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DETECTION OF PERSPECTIVE WINTER WHEAT GENOTYPES BY ELECTROPHORETIC SPECTRA OF STORAGE PROTEINS

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The paper presents results of investigation of bread winter wheat by electrophoretic spectra of storage proteins aimed to identify genetic formula of a sample by loci of storage proteins, to determine the homogeneity / heterogeneity of a genotype according to marker loci, to identify the presence of 1BL/1RS and 1AL/1RS rye translocations based on analysis of the genotypes by *Glu-A1, Glu-B1, Glu-D1* loci and taking into account the presence of translocation 1BL/1RS to predict previously grain quality level of specific genotype.

Key words: *bread winter wheat, genotype, storage proteins, homogeneity, heterogeneity, translocation, grain quality*

Introduction. Hybridization and mutations are the source of genetic heterogeneity in plant evolution and breeding. Associations of genes are being formed both in the process of evolution and in the course of breeding. Most of the achievements of modern breeding are based on developing by hybridization and selection new associations of genes that contribute to a significant increase in productivity of agronomic part of agricultural plants. Suitable complexes or associations of genes improve adaptation of genotypes, in particular increase resistance to pests and diseases, low temperatures etc.

With the purpose of identifying genotypes and estimating varietal purity and researching regularities of formation of adapted complexes of genes during selection, identifying associations of allelic variants of clusters of storage protein genes with loci that control the expression level of quantitative traits nowadays methods of molecular genetic markers are being widely used.

Analysis of literature, formulation of the problem. It is known that populations with high level of variability of external morphological characters

have elevated levels of proteins variability two. This suggests that on molecular level the same regularities are revealed as at the level of traits of the organism. It is more difficult to establish breeding value of alleles that can be identified at the molecular level than morphological traits. However, based on the existing ideas about patterns of inheritance and variability it is impossible to imagine the emergence of new properties of genotype with no changes at the molecular level. Considering the high level of genome organization in genotypes resulted from targeted selection for useful traits (performance, product quality, etc.) most processes are accurately controlled. Therefore, the variability at the molecular level has more close association with the change of traits and properties of the organism, which is especially true for self-pollinating plants [1]. Loci of storage proteins remain comfortable molecular genetic markers in wheat genetics, breeding and seed production. This is due to their features: a plurality of loci, cluster organization of genes in loci, a high level of polymorphism, direct impact of storage proteins on dough properties [1, 2].

Electrophoretic analysis of storage proteins in selection samples allows to solve the following problems: 1 – to identify genetic formula of sample by loci of storage proteins; 2 – to determine the homogeneity / heterogeneity of the sample according to the marker loci; 3 – to detect random impurities; 4 – to identify the presence of 1BL/1RS and 1AL/1RS wheat-rye translocations; 5 – based on the analysis of genotypes for *Glu-A1, Glu-B1, Glu-D1* loci and taking into account the presence of 1BL/1RS translocations previously to predict level of grain quality of specific genotype.

The aim and tasks of the research – to identify by electrophoretic spectra of grain storage proteins new perspective lines selected in final breeding links as well as bread winter wheat varieties.

Materials and methods. Perspective winter wheat genotypes in final breeding links (2013-2015) were studied at the laboratory of ecological plant genetics and biotechnology of Institute of Plant Protection of NAAS.

To carry out electrophoresis of gliadins in 10% polyacrylamide gel a method developed and modified by the authors [3, 4] was used. Electrophoresis was completed when leaving 3.5 labels of dye. Gels were stained overnight with solutions containing 0.02% coomassie R-250, 5% ethanol, 6% acetic acid, 6% Trichloroacetic acid. After staining the gels were washed in water. Dried gels were scanned to obtain images.

Electrophoresis of high molecular subunits of glutenins with sodium dodecyl sulfate (SDS) added was conducted by a modified Laemmli's method [5].

Alleles of main loci of gliadins were identified by E. V. Metakovsky's [6] Catalogue with some additions. Alleles of HMW-subunits of glutenins were identified by Catalogue of P. Payne and G. Lawrence [7].

To identify some alleles comparison of spectra of a sample with spectra of lines or varieties with known alleles by loci of storage proteins was carried

out. *Gli-B1l* allele is a marker of 1BL/1RS wheat-rye translocation [1, 6], allele designated as *Gli-A1w* is a marker of 1AL/1RS wheat-rye translocation [4].

Potential mark of baking quality was noted by the scale according to P. Payne et al. [8] based on genotypes with *Glu-A1, Glu-B1, Glu-D1* loci and taking into account the presence of 1BL/1RS wheat-rye translocation. By method of electrophoresis of gliadins in the acidic medium and SDS-electrophoresis 5-11 individual caryopsis of each sample were analyzed. Genotype of each caryopsis was fixed by *Gli-A1, Gli-B1, Gli-D1* loci of gliadins and high molecular subunits *Glu-A1, Glu-B1, Glu-D1* of glutenins.

Results and discussion. When analyzing electrophoretic spectra to identify impurities, blocks of protein components encoded with *Gli-A2, Gli-A3* loci were taken into account. Genetic formulas of breeding entries analyzed are given in Table 1.

Genotypes Lutescens 36857, Erythrospermum 37038, Erythrospermum 37189, Lutescens 37203, Lutescens 36900, Lutescens 37106, Lutescens 37129, Erythrospermum 36844, Ferrugineum 36258, Lutescens 35354, Lutescens 36926, Erythrospermum 37028, Svitanok Myronivs`kyi, individual selection (IS) from Ekonomka variety and Ekonomka variety per se were proved to be heterogeneous by one (or more) locus of storage proteins. These samples had 2 biotypes for a certain marker locus.

1AL/1RS wheat-rye translocation that carries resistance genes *Gb2, Pm 17, Cm3,* $Sr1RS^{Amigo}$ has been identified in the sample Erythrospermum 37038 (Table 1).

1BL/1RS wheat-rye translocation that carries resistance genes *Pm8, Sr31, Lr26, Yr9* [9] has been identified in 20 samples: Lutescens 36857, Lutescens 37262, Lutescens 37030, Lutescens 37203, Lutescens 36900, Lutescens 37106, Lutescens 37116, Lutescens 37292, Erythrospermum 37135, Lutescens 35232, Lutescens 37090, Lutescens 36921, Lehenda Myronivs`ka, Svitanok Myronivs`kyi, Myronivs`ka zolotoverkha, Voloshkova, Yuviliar Myronivs`kyi, Kalynova, Kolos Myronivshchyny, IS 241/05 (11/06) (the last being received from the laboratory of wheat genetics of MIW); another three samples were proved to be heterogeneous for the presence of this translocation (Lutescens 36926, IS Ekonomka and Ekonomka).

By *Gli-A1* locus in samples there were detected 8 alleles with the dominance of b and x alleles. By *Gli-B1* locus 6 alleles were detected. *Gli-B1l* allele – marker of rye translocation – dominates, *Gli-B1b* allele was the second for occurrence frequency. 5 different alleles were identified by *Gli-D1d* locus with *Gli-D1b* allele prevailing among them.

Among 3 alleles by *Glu-A1* locus alleles a and b have a high frequency. By *Glu-B1* locus 3 alleles with prevalence of *Glu-B1c* allele were detected. The d allele predominates by locus *Glu-D1* that has a significant positive effect on baking quality. Among alleles identified Glu-A1a, Glu-A1b, Glu-B1b alleles have a significant positive impact on dough quality.

Table 1

New winter wheat perspective source material by loci of storage proteins and potential mark of quality

Line, variety	Gli-A1	Gli-B1	Gli-D1	Glu-A1	Glu-B1	Glu-D1	mark of quality
LUT 36662	x	l	b	c	c	d	5
LUT 36857	x	l	b	b+a	c	d	6
LUT 37262	x	l	b	a	c	d	6
ER 37038	w	b+d 1	b	b	d	a	6
LUT 37030	o	l	b	c	c	d	5
ER 37189	b+y	b	b	b	b	d	10
LUT 37203	x	l	b	a+c	c	d	6–5
LUT 37209	b	b	b	b	c	d	9
LUT 33689	b	g	b	c	d	d	6
LUT 36900	b+c	l	b	b	d	d	5
LUT 37106	x	l	b	b+c	c	d	6–5
LUT 37116	b	l	b	b	d	d	5
LUT 37129	b	g	b	c+b	d	d	6–8
LUT 37292	f	l	b	a	b	d	7
ER 36844	g	b	g	a+b	d	a	6
FER 36258	b+o	i	f	a+b	c	d	9
ER 36846	b	b	b	b	c	d	9
ER 37135	x	l	b	a	c	d	6
ER 37157	f	b	g	b	c	d	9
LUT 35354	b+c	g	b	b	d	d	8
LUT 35232	x	l	b	b	c	d	6
LUT 37090	x	l	b	a	c	d	6
LUT 36921	x	l	b	a	c	d	6
LUT 36926	o	l+b	g+b	a	b+c	d	10–5
ER 37028 (Horlytsia MYR)	b	d	x(10)+b	b	c	d	9
LUT 36756	b	g	b	b	d	d	8
Lehenda MYR	x	l	b	a	c	d	6
Svitanok MYR	b+f	l	b	b	c	d	6

Oberih MYR	o	b	b	b	c	a	7
MYR zolotoverkha	o	l	g	b	c	d	6
LUT 36832	y	b	f	a	c	d	9
Voloshkova	x	l	b	a	c	d	6
Yuviliar MYR	x	l	b	b	c	d	6
IS Ekonomka	b+x	l+b	b	b	c	d	6–9
Ekonomka	b	b+l	b	b	c	d	9–6
Kalynova	f	l	b	b	b	d	7
Kolos MIR	b	l	b	b	b	d	7
IS 241/05, 11/062	f	l	j	b	b	d	7
IS 77558/052	f	b	b	a	b	d	10
Zernohradka / LUT 33532	b	e	g	b	b	a	8

Note: *1 – b+d, etc. – sample being heterogeneous by a particular locus of storage proteins (there are two biotypes); 2 – the sample was received from the Laboratory of Wheat Genetics of MIW).*

Counting of potential mark of baking quality in the breeding sample analyzed based on genotypes by *Glu-A1, Glu-B1, Glu-D* loci considering negative impact of 1BL/1RS translocation on the dough quality showed that samples Erythrospermum 37189, Lutescens 37209, Ferrugineum 36258, Erythrospermum 36846, Erythrospermum 37157, Erythrospermum 37028 (Horlytsia Myronivs`ka) Lutescens 36832, ID 77558/05 (2/06), Ekonomka have the highest quality marks (9-10) (Fig. 1, 2).

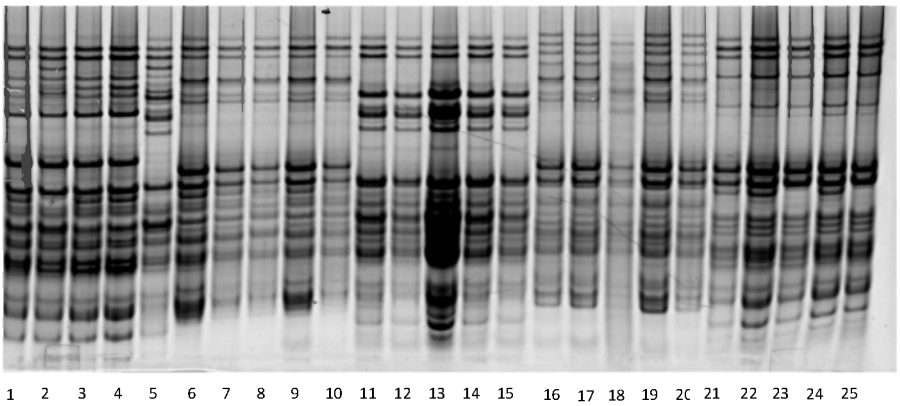

Fig. 1. Electrophoregrams of gliadins of some bread winter wheat genotypes: 1–5 – breeding sample FER 36258; 6–10 – ER 36846; 11–15 – ER 37135; 16–20 – ER 37157; 21–25 – LUT 35354

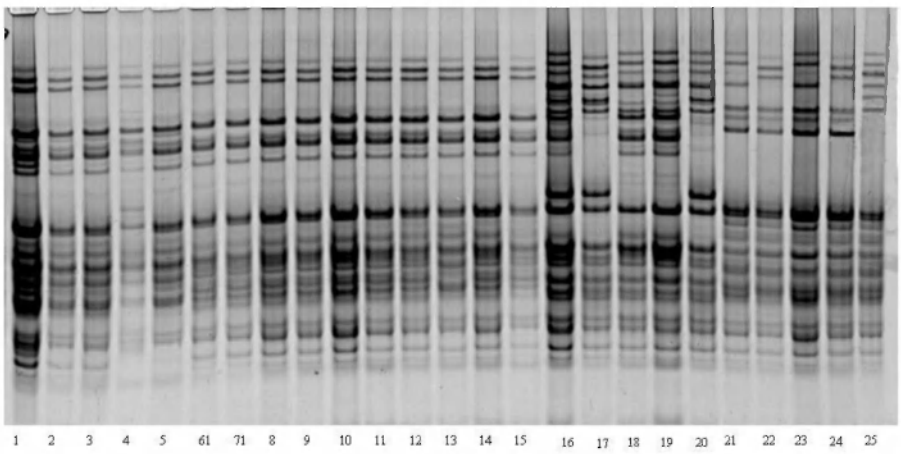

Fig. 2. Electrophoregrams of gliadins of some bread winter wheat genotypes: 1–5 – breeding sample LUT 35232; 6–10 – LUT 37090; 11–15 – LUT 36921; 16–20 – LUT 36926; 21–25 – ER 37028 (Horlytsia Myronivska)

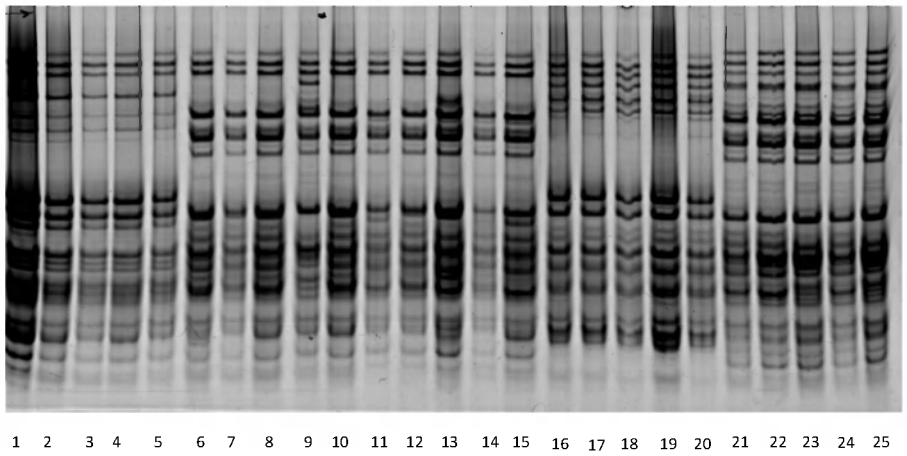

Fig. 3. Electrophoregrams of gliadins of some bread winter wheat genotypes: 1–5 – breeding sample LUT 36756; 6–10 – Lehenda Myronivs`ka; 11–15 – Svitanok Myronivskyi; 16–20 – Oberih Myronivskyi; 21–25 – MYR zolotoverkha

Comparison of data of analyzing perspective genotypes with literature data [4] regarding to the occurrence of alleles by loci of storage proteins in varieties of Myronivka breeding in different years shows that in new source breeding material analyzed some samples have alleles by *Gli-1* loci which did not previously occur in MIW varieties: № 16 (*Gli-B1i*), 15 (*Gli-A1g*), 13, 20, 26 (*Gli-B1g*) (Fig. 3). In line Erythrospermum 37028 (variety Horlytsia

Myronivs`ka) biotype that carries *Gli-D1x* (*GLD 1D10*) was detected.

Characteristics of breeding samples are given in Table 2.

Conclusions. 1. Genotypes of new source material of bread winter wheat by gliadin *Gli-A1, Gli-B1, Gli-D1* loci and high molecular subunits of glutenins *Glu-A1, Glu-B1, Glu-D1* have been identified.

2. In sample Erythrospermum 37038 1AL/1RS wheat-rye translocation has been identified, whereas in 20 samples 1BL/1RS wheat-rye translocation was identified, and three samples (Lutescens 36926, IS Ekonomka, Ekonomka) were heterogeneous for the last translocation.

3. The *Gli-A1b, Gli-A1x, Gli-B1l* alleles (marker of rye translocation), *Gli-B1b, Gli-D1b, Glu-A1 a, Glu-A1b, Glu-B1c, Glu -D1d* have been detected in material tested as prevailing ones.

Table 2

Characteristics of new source material of winter wheat by purity, heterogeneity, frequency of certain alleles, potential mark of baking quality

Characteristics	Number of lines pieces ppiecespieces pieces	% lines	Genotype
Carrying 1AL/1RS wheat-rye translocation (resistance genes *Gb2, Pm17, Cm3, Sr1RS^{Amigo}*	1	2,5	ER 37038
Carrying 1BL/1RS wheat-rye translocation (resistance genes *Pm8, Sr31, Lr26, Yr9*)	20	50	(LUT 36857, LUT 37262, LUT 37030, LUT 37203, LUT 36900, LUT T 37106, LUT 37116, LUT 37292, ER 37135, LUT 35232, LUT 37090, LUT 36921, Lehenda MYR, Svitanok MYR, MYR zolotoverkha, Voloshkova, Yuviliar MYR, Kalynova, Kolos MYR, IS 241/05(11/06)
Heterogeneous by 1BL/1RS presence	3	7,5	LUT 36926, IS Ekonomka, Ekonomka
Quality mark 9–10	8	20	ER 37189, LUT 37209, FER 36258, ER 36846, ER 37157, ER 37028 (Horlytsia MYR), LUT 36832, IS 77558/05(2/06), Ekonomka
Having alleles by the *Gli-1* loci which did not previously occur in MIW varieties	6	15	FER 36258 (*Gli-B1i*), ER 36844 (*Gli-A1g*), LUT 37129, LUT 35354, LUT 36756 (*Gli-B1g*). Biotype ER 37028 carries *Gli-D1x* (*GLD 1D10*)

4. Potential mark of baking quality in samples tested based on genotypes by *Glu-A1, Glu-B1, Glu-D1* loci considering the negative impact of 1BL/1RS wheat-rye translocation on dough quality was detected. Samples Erythrospermum 37189, Lutescens 37209, Ferrugineum 36258, Erythrospermum 36846, Erythrospermum 37157, Erythrospermum 37028, Lutescens 36832, IS 77558/05(2/06), Ekonomka have the highest quality marks (9-10).

5. The samples with alleles by Gli-1 loci which did not previously occur in varieties of Myronivka breeding: Ferrugineum 36258 (Gli-B1i), Erythrospermum 36844 (Gli-A1g), Lutescens 37129, Lutescens 35354, Lutescens 36756 (Gli-B1g) have been identified. In Erythrospermum 37028 line (Horlytsia Myronivs`ka variety) there was detected biotype carrying Gli-D1x (GLD 1D10).

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ДЕТЕКЦІЯ ПЕРСПЕКТИВНИХ ГЕНОТИПІВ ОЗИМОЇ ПШЕНИЦІ ЗА ЕЛЕКТРОФОРЕТИЧНИМИ СПЕКТРАМИ ЗАПАСНИХ БІЛКІВ

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Більшість із досягнень сучасної селекції пшениці базується на створенні шляхом гібридизації та добору нових асоціацій генів, що обумовлюють значне збільшення продуктивності господарсько цінної частини сільськогосподарських рослин.

Мета. Ідентифікувати за електрофоретичними спектрами запасних білків зерна відібраний новий вихідний матеріал і сорти пшениці м'якої озимої.

Результати. Аналізуючи електрофоретичні спектри на виявлення домішок, брали до уваги спектри білкових компонентів, кодованих локусами *Gli-2, Gli-A3*. Житня транслокація 1AL/1RS, що несе гени стійкості *Gb2, Pm17, Cm3, Sr1RS^{Amigo}*, була ідентифікована у зразка Еритроспермум 37038. Житня транслокація 1BL/1RS, що несе гени стійкості *Pm8, Sr31, Lr26, Yr9*, ідентифікована у ліній Лютесценс 36857, Лютесценс 37262, Лютесценс 37030, Лютесценс 37203, Лютесценс 36900, Лютесценс 37106, Лютесценс 37116, Лютесценс 37292, Еритроспермум 37135, Лютесценс 35232, Лютесценс 37090, Лютесценс 36921, Індивідуальний добір (І.д.) 241/05 (11/06) та сортів Легенда Миронівська, Світанок Миронівський, Волошкова, Ювіляр Миронівський, Калинова, Колос Миронівщини; ще три зразка виявилися гетерогенними за цією транслокацією (Лютесценс 36926, І.д. Економка, Економка).

За локусом *Gli-A1* серед зразків виявлено 8 алелів з домінуванням алелів b і x. За локусом *Gli-B1* виявлено 6 алелів. Домінує алель *Gli-B1l* – маркер житньої транслокації, на другому місці за частотою – алель *Gli-B1b*. За локусом *Gli-D1* ідентифіковано 5 різних алелів, серед яких переважає алель *Gli-D1b*. За локусом *Glu-A1* серед 3 алелів високі частоти мають алелі a і b. За локусом *Glu-B1* виявлено 3 алелі з переважанням алеля *Glu-B1c*. За локусом *Glu-D1* переважає алель d, що має позитивний вплив на хлібопекарську якість. Серед ідентифікованих алелів значний позитивний вплив на якість тіста мають також алелі *Glu-A1a, Glu-A1b, Glu-B1b*.

Найвищі бали якості зерна (9–10) за локусами *Glu-A1, Glu-B1, Glu-D* мають генотипи Еритроспермум 37189, Лютесценс 37209, Ферругінеум 36258, Еритроспермум 36846, Еритроспермум 37157, Еритроспермум 37028, Лютесценс 36832, І.д. 77558/05 (2/06).

Висновки. Ідентифіковано генотипи нового вихідного матеріалу пшениці м'якої озимої за локусами гліадинів *Gli-A1, Gli-B1, Gli-D1* і високомолекулярних субодиниць глютенинів *Glu-A1, Glu-B1, Glu-D1*. У лінії Еритроспермум 37038 ідентифіковано житню транслокацію 1AL/1RS, у 20 зразків – транслокацію 1BL/1RS, а три зразки (Лютесценс 36926, І.д. Економка, Економка) є гетерогенними за цією транслокацією. Виявлено, що домінуючими алелями є *Gli-A1b, Gli-A1x, Gli-B1l* (маркер житньої транслокації), *Gli-B1b, Gli-D1b, Glu-A1a, Glu-A1b, Glu-B1c, Glu-D1d.* За локусами *Glu-A1, Glu-B1, Glu-D1* високі бали якості зерна (9–10) мають генотипи Еритроспермум 37189, Лютесценс 37209, Ферругінеум 36258, Еритроспермум 36846, Еритроспермум 37157, Еритроспермум 37028 (Горлиця Миронівська), Лютесценс 36832, І .д. 77558/05, Економка.

Ідентифіковано зразки з алелями за *Gli-1* локусом, які раніше не зустрічалися в сортах миронівської селекції: Ферругінеум 36258 (*Gli-B1i*), Еритроспермум 36844 (*Gli-A1g*), Лютесценс 37129, Лютесценс 35354, Лютесценс 36756 (*Gli-B1g*). У зразка Еритроспермум 37028 виявлено біотип, що несе *Gli-D1x* (*GLD 1D10*).

Ключові слова: *пшениця м'яка озима, генотип, запасні білки, гомогенність, гетерогенність, транслокації, якість зерна*

ДЕТЕКЦИЯ ПЕРСПЕКТИВНЫХ ГЕНОТИПОВ ОЗИМОЙ ПШЕНИЦЫ ПО ЭЛЕКТРОФОРЕТИЧЕСКИМ СПЕКТРАМ ЗАПАСНЫХ БЕЛКОВ

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Большинство из достижений современной селекции пшеницы базируется на создании путем гибридизации и отбора новых ассоциаций

генов, обуславливающих значительное увеличение продуктивности хозяйственно-ценной части сельскохозяйственных растений.

Цель. Идентифицировать по электрофоретическим спектрам запасных белков зерна отобранный новый исходный материал и сорта пшеницы мягкой озимой.

Результаты. При анализе электрофоретических спектров на выявление примесей принимали во внимание спектры белковых компонентов, кодированных локусами *Gli-2, Gli-A3*.

Ржаная 1AL/1RS транслокация, несущая гены устойчивости *Gb2, Pm17, Cm3, Sr1RS^{Amigo}*, идентифицирована у образца Эритроспермум 37038. Ржаная 1BL/1RS транслокация, несущая гены устойчивости *Pm8, Sr31, Lr26, Yr9*, идентифицирована у линий Лютесценс 36857, Лютесценс 37262, Лютесценс 37030, Лютесценс 37203, Лютесценс 36900, Лютесценс 37106, Лютесценс 37116, Лютесценс 37292, Эритроспермум 37135, Лютесценс 35232, Лютесценс 37090, Лютесценс 36921, Легенда Миронівська, Світанок Миронівський, Волошкова, Ювіляр Миронівський, Калинова, Колос Миронівщини, Индивидуальный отбор (И.о.) 241/05 (11/06); еще три образца оказались гетерогенными по этой транслокации (Лютесценс 36926, И.о. Економка, Економка).

По локусу *Gli-A1* среди образцов обнаружены 8 аллелей с доминированием аллелей b и x. По локусу *Gli-B1* выявлено 6 аллелей. Доминирует аллель *Gli-B1l* – маркер ржаной транслокации, на втором месте по частоте – аллель *Gli-B1b*. По локусу *Gli-D1* идентифицированы 5 различных аллелей, среди которых преобладает аллель *Gli-D1b*. По локусу *Glu-A1* среди 3 аллелей высокие частоты имеют аллели a и b. По локусу *Glu-B1* выявлено 3 аллеля с преобладанием аллеля *Glu-B1c*. По локусу *Glu-D1* преобладает аллель d, имеющий положительное влияние на хлебопекарное качество. Среди идентифицированных аллелей значительное положительное влияние на качество теста имеют также аллели *Glu-A1a, Glu-A1b, Glu-B1b*.

Самые высокие баллы качества зерна (9–10) по локусам *Glu-A1, Glu-B1, Glu-D* имеют генотипы Эритроспермум 37189, Лютесценс 37209, Ферругинеум 36258, Эритроспермум 36846, Эритроспермум 37157, Эритроспермум 37028, Лютесценс 36832, И.о. 77558/05 (2/06).

Выводы. Идентифицированы генотипы нового исходного материала пшеницы мягкой озимой по локусам глиадинов *Gli-A1, Gli-B1, Gli-D1* и высокомолекулярных субъединиц глютенинов *Glu-A1, Glu-B1, Glu-D1*. У линии Эритроспермум 37038 идентифицирована ржаная транслокация 1AL/1RS, у 15 образцов – транслокация 1BL/1RS, а три образца (Лютесценс 36926, И.о. Економка, Економка) гетерогенны по этим транслокациям. Выявлено, что доминирующими аллелями являются *Gli-A1b, Gli-A1x, Gli-B1l* (маркер ржаной транслокации), *Gli-B1b, Gli-D1b, Glu-A1a, Glu-A1b, Glu-B1c, Glu-D1d*. По локусам *Glu-A1, Glu-B1, Glu-D1*

высокие баллы качества зерна (9–10) имеют генотипы Эритроспермум 37189, Лютесценс 37209, Ферругинеум 36258, Эритроспермум 36846, Эритроспермум 37157, Эритроспермум 37028 (Горлиця Миронівська), Лютесценс 36832, И.о. 77558/05, Економка.

Идентифицированы образцы с аллелями по *Gli-1* локусу, которые ранее не встречались в сортах мироновской селекции: Ферругинеум 36258 (*Gli-B1i*), Эритроспермум 36844 (*Gli-A1g*), Лютесценс 37129, Лютесценс 35354, Лютесценс 36756 (*Gli-B1g*). У образца Эритроспермум 37028 обнаружен биотип, несущий *Gli-D1x* (*GLD 1D10*).

Ключевые слова: *пшеница мягкая озимая, генотип, запасные белки, гомогенность, гетерогенность, транслокации, качество зерна*

DETECTION OF PERSPECTIVE WINTER WHEAT GENOTYPES BY ELECTROPHORETIC SPECTRA OF STORAGE PROTEINS

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Most of the achievements of modern wheat breeding is based on the creation by hybridization and selection of new associations of genes, causing a significant increase in the productivity of the economically valuable crops.

Aim. To identify by electrophoretic spectra of grain storage proteins selected new source material and bread winter wheat varieties.

Results. In the analysis of electrophoretic spectra to identify contaminants the spectrum of protein components encoded loci Gli-2, Gli-A3 were taken into account.

Rye 1AL/1RS translocation carrying resistance genes *Gb2, Pm17, Cm3, Sr1RS^{Amigo}* were identified in the sample Erythrospermum 37038. Rye 1BL/1RS translocation carrying resistance genes *Pm8, Sr31, Lr26, Yr9* were identified in lines Lutescens 36857, Lutescens 37262, Lutescens 37030, Lutescens 37203, Lutescens 36900, Lutescens 37106, Lutescens 37116, Lutescens 37292, Erythrospermum 37135, Lutescens 35232, Lutescens 37090, Lutescens 36921, Lehenda Myronivs'ka, Svitanok Myronivs'kyi, Voloshkova, Yuviliar Myronivs'kyi, Kalynova, Kolos Myronivshchyny, IS 241/05 (11/06), three

another samples appeared to be heterogeneous by this translocation (Lutescens 36926, IS Ekonomka, Ekonomka).

Concerning *Gli-A1* locus among the samples were found 8 alleles with the dominance of b and x alleles. By *Gli-B1* locus 6 alleles were found. *Gli-B1l* allele – rye translocation marker – dominates, *Gli-B1b* allele followes by frequency. By *Gli-D1d* locus 5 different alleles were identified with *Gli-D1b* allele dominating. By *Glu-A1* locus among the three alleles a and b ones have the highest frequency. By *Glu-B1* 3 locus 3 alleles were revealed with predominance of *Glu-B1c* allele. By loci *Glu-D1* d allele is predominant that cause a positive impact on baking quality. Among the alleles identified *Glu-A1a, Glu-A1b, Glu-B1b* alleles have significant positive impact on dough quality too.

Genotypes Erythrospermum 37189, Lutescens37209, Ferrugineum 36258, Erythrospermum 36846, Erythrospermum 37157, Erythrospermum 37028, Lutescens 36832, IS 77558/05 (2/06) have the highest scores of grain quality (9-10) at *Glu-A1, Glu-B1, Glu-D* loci.

Conclusions. Genotypes of the new source material of bread winter wheat have been identified by gliadin *Gli-A1, Gli-B1, Gli-D1* loci and high glutenin subunits of *Glu-A1, Glu-B1, Glu-D1.* 1AL/1RS wheat-rye translocation hai been identified in line Erythrospermum 37038, 1BL/1RS wheat-rye translocation has been identified in 15 samples, and three samples (Lutescens 36926, IS Ekonomka, Ekonomka) were heterogeneous by this translocation. It was revealed that Gli-A1b, Gli-A1x, Gli-B1l (a marker of rye translocation), *Gli-B1b, Gli-D1b, Glu-A1a, Glu-A1b, Glu-B1c, Glu-D1d* are dominant alleles. By *Glu-A1, Glu-B1, Glu-D1* loci genotypes Erythrospermum 37189, Lutescens 37209, Ferrugineum 36258, Erythrospermum 36846, Erythrospermum 37157, Erythrospermum 37028 (Horlytsia Myronivs'ka) Lutescens 36832, IS 77558/05, Ekonomka have high points of grain quality (9-10).

The samples with alleles by *Gli-1* loci which did not previously occur in varieties of Myronivka breeding: Ferrugineum 36258 (*Gli-B1i*), Erythrospermum 36844 (*Gli-A1g*), Lutescens 37129, Lutescens 35354, Lutescens 36756 (*Gli-B1g*) have been identified. In Erythrospermum 37028 line (*Horlytsia Myronivs`ka variety*) there was detected biotype carrying *Gli-D1x* (*GLD 1D10*).

Key words: *bread winter wheat, genotype, storage proteins, homogeneity, heterogeneity, translocation, grain quality*