

GENETIC ANALYSIS OF WET GLUTEN CONTENT IN GRAIN IN DIALLEL CROSS OF DURUM WHEAT

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Abstract

In the period 2014-2016, a diallel cross design was performed and harvested without the reciprocal crosses. The study includes five modern durum wheat varieties: Victoria (BG), Deni (BG), Superdur (AT), Progress (BG), Predel (BG). Parents and hybrids were sown by block method with three replications in the experimental field of the Field Crops Institute in Chirpan, Bulgaria. The trait studied was wet gluten content in grain. The results of the technological analysis were statistically processed by Hayman - Jinks methods. Both the additive and dominant parameters have influenced the inheritance of the studied character. The dominant parameters are higher and they have a greater role in inheritance. To increase the wet gluten content, recessive genes are accumulated in the genotype. Heritability coefficients indicate that efficient genotype selection is possible by phenotype, but it should start in the later segregated generations. The graphical analysis points out that the trait is under the control of an additive-dominant genetic system with manifestations of epistasis. In all cases the epistasis is of a complementary type with involved overdominance.

Key words: breeding, durum wheat, genetics, inheritance, wet gluten.

INTRODUCTION

Inheritance of quantitative traits is the subject of numerous scientific studies. Knowledge of genetic architecture and the inheritance of various traits is of particular importance for the development of varieties that meet modern requirements. The use of diallel crosses and the information received from them gives a clear idea of the manipulations that may be carried out on the trial objects. Studies are topical since the manifestation of various components in inheritance is essential to set the right strategy for breeding in durum wheat. Knowledge about the genetic capabilities of various genotypes is the basis of their effective use as donors in the development of new high-quality varieties. The prevailing content of dominant or recessive genes in parents is critical to their breeding value. Determining what kind of genes are accumulated to increase the magnitude of the trait allows for an effective estimate defining the rate of the expected result. The results of various studies exhibit a diversity of inheritance mechanisms for wet gluten content in grain. Rathod et al. (2008); Singh et al. (2009) report that additive and dominant parameters are significant in the inheritance of the wet gluten content in grain. According to

Akram et al. (2007) wet gluten content is influenced by dominant gene effects with preponderance of overdominance and manifestations of non-allelic interactions. They conclude that this will hinder effective selection in earlier generations. The correlation between the mean value of parents and their sum (V_r+W_r) indicated a tendency for high wet gluten content to be associated with accumulated of dominant genes. Sadeghi et al. (2013) determine that non-additive gene effects have a greater role in inheritance of the wet gluten content. According to them, the inheritance of the character exhibits a simple additive-dominant genetic system with overdominance and the trait values increase with the accumulation of recessive genes. The authors note that effective selection has to begin in later segregated generations. The calculation of the heritability coefficients determines the opportunities both for running efficient selection and the appropriate units to start it from. Aydogan and Yagdi (2004) examine a 6 x 6 diallel cross to establish the genetic nature of the wet gluten content in grain. They find significant D, H₁, and H₂ parameters, noting that the dominant ones are higher. They establish medium heritability coefficients in narrow sense and high ones in

broad sense. From the graphical diallel analysis they report that partial dominance is fundamental to inheritance.

The results presented by the various authors show that in the inheritance of the character of great importance are the parents used and they determine the differences in the genetic architecture of the hybrids. This necessitates the study of this trait in durum wheat with modern genotypes. The aim of this study is to investigate the genetic components and their variances for wet gluten content in the grain. Receiving inheritance information for this trait will allow recommendations to be made to lead an effective selection and speed up the breeding process.

MATERIALS AND METHODS

The study was conducted under field conditions in the Field Crops Institute, Chirpan. The experiment included five durum wheat varieties: Victoria (BG), Deni (BG), Superdur (AT), Progress (BG) and Predel (BG) and 10 crosses with them. A diallel cross was made and tested for three years (2014, 2015 and 2016). This allowed the cultivation of three generations - F₁ and two F₂. The experiment was carried out by a block method in three replications by the approved technology for growing durum wheat. The length of the row was 2 m, the row spacing was 20 cm and in the row 5 cm. 20 plants from parents and F₁ generation were randomly plucked off and from F₂ - 30 plants. The grain from the replication was pooled and used for technological analysis under laboratory conditions. The studied trait was wet gluten content in grain from an average sample for each replication and the technological analysis was carried out under BDS EN ISO 21415-2: 2008. Half of the seeds of F₁ were used to sow F₂ generation.

The obtained results were processed with graphic and parametric diallel analysis by Jinks (1954); Hayman (1954; 1957); Mather (1967). The obtained results are processing using the publication of Aksel and Johnson (1962) for diallel analysis. Suitability of data for diallel analysis was assessed by the regression coefficient *b* and *t* (*W_r-V_r*) (Mather and Jinks, 1982; Singh and Chaudhary, 1985). Heritability

coefficients were calculated by the formulas of Mather and Jinks (1982). The calculated parameters are as follows: *D* - Component of genetic variance due to additive effect of genes, *H₁* - Components of genetic variance due to dominance effect, *H₂* - Proportion of dominance variance due to the positive and negative effects of the genes in the parents, *h₂* - Dominance effects, as algebraic sum over all the loci in heterozygous phase in all the crosses, *F* - Co-variance of additive and non-additive effects in a single array. It may be positive or negative. The parameters served for calculation of indicators: (*H₁/D*)^{1/2} - Mean degree of dominance, *H₂/4H₁* - Proportion of genes with positive and negative effects on the parents, *K_d/K_r* - Proportion of dominant and recessive genes in the parents, *h₂/H₂* - number of groups of genes with positive and negative effects on the parents, *r_{Y_r(W_r+V_r)}* - correlation coefficient between the value of the parent and their respective sum *W_r + V_r*, indicate the direction of action of the dominant or recessive factors.

RESULTS AND DISCUSSIONS

The variance analysis exhibits reliable differences between genotypes in the three generations F₁ and the two F₂ (See Table 1). This allows the data to be processed statistically and to obtain significant information from them. Table 2 lists the genetic parameters and indicators by Hayman (1954); Jinks (1954) from the diallel cross for all tested cases.

Table 1. Mean squares (MS) from ANOVA by years

Source of variation	F ₁ -2014 MS	F ₁ -2015 MS	F ₁ -2016 MS	F ₂ -2015 MS	F ₂ -2016 MS
Genotype	20.13***	8.93**	18.58***	9.79**	12.47**
Replication	21.88***	6.37*	12.52***	36.96**	18.57**
Error	0.44	3.45	1.57	2.37	3.55

*P >0.05; **P >0.01; ***P >0.001

Parameter *D* has significant values for the F₁ and F₂ generations (Table 2). These reliable values show the remarkable impact of the additive gene action in the inheritance of the character. That correlates to the results obtained by other authors (Aydogan and Yagdi, 2004; Rathod et al., 2008; Singh et al., 2009). The table presents the dominant parameters of *H₁*

and H_2 , which are also significant. They are greater than (D) and prove that dominance has a major role in the inheritance of the wet gluten content in grain (See Table 2). Other researchers also report proven dominant

parameters from experiments with diallel analysis for wet gluten content (Aydogan and Yagdi, 2004; Rathod et al., 2008; Singh et al., 2009).

Table 2. Genetic parameters and indicators for wet gluten content in grain of durum wheat from the diallel cross

Parameters and indicators	F ₁ - 2014 y.	F ₁ - 2015 y.	F ₁ - 2016 y.	F ₂ - 2015 y.	F ₂ - 2016 y.
D	6.54 ± 0.37	1.61 ± 0.59	5.14 ± 3.25	1.55 ± 0.73	4.42 ± 1.76
F	-2.25 ± 0.93	-2.02 ± 1.47	10.48 ± 8.13	-1.30 ± 1.84	9.72 ± 4.42
H ₁	13.04 ± 1.01	3.70 ± 1.59	30.87 ± 8.79	5.79 ± 1.99	20.83 ± 4.78
H ₂	12.70 ± 0.92	3.76 ± 1.44	23.20 ± 7.97	5.14 ± 1.80	14.99 ± 4.33
h ₂	20.27 ± 0.15	-0.10 ± 0.24	2.76 ± 1.32	2.05 ± 0.30	0.87 ± 0.72
(H ₁ /D) ^{1/2}	1.41	1.51	2.45	1.93	2.17
H ₂ /4H ₁	0.24	0.85	0.18	0.22	0.17
Kd/Kr	0.78	0.41	2.42	0.64	3.05
h ₂ / H ₂	1.59	0.02	0.11	0.39	0.05
r _{Yr_i(W_r+V_r)}	0.28	-0.82	0.78	0.26	0.78
H ²	0.94	0.69	0.91	0.7	0.74
h ²	0.55	0.45	0.15	0.40	0.05

D - Component of genetic variance due to additive effect of genes, H₁ - Components of genetic variance due to dominance effect, H₂ - Proportion of dominance variance due to the positive and negative effects of the genes in the parents, h₂ - Dominance effects, as algebraic sum over all the loci in heterozygous phase in all the crosses, F - Covariance of additive and non-additive effects in a single array. (H₁/D)^{1/2} - Mean degree of dominance, H₂/4H₁ - Proportion of genes with positive and negative effects on the parents, Kd/Kr - Proportion of dominant and recessive genes in the parents, h₂/H₂ - number of groups of genes with positive and negative effects on the parents, r_{Yr_i(W_r+V_r)} - correlation coefficient between the value of the parent and their respective sum W_r + V_r, indicate the direction of action of the dominant or recessive factors, H² - broad sense heritability coefficient and h² - narrow sense heritability coefficient.

A number of authors find major impact of the dominant parameters, expressed by greater dominant parameter than the additive one (Aydogan and Yagdi, 2004; Akram et al., 2007; Sadeghi et al., 2013). The mean degree of dominance presented by the parameter (H₁/D)^{0.5} exhibits that overdominance has a major role in the inheritance of the character. Other researchers also report the same results for this trait (Akram et al., 2007; Sadeghi et al., 2013). The values of the parameter F suggest that positive genes are not particularly balanced. In cases where the parameter F has a negative sign, it indicates that there are more recessive genes. The values of indicator (H₂/4H₁) (which differ by 0.25) confirm the uneven distribution of genes with positive and

negative effects on parents. The exception is only F₁-2014 where this indicator has values very close to 0.25. The ratio of the number of dominant to the number of recessive genes Kd/Kr shows that recessive genes dominate over the dominant genes in F₁-2014, F₁-2015, and F₂-2015, while in 2016 it is the opposite in the F₁ and F₂ generations. This is confirmed by other researchers such as Mandloi et al. (1974) and Akram et al. (2007). Throughout all years of study, the component H₁ is greater than H₂, indicating that positive and negative alleles in the loci exhibiting dominance in parents are not proportional. It should be borne in mind that H₁ and H₂ differ reliably with proven values. For the F₁-2015 case only, the H₂ parameter is greater than H₁. The indicator (h₂/H₂) refers to

the participation of 1 gene or group of genes exhibiting dominance in the control of the trait, except for F₁-2014 where the involvement of two genes or a group of genes is assumed. Other authors also report the involvement of a gene or a group of genes in inheritance of trait (Aydogan and Yagdi, 2004; Akram et al., 2007). The correlation coefficient ($r_{Yr:(Wr+Vr)}$) between the magnitude of the trait in parents and their sum (Wr+Vr) shows that the increase of the amount of wet gluten in the grain is connected to the accumulation of recessive genes in the genotype (Table 2). Authors Aydogan and Yagdi (2004) also reported that the increase in trait values has resulted from the accumulation of recessive genes. Only in F₁-2015 the correlation coefficient changed its sign, which points to the phenomenon of redefinition of the genetic formulas of the trait. This indicates that under different environmental conditions, the increase of the trait depends both on dominant and recessive genes. Akram et al. (2007) also report the accumulation of dominant genes would increase the values of the trait. The obtained heritability coefficients in broad sense H^2 are high in F₁-2014 and F₁-2016 and medium in F₁-2015, F₂-2015, and F₂-2016, which means that it is possible to conduct efficient genotype selection by phenotype. Others also report such heritability coefficients in broad sense (Aydogan and Yagdi, 2004; Khodadadi et al., 2012). Heritability coefficients in narrow sense h^2 are from low to medium. These coefficients denote that selection needs necessarily to start in later segregated generations. This conforms to the results obtained by a number of other authors (Vallega, 1985; Blanco et al., 2002; Aydogan and Yagdi, 2004; Khodadadi et al., 2012). Researchers Akram et al. (2007); Sadeghi et al. (2013) also reported that selection by wet gluten content in grain will be hindered in the early segregated generations and they recommend to start it in the later ones. The graphic diallel analysis gives the visual idea about the genetic nature of the trait in the

parents used. On Figures 1, 2, 3, 4 and 5, one can see a graphical analysis of individual environments by generation and year: F₁-2014, F₁-2015, F₁-2016, F₂-2015, F₂-2016. Figures 1, 2 and 5 (F₁-2014, F₁-2015, F₂-2016) show that the wet gluten content in durum wheat is determined by a simple additive-dominant genetic system since b differs reliably from 0 and does not differ from 1. The two cases shown on Figures 3 and 4 (F₁-2016 and F₂-2015) illustrate that complementary epistasis is involved in the inheritance of the character.

This becomes clear from the regression coefficient (b), which has values reliably different from 1 and inclines the regression line down to the abscissa (Vr). Akram et al. (2007); Sadeghi et al. (2013) also report that the trait is under the control of a simple additive-dominant genetic system with manifestations of epistasis. In F₁ regression line crosses Wr below the start of F₁-2014 (Figure 1) and around the start of F₁-2015 (Figure 2) and F₁-2016 (Figure 3). This exhibits that the inheritance in F₁ generation is dominated by complete dominance and only in F₁-2014 over dominance prevails. For F₂-2015 (Figure 4) and F₂-2016 (Figure 5) partial dominance and over dominance in the expression of the trait are respectively expressed in inheritance. Aydogan and Yagdi (2004) report about the manifestation of partial dominance. The figures present the location of the parental points through which it can be determined which varieties contain more dominant and which more recessive genes. The graphs show that parental points exchange their places in different years and generations, which is explained by the genotype-environment interaction. These parents, who are closer to the beginning of the coordinate system, contain more dominant ones, and vice versa, those who are closer to the interception point of the regression and the parabola contain more recessive ones.

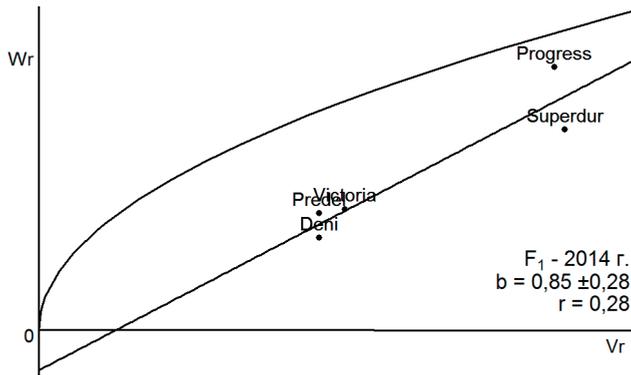


Figure 1. Graphical diallel analysis for wet gluten content in F₁-2014 year; Wr - Mean parent-offspring covariance of arrays; Vr - Mean variance of arrays; b – regression coefficient

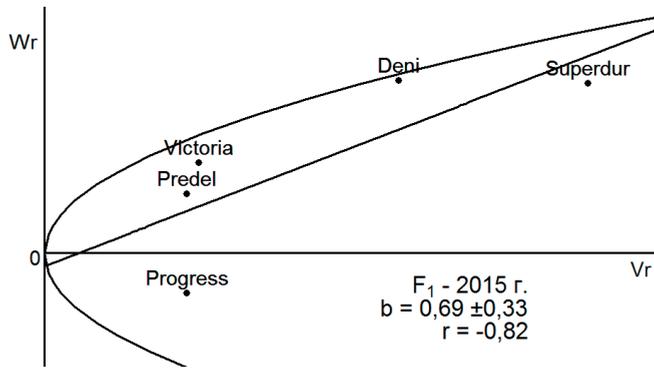


Figure 2. Graphical diallel analysis for wet gluten content in F₁-2015 year

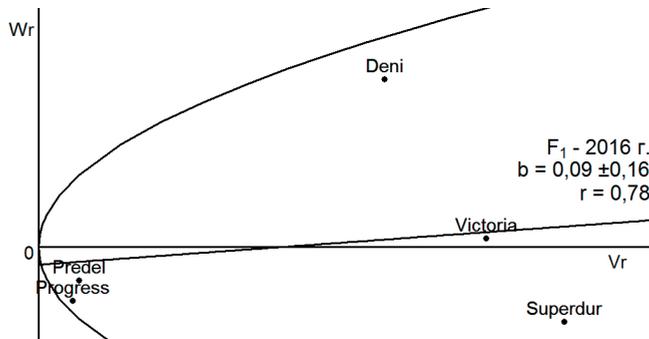


Figure 3. Graphical diallel analysis for wet gluten content in F₁-2016 year

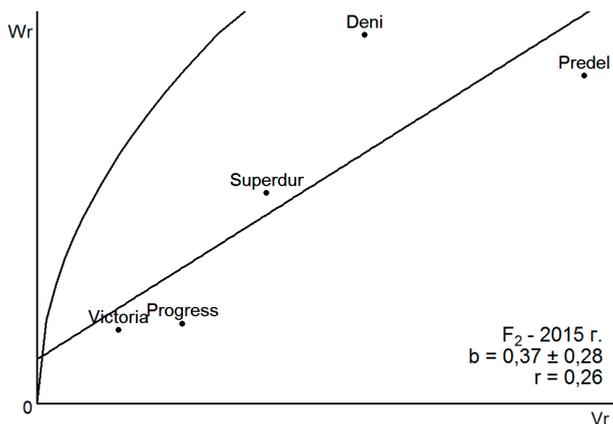


Figure 4. Graphical diallel analysis for wet gluten content in F₂-2015 year

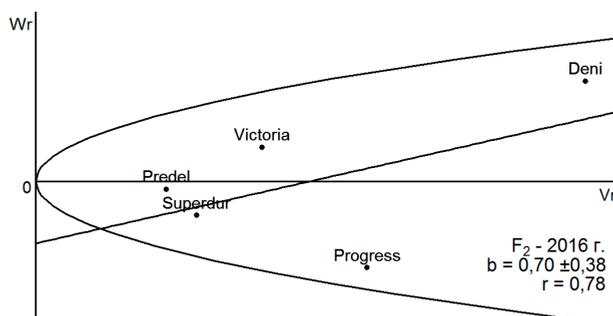


Figure 5. Graphical diallel analysis for wet gluten content in F₂-2016 year

In F₁-2014 (Figure 1), varieties Deni, Victoria and Predel had the greatest number of dominant genes, while the rest move away and occupy a more distant position from the beginning (or closer to the parabola and regression intersection point) and therefore contain more recessive genes. In the F₁-2015 (Figure 2) case, varieties Victoria, Predel and Progress have more dominant genes, while Superdur variety contains more recessive genes. In the third year F₁ (figure 3) the studied varieties are located close to the beginning of the coordinate system and contain more dominant genes. In the F₂ generations (Figures 4 and 5) varieties are located relatively close to the beginning of the coordinate system. The impression is that Superdur variety changes its place and in F₂ it contains more recessive genes. Victoria and Progress varieties retain their positions against the F₁ generation and therefore contain more dominant genes. Deni and Predel varieties are located in the farthest part, indicating that they contain more recessive genes for this trait.

CONCLUSIONS

The results obtained lead to the following conclusion. The trait wet gluten content in the grain is controlled by a simple additive-dominant genetic system.

In some cases, inheritance control is achieved by the involvement of non-allelic interactions, too, in the form of complementary epistasis. Partial to overdominance in the inheritance of the character wet gluten content in grain is observed. It has been found that increasing the values of the wet gluten content trait is associated with the accumulation of recessive genes in the genotype.

The heritability coefficients make it apparent that efficient genotype selection is possible by phenotype, but it should begin in later segregated generations.

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