genetic features in phenotypical variability, and mainly additive monitoring of an attribute. **Conclusions.** Selection-genetic features are determined in the probed genotypes on an attribute «mass of 1000 grains». They allow to forecast efficiency of selections directed on augmentation of an attribute in the framed hybrid material. Efficient genetic sources for increase of weight of 1000 grains in combinational selection are grades Zhana, KWS Aliciana, Virazh.

Key words: genetics, grain, hybridization, crossing, combining ability, heritability.

Goal. To reveal plant breeding and genetic characteristics of modern spring barley varieties by 1000 kernel weight in the Central Forest-Steppe of Ukraine and to identify genetic sources of increased combining ability for including in hybridization. **Methods.** The research was carried out at the V.M. Remeslo Myronivka Institute of Wheat of NAAS in 2014-2016. Modern varieties of domestic and foreign breeding were involved in crossings by full diallel scheme (7 x 7). Analysis of the results and the interpretation of genetic parameters were carried out in accordance with common methods (M.A Fedin et al., 1980). **Results of the research**. The varieties Zhana (1.31-1.62) and KWS Aliciana (0.48-0.89) were distinguished by stable high effects of general combining ability (GCA) in all years of research. The varieties Virazh and Explorer were characterized with reliable effects of GCA in two years. In 2014 and 2016, the advantage of additive effects (D) *vs* dominant (H_1 and H_2) was noted. In 2015, on the contrary, dominant effects were higher. Dominance in 2014 and 2016 and overdominance in 2015 were revealed by indices of average degree of dominance (H_1/D) both in general and in individual loci ($\sqrt{H_1/D}$). The dominance turned upon the trait increase, but with different values of correlation $r[W_r+V_r)_i; x_i]$: from -0.85 ± 0.24 in 2016 to -0.57 ± 0.37 in 2015. Quantitatively, in this set of varieties recessive genes (effects) prevailed. The most number of dominant genes (effects) was noted in the varieties Zhana, KWS Aliciana, Virazh, recessive ones was noted in the varieties Talisman Myronivskyi and Explorer. The varieties Komandor and KWS Bambina were characterized by redefining the effects of genes over the years of research. High values of heritability coefficients both in the broad (H^2 = 0.98-0.99) and in the narrow sense (h^2 = 0.73-0.82) were found thus indicating a significant contribution of genetic characteristics and mainly addictive control of the trait to the phenotypic variability, respectively. **Conclusions.** Plant breeding and genetic characteristics being revealed in genotypes studied for the trait "1000 kernel weight" can predicting efficiency of selections aimed at increasing the trait in hybrid material created. The varieties Zhana, KWS Aliciana, Virazh should be used as effective genetic sources for increasing 1000 kernel weight in combination breeding.

Thousand kernel weight is one of spring barley yield components and is an important agronomic trait, which largely determines consumer, technological, and seed characteristics of the crop. To carry out purposeful breeding varieties with a given grain size, the availability of effective genetic sources of sufficient expression level of the trait 1000 kernel weight and information on its genetic control is of great importance.

A large number of publications of domestic and foreign researchers are devoted to study of genetic determination of quantitative traits associated with barley productivity, including 1000 kernel weight, in system of diallel crossings. In particular, V.V. Vashchenko has found the prevalency of dominant gene effects in genetic control of 1000 kernel weight [1]. The trait was increased by dominant genes. In experiment with another set of varieties, the same researcher has noted intra-locus overdomination and additivity between loci [2]. However, in some years, the redefining genetic systems of control of the trait was revealed. Proceeding from the lack of domination direction, the author points out that large grain forms can be selected both on dominant and recessive basis.

In one of the experiments, L. I. Koroleva has found an additive control of the 1000 kernel weight [3]. Instead, in the study with another set of accessions, the same author notes the prevalency of dominant effects and overdomination [4]. The domination was directed. Dominant genes increased the size of kernels.

A. A. Usikova notes one-direction dominance toward increasing the 1000 kernel weight. In genetic control of the trait overdomination both in system as a whole and in individual loci was detected [5].

In the studies by M. R. Kozachenko and O. V. Solonechna, a significant prevalency of dominant effects of genes on additive and overdomination in genetic control of the trait was noted [6, 7]. The same regularities were revealed when involving forms with various expression of awness diallel [8], as well as varieties with different qualitative indices of protein and starch [9-11] into diallel crosses.

Instead, in a three-year study of two schemes of crossing accessions from global collection belonging to different varieties and mutants obtained experimentally dominant effects prevailed in two years, but in the third additive effects did [12, 13].

Concerning hulless barley forms it was marked reliable contribution of both dominant and additive effects with a slight advantage in F_1 additive effects, whereas in F_2 dominant ones [14]. Other authors also noted the significant contribution of additive and dominant effects with the latter prevailing. In inheritance there was noted overdomination [15]. The contribution of dominant effects was also found for multi-row barley [16].

Eshghi R. et al. [17] in Iran investigated hybrids derived from crossing multi-row hulled and hulless barley forms under natural precipitation and artificial irrigation. In no stress (irrigation), prevalency of dominant effects was noted, although the additive ones were also reliable. Instead, in stressful conditions additive effects prevailed over the dominant ones. Under humid conditions recessive genes increased the trait, and under stresses dominant genes did. In general, the authors conclude that dominant effects and non-allelic interactions to are the most determining in genetic control of the trait under both conditions of the research.

Non-allelic interaction in various combinations with additive and dominant effects was noted by a number of other researchers [18-21].

Thus, the literature sources analyzed contain ambiguous data on the genetic control of 1000 kernel weight which is obviously due to diverse genetic material involved in crossing, locations and conditions of researches. Consequently, study on plant breeding and genetic characteristics of new spring barley varieties by 1000 kernel weight in specific environments is actual for practical breeding this crop.

The purpose of the research is to reveal breeding and genetic features of modern barley varieties for 1000 kernel weight in the Central Forest-Steppe of Ukraine and to identify genetic sources of increased combining ability for including in hybridization.

Materials and methods of the research. The research was carried out at the V. M. Remeslo Myronivka Institute of Wheat of NAAS (the V. M. Remeslo MIW of NAAS). Hybridization for a full (7 x 7) diallel scheme was performed annually in 2013-2015. As components of crossing there are modern varieties of the native (Virazh, Talisman Myronivskyi (hereinafter in tables Talisman) (the V. M. Remeslo MIW of NAAS), Komandor (Plant Breeding and Genetics Institute – National Centre of Seed and Cultivar Investigation of NAAS) and foreign (KWS Aliciana, KWS Bambina (DEU), Zhana, Explorer (FRA)) breeding. Plants of parental forms and F_1 were grown under field conditions in 2014-2016 with 3 replications. 1000 kernel weight was determined for parental components and hybrid combinations for each replication. Analysis of variance was carried out according to B. A. Dospekhov [13]. Combining ability and genetic parameters were calculated in accordance with M. A. Fedin, D. Ya. Silis, A. V. Smiryaev [14]. Data were calculated using Excel 2010 and Statistica 8.0.

Results of the research. Table 1 describes the mean value of 1000 kernel weight in the varieties involved in crossing and hybrids with their participation. There are reliable differences between both the components of crossing and F_1. The maximum level of occurrence of the sign is noted in varieties of Zhana, KWS Aliciana, Virazh, Explorer.

1. Expression level of the trait "1000 kernel weight" in components of crossing and F_1 with their participation

Variety	2014		2015		2016		**Mean**	
	P	F_1	P	F_1	P	F_1	**P**	**F_1**
KWS Aliciana	52.56	53.60	53.92	56.00	48.36	49.79	**51.61**	**53.13**
KWS Bambina	51.68	53.10	52.94	55.09	47.75	49.20	**50.79**	**52.46**
Zhana	53.83	54.29	55.04	56.63	49.87	50.61	**52.91**	**53.84**
Explorer	51.92	53.73	53.86	56.03	47.87	49.20	**51.22**	**52.98**
Komandor	50.59	53.10	51.68	55.10	47.66	48.96	**49.97**	**52.38**
Talisman	46.86	51.11	47.80	52.54	43.60	47.24	**46.09**	**50.29**
Virazh	52.09	53.50	52.87	55.41	48.76	49.81	**51.24**	**52.91**
Mean	**51.36**	**53.20**	**52.59**	**55.26**	**47.70**	**49.26**	50.55	52.57
LSD_{05}	0.46	0.50	0.57	0.63	0.31	0.37	-	-

The ANOVA showed reliable values of both general (GCA) and specific combining ability (SCA), but with a significant advantage of the former (Table 2). The reciprocal effect in all years was unreliable.

2. Analysis of variance of combining ability of the spring barley varieties by the trait "1000 kernel weight"

Source of variation	2014			2015			2016		
	MS	F	%	MS	F	%	MS	F	%
GCA	14.72	548.77*	94.06	25.12	682.73*	95.70	15.82	1070.07*	96.58
SCA	0.87	32.6*	5.56	1.07	29.0*	4.08	0.54	36.58*	3.30
RE	0.03	0.94	0.19	0.03	0.88	0.11	0.01	0.77	0.06
Error	0.03	-	0.19	0.04	-	0.15	0.01	-	0.06

Note: MS – mean square; F – Fisher criterion (actual value); GCA – general combining ability; SCA – specific combining ability; RE – reciprocal effect; * – significant at the 0.01 level

Characteristics of the varieties studied for GCA effects, SCA constants, and variances of GCA and SCA are given in Tables 3 and 4. As for GCA effects in all years of research the variety Zhana (1.31-1.62) significantly exceeded other varieties. The variety KWS Aliciana (0.48-0.89) in all the years had significantly higher than zero GCA effects. The variety Explorer has shown positive effects in 2014-2015, but in 2016 they were not statistically different from zero. The variety Virazh was characterized by reliable GCA effects in 2014 and 2016, but unreliable positive in 2015. The most negative value of GCA effects has been marked all year in the variety Talisman. The varieties Komandor and KWS Bambina were characterized by slight negative GCA effects which in some years did not differ significantly from zero.

3. Effects of general, variances of general and specific combining ability

Variety	GCA effects			GCA variance			SCA variance		
	2014*	2015	2016	2014	2015	2016	2014	2015	2016
KWS Aliciana	0.48	0.89	0.64	0.22	0.79	0.41	0.32	0.47	0.06
KWS Bambina	-0.12	-0.20	-0.07	0.01	0.03	0.00	0.28	0.27	0.32
Zhana	1.31	1.65	1.62	1.70	2.71	2.62	0.46	0.46	0.14
Explorer	0.63	0.92	-0.07	0.39	0.84	0.00	0.55	0.49	0.32
Komandor	-0.13	-0.19	-0.36	0.01	0.03	0.13	0.15	0.25	0.13
Talisman	-2.52	-3.26	-2.43	6.33	10.59	5.88	0.26	0.20	0.03
Virazh	0.36	0.18	0.66	0.12	0.02	0.44	-0.01	0.27	0.26
LSD$_{05}$ (gi)	0.16	0.19	0.12	-	-	-	-	-	-
LSD$_{01}$ (gi)	0.21	0.25	0.16	-	-	-	-	-	-
LSD$_{05}$ (gi–gj)	0.25	0.29	0.18	-	-	-	-	-	-
LSD$_{01}$ (gi–gj)	0.33	0.38	0.24	-	-	-	-	-	-

Mote: * – years of the research

4. Constants of specific combining ability

Сорти	Year	KWS Aliciana	KWS Bambina	Zhana	Explorer	Komandor	Talisman
KWS Bambina	2014	0.01					
	2015	-0.33					
	2016	-0.33					
Zhana	2014	-1.17	-0.60				
	2015	-1.37	-0.07				
	2016	-0.24	-0.70				
Explorer	2014	0.55	1.00	0.45			
	2015	0.55	0.95	0.54			
	2016	0.22	0.72	0.48			
Komandor	2014	0.11	0.26	0.49	-0.85		
	2015	0.29	0.40	0.72	-0.84		
	2016	0.51	-0.02	0.25	-0.56		
Talisman	2014	0.51	-0.40	0.63	-0.86	-0.14	
	2015	0.29	-0.48	0.10	-0.61	-0.14	
	2016	-0.09	-0.39	0.00	-0.04	0.20	
Virazh	2014	-0.02	-0.27	0.20	-0.30	0.13	0.26
	2015	0.57	-0.47	0.09	-0.58	-0.45	0.84
	2016	-0.06	0.73	0.22	-0.81	-0.39	0.32

Note: in 2014 LSD$_{05}$ = 0.32, LSD$_{01}$ = 0.42; in 2015 LSD$_{05}$ = 0.38, LSD$_{01}$ = 0.49; in 2016 LSD$_{05}$ = 0.24, LSD$_{01}$ =0.31

The results of ANOVA of diallel tables indicate the reliability of parameter *b* characterizing effects of domination in loci (Table 5). Component b_1 informs that mean values of the parent components do not equal mean value of the hybrids with their participation, and accordingly mean degree of dominance (H_1/D) is not zero. Parameter b_2 indicates the asymmetry of gene distribution in loci that express domination. It is confirmed with asymmetry of the ratio of parameter $H_2/4H1 \neq 0.25$ (Table 6). Thus, it can be argued that mean square of parameter *a* evaluates general genetic variation. Component *d* confirms the absence of reciprocal differences.

5. Analysis of variance of dial-up tables by the trait "1000 kernel weight"

Components of variation	2014		2015		2016	
	MS	F	MS	F	MS	F
a	58.30	684.57*	90.25	722.41*	58.03	1306.33*
b	4.80	56.36*	8.76	70.10*	3.45	77.65*
b_1	61.01	716.36*	128.28	1026.78*	43.80	985.92*
b_2	0.51	6.00*	1.81	14.45*	0.99	22.22*
b_3	2.62	30.80*	3.20	25.62*	1.62	36.53*
c	0.10	1.22	0.09	0.73	0.05	1.22
d	0.06	0.75	0.10	0.79	0.03	0.59
Pt	0.09	-	0.12	-	0.04	-

Note: * – significant at the 0.01 level

6. Genetic components and coefficients of heritability by the trait "1000 kernel weight"

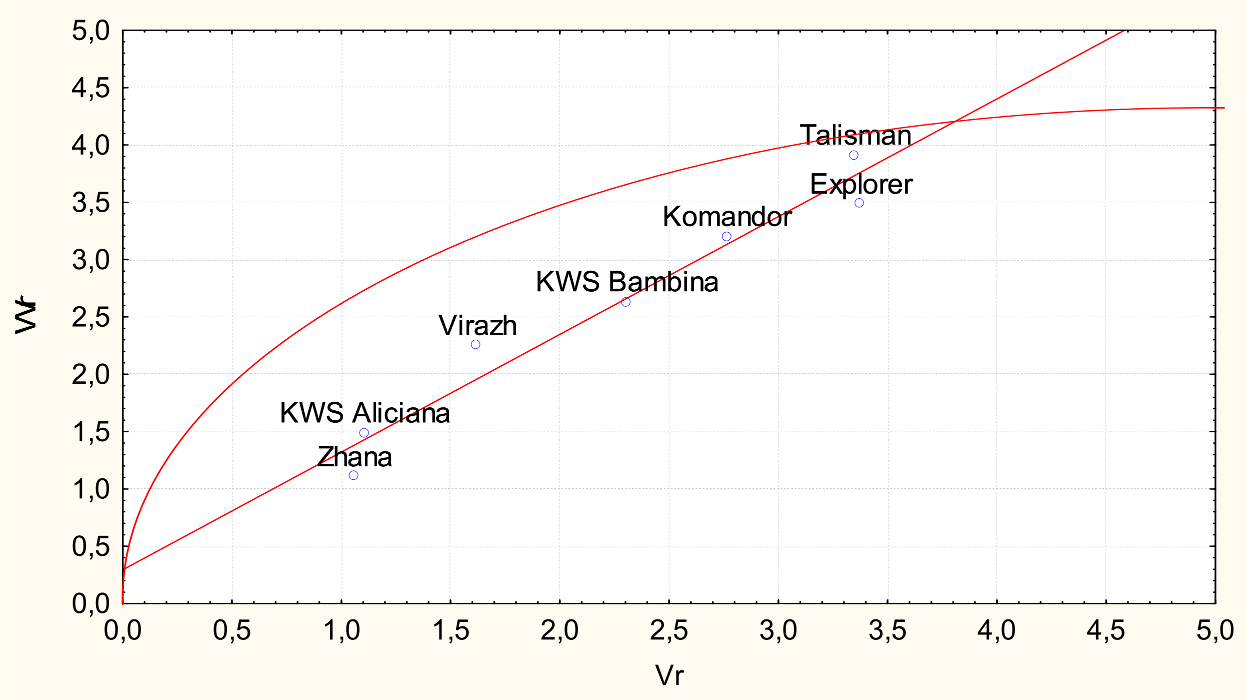
Genetic components	2014	2015	2016
D	4.83	5.49	3.82
H_1	3.27	6.21	2.52
H_2	3.80	5.83	2.29
F	-0.62	-2.72	-1.47
H_1/D	0.68	1.13	0.66
$\sqrt{H_1/D}$	0.82	1.06	0.81
$1/2F/\sqrt{[D(H_1-H_2)]}$	-0.47	-0.95	-0.79
$(\sqrt{4DH1} + F)/(\sqrt{4DH1}-F)$	0.85	0.62	0.62
h^2/H_2	4.25	4.88	4.23
$H_2/4H_1$	0.24	0.23	0.23
$r[(W_r+V_r)_i; x_i]$	–0.77±0.28	–0.57±0.37	–0.85±0.24
F_1–P	1.84	2.67	1.56
H^2	0.98	0.98	0.99
h^2	0.76	0.73	0.82

In 2014 and 2016, the prevalency of additive effects (D) over dominant ones (H_1 and H_2) was noted. In 2015, on the contrary, dominant effects were higher. Accordingly, the mean degree of dominance (H_1/D) has pointed to domination in 2014 and 2016 and overdomination in 2015. The same regularity was also typical for the index of the mean degree of domination in the loci (($\sqrt{H_1/D}$). The ratio $1/2F/\sqrt{[(D(H_1-H_2)]}$ significantly differing from 1.0 indicates an uneven mean degree of domination in different loci in all years.

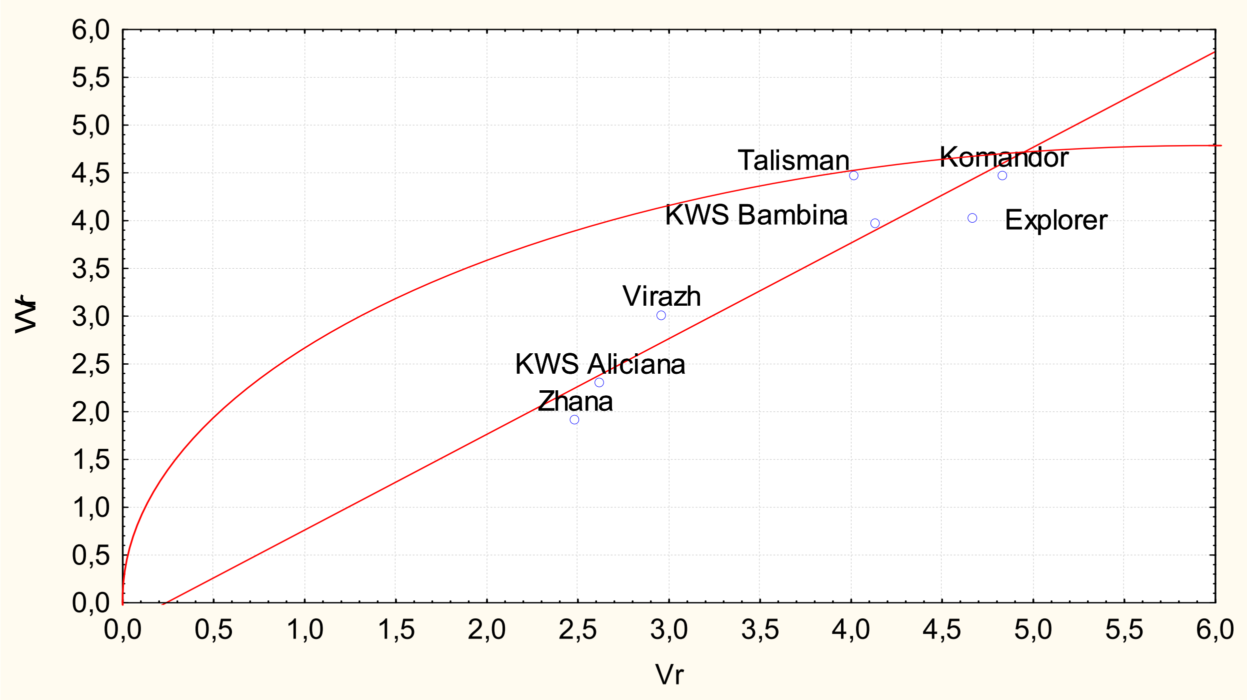
The index of frequency distribution of dominant and recessive alleles ($F<0$) indicates quantitative prevalency (expression) of recessive genes (effects) in all the years. Parameter $(\sqrt{4DH1}+F)/(\sqrt{4DH1}-F)$ demonstrates the ratio of the total number of dominant genes to the total number of recessive genes in all varieties involved into crossings.

The value of the ratio h^2/H^2 indicates that 4 genes (groups of genes) revealed domination effects. Correlation coefficient $r[(W_r+V_r)_i;\ x_i]$ in all the years testifies to the tendency of dominance toward increasing the trait. However, its value varied over the years from $r[(W_r+V_r)_i;\ x_i] = -0.85\pm0.24$ in 2016 up to $r[(W_r+V_r)i;\ x_i] = -0.57\pm0.37$ in 2015. That is, the trait was increased by mainly dominant genes. This is confirmed with parameter F_1–P. Heritability coefficient in the broad sense (H^2) was high in all the years of the research (0.98-0.99), thus indicating significant contribution of genetic characteristics to phenotypic variability. Heritability coefficient in the narrow sense (h^2) was also high (0.73-0.82) to confirm significant additive control of the trait.

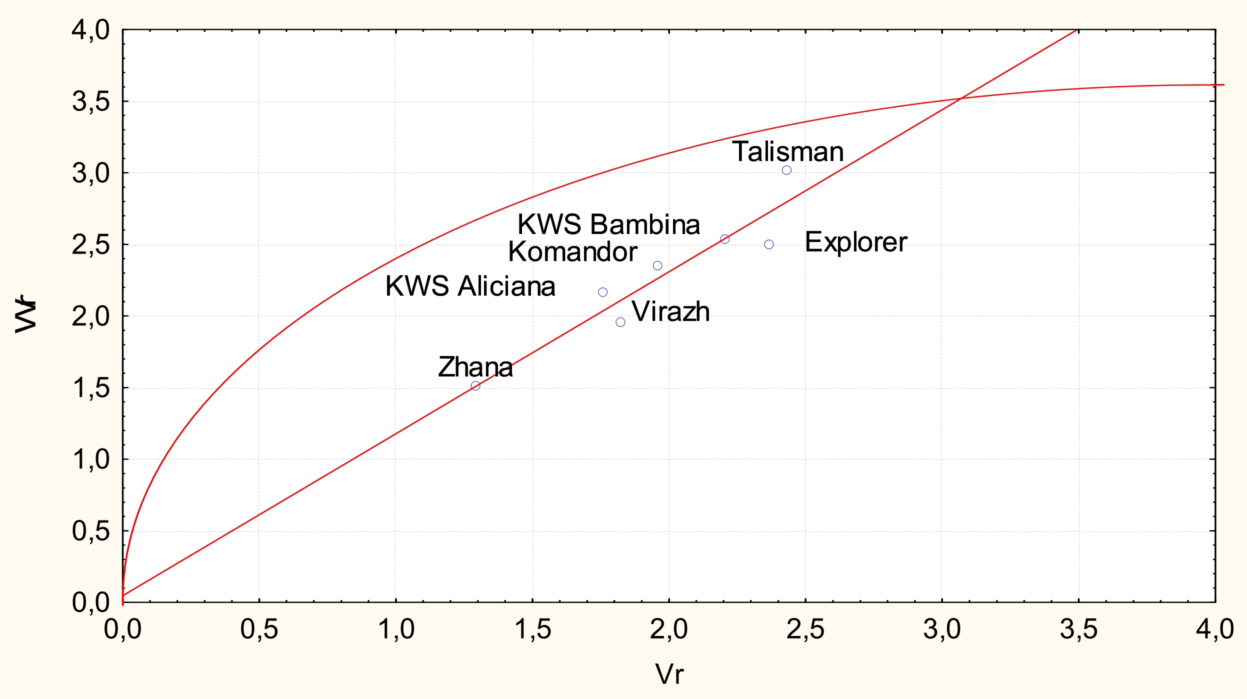
Graphical analysis of regression of covariance (Wr) on variance (Vr) between mean value of parent components and hybrids with their participation confirms and complements information on genetic components with respect to dominance in 2014 and 2016 and the overdominance in 2015 (Figure 1). The distribution of varieties by relative ratio of dominant and recessive alleles is clearly represented. In all the years, the varieties Zhana, KWS Aliciana, Virazh were stably in dominant zone, while the varieties Talisman and Explorer were in recessive zone. As for the varieties Komandor and KWS Bambina, there was a certain redefinition of gene effects over the years of the research.



2014



2015



2016

Fig. 1. Regression graphs Wr/Vr for the trait "1000 kernel weight", 2014-2016

Conclusions.

Plant breeding and genetic characteristics being revealed in the varieties involved into crossing for the trait "1000 kernel weight" can predicting efficiency of selections aimed at increasing the trait in hybrid material created. The varieties Zhana, KWS Aliciana, Virazh should be used as effective genetic sources for increasing 1000 kernel weight in combination breeding.

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