

# Inheritance Of The Seed Storage Proteins In Wheat-Aegilops Hybrids And Their Relationship With Grain Quality

Hasanova Sudaba<sup>1</sup>, Asadov Elsevar<sup>1\*</sup>, Sultanova Natella<sup>2</sup>, Babayeva Fatima<sup>1</sup>

<sup>1</sup>Department of Basic Medical Sciences, Nakhchivan State University, Nakhichevan, Azerbaijan; <sup>2</sup>Department of Biology, Sumgayit State University, Sumgayit, Azerbaijan

## Research Article

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**\*For Correspondence:**

Asadov Elsevar, Department of Basic Medical Sciences, Nakhchivan State University, Nakhichevan, Azerbaijan

**E-mail:** asadoves@mail.ru

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## ABSTRACT

In the article, biochemical and technological qualities of wheat-Aegilops hybrids, the inheritance of the electrophoretic storage protein components was studied, and it was found that wheat-Aegilops hybrids with stable morphological features are homogeneous and heterogeneous in the electrophoretic spectrum. Amino groups passed from parental forms to the next generation. The study of the inheritance of components of hybrid storage proteins confirmed that wheat Aegilops is the source of the D genome to bread wheat varieties.

## INTRODUCTION

A direct relationship between the electrophoretic spectra of gliadin and the seed protein content, gluten content, and the bread volume was found. The blocks components of with a positive impact on these features were identified as well [1].

Today, to obtain high-quality productive crops, various methods of biochemistry, genetics, and molecular biology are used in the breeding process. Identification of protein molecules by using a number of modern methods, such as electrophoresis, gel filtration, immune electrophoresis, makes possible to obtain more accurate information about the diversity of macromolecules, including genotypes. Comparative analysis of wheat-Aegilops hybrids and EF-

spectra of parents confirms that the wheat Aegilops is the source of the D genome to bread wheat. Thus, each polypeptide can be a marker of its encoding gene. The quality of bread made from bread wheat and the quality of pasta made from durum wheat determined the quality of the gluten complex, consisting of gliadin and gluten-a storage protein of cereal crops. The study of seed storage protein polymorphism is of great importance for genetics and crop breeding [2].

### METHODOLOGY

The study was carried out on wheat-Aegilops hybrid with stable features of F13-F15 generation. Two types of Aegilops were used for hybridization: *Ae. ovata*, *Ae.ventricosa* and *T.dicoccum v. atratum*, *T.durum v. leucurum*, Teyakan-60. Bezostaya-1 and durum wheat varieties Vostochny were used as standard bread wheat varieties for comparison.

Total nitrogen in the grain was determined based on the Kjeldahl method, the amount of starch by using the Evers method, the amounts of lysine and tryptophan according to the method of Yarosh [2]. Osborne fractionation method for extraction of wheat bran proteins, enzyme and seed storage protein electrophoresis was carried out according to the method developed in the biochemical genetics laboratory of the Plant Breeding and Genetics Institute, Odessa, and the physical and technological features were analyzed by using standard methods [3,4].

### RESULTS AND DISCUSSION

The study was conducted in five hybrid combinations. The relationship between the biochemical and technological properties of hybrids, component composition, and inheritance of seed storage proteins, electrophoretic protein components, and seed quality was studied [5]. The protein content, essential amino acids, lysine and tryptophan, starch, and ash in hybrids, and their physical and technological parameters also were determined (Table 1).

**Table 1.** Biochemical parameters of wheat-Aegilops hybrids (F13–F15).

Lines	Protein%		Lysine (acc.to protein%-x)		Tryptophan (acc.to protein %-x)		Starch%		Ash element%	
	X ± Sx	CV%	X ± Sx	CV%	X ± Sx	CV%	X ± Sx	CV%	X ± Sx	CV%
1	15.63 ± 0.28	3.15	2.1 ± 0.016	1.37	1.4 ± 0.056	7.03	64.43 ± 0.34	0.93	1.97 ± 0.02	1.91
2	15.55 ± 0.63	7.09	1.99 ± 0.06	5.76	1.08 ± 0.058	9.3	64.1 ± 2.43	6.56	1.86 ± 0.041	3.88
3	15.77 ± 0.42	4.68	2.99 ± 0.023	1.76	1.35 ± 0.08	10.3	63.86 ± 0.34	0.94	1.84 ± 0.083	7.85
4	15.29 ± 0.56	6.42	2.13 ± 0.058	4.76	1.35 ± 0.10	13.1	65.36 ± 0.94	2.43	1.96 ± 0.10	8.94
5	16.38 ± 0.21	2.25	2.42 ± 0.03	2.18	1.33 ± 0.054	7.18	61.4 ± 1.38	3.9	1.96 ± 0.036	3.23
6	16.18 ± 0.41	4.47	2.09 ± 0.095	7.9	1.09 ± 0.04	6.42	64.33 ± 0.63	1.71	1.93 ± 0.035	3.15

7	15.6 ± 0.73	8.18	2.14 ± 0.01	10.0 1	1.47 ± 0.04	9.52	62.5 ± 1.05	2.93	1.96 ± 0.008	0.77
<i>T.durum v. leucurum</i> x <i>Ae ventricosa</i>										
8	16.31 ± 0.99	10.5	2.10 ± 0.01	9.63	1.16 ± 0.14	20.93	61.93	4.27	2.11 ± 0.056	4.58
9	15.7 ± 0.56	6.27	2.49 ± 0.057	4.01	1.53 ± 0.13	14.98	60.6	2.74	2.18 ± 0.061	4.85
10	15.36 ± 0.18	2.09	2.23 ± 0.16	12.4 2	1.59 ± 0.13	14.94	63.43	0.55	2.2 ± 0.057	4.54
11	19.3 ± 0.60	5.48	2.25 ± 0.08	6.84	1.51 ± 0.035	4.02	55.63	5.97	2.48 ± 0.012	0.83
12	15.68 ± 0.59	6.52	2.04 ± 0.09	8.04	1.18 ± 0.072	10.58	62.43	3.14	2.14 ± 0.031	2.56
Teyakan 60 x <i>Ae ovata</i>										
13	16.88 ± 0.84	8.63	2.34 ± 0.16	12.3 2	1.49 ± 0.066	7.73	59.83 ± 1.19	4.91	2.25 ± 0.12	9.41
14	18.98 ± 0.41	3.8	2.55 ± 0.089	6.09	1.19 ± 0.086	12.57	56.03 ± 0.8	2.5	2.14 ± 0.047	3.79
15	17.82 ± 1.02	9.94	2.68 ± 0.13	8.63	1.46 ± 0.24	29.49	58.76 ± 1.08	3.18	2.30 ± 0.048	3.64
Teyakan 60 x <i>Ae ventricosa</i>										
16	16.18 ± 0.16	1.71	3.03 ± 0.037	2.14	1.60 ± 0.16	17.52	59.93 ± 0.37	1.08	2.18 ± 0.18	9.37
<i>Ae ventricosa</i> x Teyakan										
17	16.71 ± 0.57	5.96	2.86 ± 0.043	2.64	1.46 ± 0.053	6.34	57.36 ± 0.37	1.13	2.11 ± 0.12	10.08
18	16.33 ± 0.72	7.63	2.32 ± 0.01	8.9	1.19 ± 0.037	5.51	58.33 ± 1.29	3.85	2.12 ± 0.028	2.56
19	15.01 ± 0.36	4.26	2.37 ± 0.087	6.37	1.29 ± 0.075	10.09	58.9 ± 2.51	7.38	2.20 ± 0.052	4.08
20	16.35 ± 1.17	12.4 4	2.81 ± 0.2	12.6 2	1.40 ± 0.08	10.55	59.73 ± 2.63	7.63	2.19 ± 0.012	0.57
21	16.20 ± 0.92	9.93	2.68 ± 0.11	7.54	1.45 ± 0.033	3.97	58.13 ± 1.69	5.05	2.25 ± 0.05	4.44
22	17.64 ± 0.52	5.15	2.14 ± 0.51	4.15	1.31 ± 0.11	15.38	55.16 ± 1.19	3.76	2.18 ± 0.13	10.32
23	16.47 ± 0.83	8.74	2.9 ± 0.12	7.4	1.39 ± 0.18	23.05	55.56 ± 1.03	3.24	2.18 ± 0.05	4.24

B-I	13.55 ± 0.52	6.69	2.77 ± 0.19	12.3 1	1.52 ± 0.078	8.01	63.56 ± 3.49	9.52	2.12 ± 0.17	14.06
East	15.8 ± 1.52	1.67	2.24 ± 0.13	10.7	1.60 ± 0.015	1.65	60.33 ± 1.55	4.46	2.11 ± 0.12	9.83

These features were studied to evaluate their economic value as a product of hybridization, as well as for determining the correlated relationship between the electrophoretic proteins components and these features.

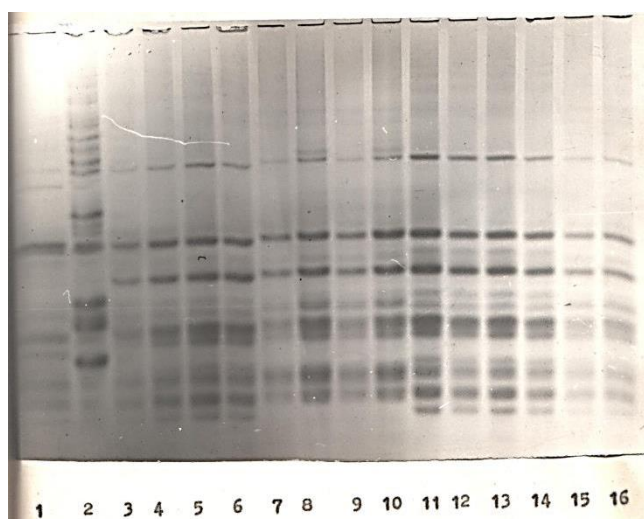
Studies showed that among the stable wheat-Egilops hybrids of *T. durum v. leucurum* x *Ae. Ovata* no 11, Teyakan-60 x *Ae.ventricosa* no 22 combinations are high-protein hybrid lines, and hybrid lines no 17, 20, and 23 of the hybrid combination of *Ae. ventricosa* x Teyakan 60, have a high protein content and a significant economic value, it shows that hybridization, carried out between the genes of *Triticum* and *Aegilops*, has both theoretical and practical value<sup>[6]</sup>.

### Component composition and inheritance of gliadin in wheat-Aegilops hybrids

A comparative analysis of parent forms and the electrophoretic spectra of grain storage proteins in wheat-Aegilops hybrids were conducted and their inheritance was studied.

Spectral line analysis of hybrid combination of *T.diccocum v. atratum* x *Ac.ovata* shows that there is intrinsic homogeneity and heterogeneity between these lines according to the EF spectra (Figure 1).

**Figure 1.** Gliadin electrophoretic spectra of separate grains of *T.diccocum v. atratum* x *Ae.ovata* hybrid combination lines. (\*Note: 1-*T.diccocum v. atratum*, 2-*Ae.ovata*, 3-6-samples from hybrid line no 1, 7-10-samples from hybrid line no 2, 11-14-samples from hybrid line no 3, 15-16-samples from hybrid line no 4).



Some of the components have been passed down from parents to next generation in group. However, it can be assumed that other parents are also involved in open pollination.

Comparative analysis of EF spectra of different lines and primary parent forms shows observation of certain similarities in *T.diccocum v. atratum* and different lines. This gives the opportunity to assume the existence of an

alliance between them. For example, the components of movement in *T.diccocum v. atratum* and lines–no 1 are identical [7].

Studies conducted on durum wheat varieties [2] have shown that the synthesis of components of this band is regulated by the gliadin locus located on chromosome 6A. As well as the similarity of α band (6A) of no 4 line and *T.diccocum v. atratum* was observed. Specific components in ω - and γ bands exist in the either line, and some components in both parental forms. However, this does not mean that these components passed exactly from these parents. Comparison of lines from these hybrid combinations showed the similarity of these components for a group of gliadin components. For example, no differences was found between no 1 and 3 lines on the EF spectrum [8].

According to the printed catalog of bread and durum wheat varieties for all chromosomes blocks, we can assume that the synthesis of components–α band is regulated by chromosome 6A, β band-by chromosome 6B, γ-by chromosome 6B, 1A, 1B, ω-1A and 1B. In this case, the results of a comparative analysis of the spectra of the EF line of a hybrid combination of *T.diccocum v. atratum* x *Ae.ovata* can be symbolically separated into groups and shown in the following table (Table 2).

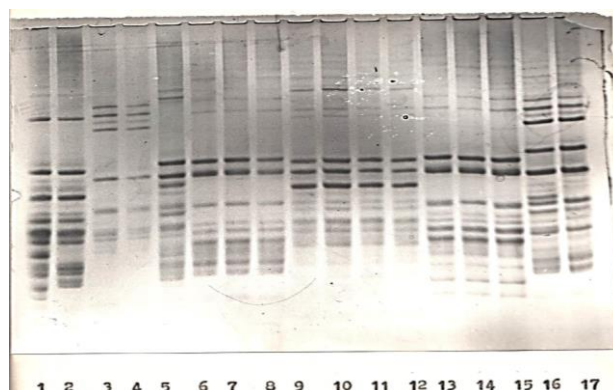
**Table 2.** Grouping of *T.diccocum v. atratum* x *Ae.ovata* hybrid combination lines on probable chromosomes.

Probable chromosomes	Lines						
	1	2	3	4	5	6	7
I (1A)	1	1	1	1	2	3	3
II (1B)	1	1+2	1	1	3	4	4
III (6A)	1	2	1	1	3	2	2
IV (6B)	1	2	1	2	3	1	2

In the EF spectra, included into a hybrid combination of *Ae.ventricosa* x Teyakan 60, is clearly visible the oil component in the band, which belongs to the gene D in *Ae.ventricosa*. This proves the normal expression of the genome D in these lines. However, the existence of ω band gliadin components in *Ae.ventricosa* hybrid species was not detected, so the existence of the gliadin component belonging to other genomes (A and B) in this spectrum was revealed.

In line no 19 (in the γ band) the presence of two oil components, belonging to Teyakan 60 is noticed. It is assumed that the synthesis of these components is cotrolled by chromosome 1B. In line no 21 existence of gliadin components, belonging to the band (in 1<sup>st</sup> and 3<sup>rd</sup> samples) was detected (Figure 2) [9].

**Figure 2.** Gliadin electrophoretic spectra of separate grain lines of hybrid combinations *Ae.ventricosa* x Teyakan 60. (\*Note: 1-2-Teyakan 60, 3-4-*Ae.ventricosa*, 5-8-samples from hybrid line no 18, 9-12-samples from hybrid line no 19, 13-15-samples from hybrid line no 20, 16-17-samples from hybrid line no 21).



Thus, a comparative analysis of the electrophoretic spectra of the parents and hybrids showed that a group of gliadin components were passed down from parents to the next generation and same blocks between the hybrid lines are observed (Table 3) [10].

**Table 3.** Grouping of *Ae.ventricosa* x Teyakan 60 hybrid combination lines on probable chromosomes.

Probable chromosomes	Lines					
	18	19	20	21	22	23
I (1A)	1	2	1	3	4	1
II (1B)	1	2	1	3	1	3
III (1D)	1	1	1+2	1	2	1
IV (6A)	1	2	3	1+4	1	1
V (6B)	1	2	1	3+4	3	2+3
VI (6D)	1	2	1	3	3	1

Analysis of the EF spectrum of all hybrid combinations shows that particular similarities and differences exist between parents and hybrids. It is assumed that number of components passed from aegilops to hybrids is very little. In lines where *Ae.ventricosa* participates as a parent, components belonging to the genome D are visible in the spectrum of gliadin EF [11].

**Connection of electrophoretic components of gliadin with the grain quality in wheat-Aegilops hybrids**

The relationship between the block of components in large hybrid combinations and parameters of grain quality was studied [12]. It is assumed that the gliadin synthesis of the lines included into the hybrid combination *T.diccocum v. atratum* x *Ae.ovata*, are controlled by chromosomes 1A, 1B, 6A and 6B.

In the synthesis of proteins with genomes A and B in *Ae.ventricosa* x *Teyakan* 60, also the participation of genome D belonging to *Ae.ventricosa* is assumed. Studies showed the relation between the grain quality and the spectrum of EF gliadin.

In a hybrid combination of *T.diccocum v.atratum* x *Ae.ovata*, blocks of GLd 1A1, GLd 6A1, GLd 6B1 have a positive impact on the 1000 seeds weight, blocks of GLd 6A2, GLd 6e1d to grain vitreousness, and blocks of GLd 6B3, GLd 1A2 have a positive impact on the protein content and bread volume.

A positive impact of GLd 1A3, GLd 1A4, GLd 1B1, GLd 6A1, GLd 6B3, GLd 6D3 to the on protein content of hybrid combination of *Ae.ventricosa* x Teyakan 60, GLd 1A4, GLd 6A3, GLd 1B1, GLd 6D3, GLd 1A4, GLd 6B3, GLd on gluten contents, 1B1, GLd 6D3, GLd 1A4, GLd 6B3, GLd 6D3 on 1000 seed weight, GLd 1A2, GLd 1B2, GLd 6A2, GLd 6B2 on vitreousness was detected. Also a positive impact of the blocks of GLd 1B3 on bread volume was found (Table 4) [13-15].

**Table 4.** Impact of grain gliadin blocks on qualitative indicators obtained in PAAG in wheat-Aegilops hybrids.

Compared components	1000 seeds weight			Vitreousness%			Protein%			Gluten%			Bread volume h/d	
<i>T.diccocum v. atratum</i> x <i>Ae. ovata</i>														
GLd 1A1 ± GLd 1A2	+12,2	18,4	14,9	+	+	+	-1,9	-0,4	-0,4	-2,5	-0,8	-1,0	-3,5	-145
GLd 1A1 ± GLd 1A3	+4,7	+8,3	+7,5	-8	0	-15	-0,6	0,2	-0,7	-2,8	-1,6	-1,5	5	-25
GLd 1A2 ± GLd 1A3	-7,5	-10,1	-7,4	-	-	-	+1,3	+0,6	-0,4	-0,3	-0,8	-0,5	40	120
GLd 1A1 ± GLd 6A2	+5,1	+7,9	+8,1	-7,7	-6,0	16,6	-0,2	+0,4	-0,7	-3,9	-0,9	-0,7	13,4	-20,3
GLd 6A1 ± GLd 6A3	+13,2	19,7	16,5	+	+	+	-1,8	-0,2	-0,5	-3,5	-0,7	-0,8	-30	-147
GLd 6A2 ± GLd 6A3	+8,1	11,8	+8,4	+	+	+	-1,6	-0,6	+0,2	+0,4	+0,2	-0,1	43,3	126,7
GLd 6B1 ± GLd 6A2	+1,9	+6,5	+4,1	+5,7	+1,1	-3,3	+0,06	+0,7	-0,1	+1,1	+3,2	+3,1	13	6
GLd 6B1 ± GLd 6B3	+11,6	-19	14,5	+	+	+	-1,4	-0,1	-0,2	-1,0	+1,3	+1,1	-37	-134
GLd 6B2 ± GLd 6B3	+9,7	12,5	10,4	+	+	+	-2,0	-0,1	-0,1	-2,1	-1,9	-2	-50	-140
<i>Ae. ventricoso</i> x <i>Teyakan 60</i>														
GLd 1A1 ± GLd 1A2	+5,1	+2,7	-4,8	-8	-41,7	-21,7	+0,1	+1,5	+2,5	15,6	19,2	18,2	-160	40

GLd 1A1 ± GLd 1A3	+2, 7	-1,7	-2,4	-5	-	41, 7	11, 7	+0,8	-0,9	+0, 6	+3, 5	+2, 8	+1, 7	-30	-10	
GLd 1A1 ± GLd 1A4	-1,6	-9,9	-10	-10	-	36, 7	-1,7	-1,4	-2,4	0	-8,9	-8,9	-4,8	-	110	-130
GLd 1A2 ± GLd 1A3	-2,4	-4,4	+2, 4	3	0	10	+0,7	-2,4	-1,9	-	12, 1	16, 4	16, 5	130	-50	
GLd 1A2 ± GLd 1A4	-6,7	-12,6	-5,2	-2	5	20	-1,5	-3,9	-2,5	-	24, 5	28, 1	-23	50	-170	
GLd 1A3 ± GLd 1A4	-4,3	-8,2	-7,6	-5	5	10	-2,2	-1,5	-0,6	-	12, 4	11, 7	-6,5	-80	-120	
GLd 1B1 ± GLd 1B2	+5, 3	+3,9	+4, 3	+4, 7	-	36, 7	23, 4	+0,6	+2, 0	+2, 5	19, 2	22, 7	20, 6	-	113	86
GLd 1B1 ± GLd 1B3	+0, 9	-2,9	-4,9	+0, 8	-	26, 7	10, 9	+1,0	+2, 0	+0, 4	+6, 3	+4, 9	+4, 4	46, 6	46,6	
GLd 1B2 ± GLd 1B3	+4, 4	+6,8	-0,6	+5, 5	10	12, 5	+0,4	-2,3	-2,1	-	12, 9	17, 5	16, 2	160	-40	
GLd 1D1 ± GLd 1D2	-2,8	-9,4	-7,5	-	10, 5	-5	+3, 7	-1,7	-2,4	-1,0	-	14, 4	14, 3	10, 1	62, 5	-152

### CONCLUSION

Based on the comparative analysis of spectra of gliadin EF in wheat-Aegilops hybrids, the following conclusions was made:

1. Wheat Aegilops hybrids with stable morphological features according to the EF spectrum are homogeneous and heterogeneous.
2. The happened open pollination caused the transfer of groups of some protein components by blocks from well-known parents to offspring. But the passing of other blocks from alien (unknown) samples can be assumed.
3. Comparative analysis of wheat-Aegilops hybrids and EF-spectra of parents confirmed that wheat Aegilops is the source of the D genome to bread wheat varieties.



4. The relationship between protein components and grain quality blocks has been studied.

The study of the positive effects of these components on the quality and number of economic parameters has a significant value for the exclusion of unproductive hybrids in the first stages of breeding.

## REFERENCES

1. Ermakov VI. Methods of biochemical research of plants. *Methods Biochem Anal.* 1972; 224.
2. Pleshkou BP. Workshop on biochemistry plant. 1976; 254.
3. Akhmetov MG. Polymorphism and genetic analysis of replacement varieties of wheat zoned in Azerbaijan- Abstract dis Ph.D in Biological Sciences. Tank. 1992; 21.
4. Konarev AV. The use of molecular markers in work with plant genetic resources. *Biol.* 1998; 55-62.
5. Sozinov AA. Polymorphism of proteins and its significance for genetics and breeding. 1985; 272.
6. Kudryavtsev AM, et al. Catalog of components blocks of gliadin chromosome 6A summer durum wheat. *Genetic.* 1987; 1465-1479.
7. Ribalka AI, et al. Mapping of the locus controlling the biosynthesis of spare wheat proteins. *Cytol Genet.* 1979;13: 276-282.
8. Popereya FA. Gliadin polymorphism and its relationship with grain quality, productivity and adaptive properties of winter wheat varieties. *Agropromizdat.* 1989; 138-149.
9. Kudryavtsev AM. Intravarietal heterogeneity of durum wheat is an important component of species biodiversity. *Genetics.* 2006;42: 1208-1211.
10. Sadigov HB. Genetic diversity of gliadin coding loci in local samples of tetraploid wheat ( $2n=28$ ). International Conference of plant genetic resources for enhanced resilience to climate change. Diversity, characterization, and utilization. 2011; 191-193.
11. Aksenov IV, et al. Using the storage proteins of sunflower seeds to determine the genetic purity of lines and hybrids, *Nauch. Tekh Byull Inst Maslichn Kul't.* 2007; 12: 3-11.
12. Reginald H, et al. *Grisham biochemistry.* Cengage learning University Virginia USA. 2016; 146:1219.
13. Sadigov HB. Gliadin and glutenin polymorphism in durum wheat landraces and breeding varieties of Azerbaijan . *Genetika, Serbiya.* 2015;47: 839-848.
14. Sadigova SB, et al. Genetic structure and geographical differentiation in barley landraces based on storage proteins. *IJACS.* 2012; 960-970.
15. Joshi J, et al. Comparison of gene families: seed storage and other seed proteins. *The Common Bean Genome.* 2017;201-219.