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Genetic variation of *GLI-B1* locus in Ukrainian bread wheat varieties and lines

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Aim. To investigate polymorphism of *Gli-B1* locus in modern Ukrainian bread wheat cultivars, to analyze the distribution of alleles and to compare the received data with the "core-collection of wheat cultivars" presented by Dr. E. Metakovsky. **Methods.** Eighty one bread wheat cultivars and lines from different plant breeding institutions and stations of Ukraine were tested using allele-specific primers to *Gli-B1* locus developed by Zhang *et al.* [2003]. PCR products were fractionated in polyacrylamide gel (PAG) and then were stained by silver nitrate. Allelic variants of gliadins were analyzed by electrophoresis in acid polyacrylamide gel (APAGE). **Results.** Nine allelic variants of gliadins were revealed by APAGE and six alleles of *Gli-B1* locus were detected by PCR-analysis. In 52 % of modern Ukrainian bread wheat cultivars we revealed Gli-B1b allelic variant, according to PCR - *Gli-B1.1* allele with a 369 bp amplification fragment. In the genotypes of Ukrainian wheat cultivars, the 1RS.1BL translocation, which carries resistance genes, is frequent, as was detected by the absence of any amplification fragments with *Gli-B1* primers. The correspondence between allelic variants of gliadins and alleles of *Gli-B1* locus is discussed. **Conclusions.** DNA polymorphism of *Gli-B1* locus examined in our research coincides with the diversity of allelic variants of gliadins, which were detected by APAGE method for Ukrainian bread wheat cultivar. However, PCR-analysis with applied primers carried out in this study does not distinguish the alleles that correspond to the Gli-B1c, Gli-B1g and Gli-B1e allelic variants of gliadins. The most common allele (52 %) for the investigated Ukrainian wheat varieties is *Gli-B1.1* allele, which was characterized by the amplification fragment of 369 bp, and the presence of 1RS.1BL translocation, which corresponds to Gli-B1b and Gli-B1l allelic variants of gliadins obtained by APAGE, respectively.

Keywords: *Triticum aestivum L.*, *Gli-B1*, gliadins, polymorphism, PCR analysis.

Introduction

Gliadins are large families of wheat storage proteins with similar amino acid sequences. Monomeric gliadin peptides are held together with glutenin polymers via intramolecular disulfide bonds and form gluten complex during mixing wheat grain flour and water [1]. It is considered that gliadins contribute to dough properties such as viscosity and extensibility, whereas glutenins affect strength and elasticity [2, 3]. Moreover, gliadins contain CD epitopes, that can cause coeliac disease in 1–3 % of population. Thus, studying the gliadins gene sequences will advance the development of low gluten wheat by using RNA interference or Crispr/Cas 9 technologies in order to create safe food for people with this disease [4–8].

Gliadins are classified as α-, γ-, δ- and ω-gliadins, based on their electrophoretic mobility and primary amino acid sequence [9, 10]. The gliadin gene families are localized at six major loci on chromosomes of homoeologous group 1 and 6. *Gli-A1, Gli-B1, Gli-D1* loci are coding γ-, δ- and ω-gliadins, whereas *Gli-A2, Gli-B2, Gli-D2* loci are coding α-gliadins [10, 11]. *Gli-1* loci have higher impact on flour quality than *Gli-2*, but major impact is provided by glutenins. Nonetheless, *Gli-1* loci are linked to LMW glutenin genes (*Glu-3*) and some important resistance genes, called *R* genes [11, 13, 15].

Each *Gli* locus encodes a group of gliadin polypeptides (allelic variant) inherited together as a simple Mendelian trait. There is a range of 40 to 150 copies of α-genes in *Gli-2* loci, 15–40 and 15–18 copies of γ- and ω-gliadin genes at *Gli-1* loci respectively [14–16], depending on the wheat cultivar. A large number of pseudogenes have also been reported for each gene family, and some of them had very low expression level.

Multiple allelism of gliadins has been revealed by the acid polyacrylamide gel electrophoresis method [17, 18]. Allelic variants differing from each other in a number of bands and their electrophoretic mobility are encoded by one *Gli* locus. 182 allelic variants for six main gliadin loci in more than 1000 common wheat cultivars have been described by Metakovsky *et al.* [18]. The most frequent allelic variants are Gli-B1b (28.2 %) and Gli-D1b (39.4 %) [18].

Contribution of *Gli-B1* locus to breadmaking quality is higher than that of *Gli-A1* and *Gli-D1* loci [19]. Better quality is observed in cultivars with GLD 1B1 and GLD 1B2 (Gli-B1b and Gli-B1d) allelic variants of gliadins. To date, 26 allelic variants of gliadins of *Gli-B1* locus were described and cataloged [18].

Only one consensus sequence (MG560141.1) of *Gli-B1* locus with length 6 535 908 bp was generated. Based on PacBio platform sequencing data, six γ-, one ω- and one δ-gliadin active genes and eight pseudogenes were reported for *Gli-B1* locus of Chinese Spring cultivar, which have Gli-B1a allelic variant [18, 20]. To date, there are no full nucleotide sequences of *Gli-B1* locus of other wheat cultivars with different allelic variants of *Gli-B1* locus. Based on AF234646 and M13712 sequences, allele-specific SNP markers (*Gli-B1.1* and *Gli-B1.2*) for γ-gliadin pseudogene of *Gli-B1* locus were developed by Zhang *et al.* [21]. Amplification

fragments lengths variation obtained with marker *Gli-B1.2* in wheat varieties was observed due to the presence of microsatellite in the sequence, as reported by Devos *et al.* [22]. Polischuk *et al.* [23] applied PCR with the allele-specific primers for the analysis of six near-isogenic lines and 12 Ukrainian bread wheat cultivars and showed the correspondence between allelic variants of gliadins and *Gli-B1* alleles. Also, the correspondence between PCR fragments length polymorphism (detected using primers developed by Zhang [21]) and allelic variants of gliadins at *Gli-B1* locus had been reported for 46 common wheat cultivars in our previous studies [24]. In this research we aimed to explore polymorphism of *Gli-B1* locus in modern Ukrainian bread wheat cultivars (most of which have been registered in The State Register of Plant Varieties Suitable for Dissemination in Ukraine after 2000 year), to analyze the distribution of alleles and to compare received data with "core-collection of wheat cultivars" presented by Dr. E. Metakovsky.

Materials and Methods

A set of 62 modern Ukrainian bread winter wheat cultivars and lines was received from different plant breeding institutes and stations as follows: The V. M. Remeslo Myronivka Institute of Wheat (MIW; 19 cultivars), Bila Tserkva Breeding Research Station (11 cultivars), The Institute of Irrigated Agriculture of the NAAS (10 cultivars), Poltava State Agrarian Academy (10 cultivars), Nosivska Selection and Research Station (3 cultivars and 5 lines), Donetsk Institute of Agricultural Production (2 cultivars), Driada Research and Production Company (1 cultivar), Luhansk Institute of Breeding and Technologies (1 cultivar). Six near-isogenic lines (Gli-A1–1, Gli-B1–3, Gli-B1–4, Gli-B1–12, Gli-D1–4, Gli-D1–5) created by Dr. M. M. Kopus [25] and 13 reference wheat cultivars — Mironovskaya 808, Mironovskaya 61, Donskaya Polukarlikovaya, Albatros, Strumok, Suneca, Federation, Bezostaya 1, Escualo, Ardec, Caia, Prinqual, Krasnodonka (the reference cultivars from "core collection of common wheat", which have been collected by Dr. E. Metakovsky with the aim to represent the widest polymorphism of allelic variants of *Gli-B1* locus), were used for comparison and verification of amplification fragments length.

For research we used five grains per variety. Each grain was divided into two parts. One half of the grain was used for analysis of allelic variants of gliadins by using electrophoresis according to F. O. Poperelya's method in acid polyacrylamide gel (APAGE) [26]. Gliadin allelic variants were identified using the catalogue of E. Metakovsky [18].

DNA was extracted from another half of grain by CTAB method [27]. PCR was performed with primers Gli-B1.1 (F: tgatctggccacaaaggga, R: cattggccaccaattcctgt) and Gli-B1.2 (F: tgatctggccacaaagggg, R: cattggccaccaattcctgt) developed by Zhang *et al.* [21]. A total volume of PCR reaction mixture was 10 µl (1µl genomic DNA, 1µl DreamTaq buffer (10x), 0.5 µl dNTP (10 µM), 5 pmol each primer (1ng/µl), 0.25 U DreamTaq DNA polymerase). Initial denaturation temperature was 95 °C. The denaturation, annealing, and polymerization temperatures for 38 cycles were 95 °C, 56 °C, and 72 °C respectively and final elongation 10 min, 72 °C. The electrophoresis of amplification products in the 7 % polyacry-

lamide gel stained with silver nitrate was used to visualize amplification fragments [28]. The length of amplification fragments was calculated using GelAnalyser software.

Allele frequency was calculated considering heterogeneous cultivars [29]. Nei's genetic variation index [30] was calculated according to the formula

$$H = 1 - \sum p_i^2$$

where p_i is the frequency of the certain allele at the locus.

Results and Discussion

Nine allelic variants of gliadins were revealed among 62 Ukrainian bread wheat cultivars and 6 wheat lines created by M. M. Kopus tested by acid polyacrylamide electrophoresis. The most frequent allelic variant was Gli-B1b (p=0.52) found in 35 cultivars (Table 1). Gli-B1l allelic variant (p=0.32) was found in 21 cultivars. Genotypes with this allelic variant have 1RS.1BL wheat-rye translocation, which carries resistance genes *Pm8, Sr31, Lr26, Yr9*, and reduces bread-making quality. Other allelic variants Gli-B1e (p=0.045), Gli-B1d (p=0.03), Gli-B1f (p=0.03), Gli-B1c (p=0.015), Gli-B1h (p=0.015), Gli-B1o (p=0.015), Gli-B1g (p=0.015) were rare and found in two or one cultivars. Nei`s genetic variation index was H=0.61.

Based on PCR analysis all cultivars were divided into six groups. The first and the second groups included wheat cultivars with *Gli-B1.1* allele, the third group combined cultivars that did not have any amplification fragments, and other three groups were characterized by *Gli-B1.2* allele.

The first group was the largest and included cultivars Vyshyvanka, MIP Assol, Oberih Myronivsky, Mariia, Sonata and other with the amplification fragment of 369 bp in *Gli-B1.1* locus. The same size amplification products were identified in cv. Bezostaya 1, Mironovskaya 808 and Albatros (Fig. 1). This group included 36 wheat cultivars and lines with Gli-B1b allelic variant of gliadins (Table 1).

Only one wheat line Gli-B1–12 belonged to the second group. In PCR with allele-specific primers line Gli-B1–12 produced a 400 bp amplification fragment of *Gli-B1.1* allele as in variety Federation (Fig. 1). Both cultivar and line were characterized by Gli-B1o allelic variant.

The third group included 21 wheat cultivars that did not produce in PCR any amplification fragments (null allele) due to the 1RS.1BL wheat-rye translocation (cultivar Ledia, Fig. 1, Fig. 2). All cultivars in the group had Gli-B1l allelic variant as expected (Table 1).

Seven wheat cultivars and lines that produced a 397 bp amplification fragment of *Gli-B1.2* allele as in reference varieties Escualo and Prinqual, were assigned to the fourth group

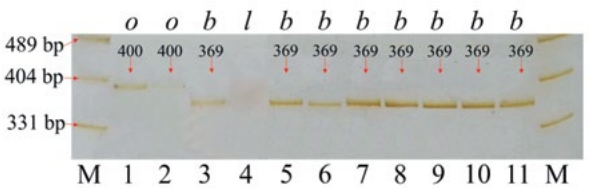

Fig. 1. Electrophoregram of amplification fragments produced by PCR with allele-specific primers to *Gli-B1.1* allele and DNA of wheat cultivars: 1 — Gli-B1–12; 2 — Federation; 3 — Vyshyvanka; 4 — Ledia; 5 — Bezostaya 1; 6 — Mironovskaya 808; 7 — Anatoliia; 8 — MIP Assol; 9 — Oberih Myronivsky; 10 — Mariia; 11 — Sonata; *M* — molecular weight marker pUC 19/Msp I.

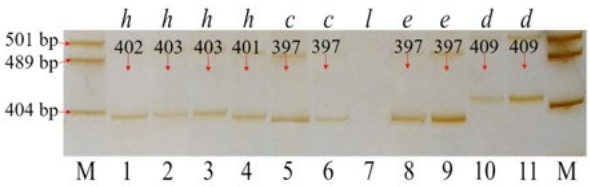

Fig. 2. Electrophoregram of amplification fragments produced by PCR with allele-specific primers to *Gli-B1.2* allele and DNA of wheat cultivars: 1 — Ardec; 2 — Caia; 3 — Madiarka; 4 — Krasnodonka; 5 — Prinqual; 6 — L 59/95; 7 — Ledia; 8 — Escualo; 9 — Liutenka; 10 — Suneca; 11 — KS 22–04; *M* — molecular weight marker pUC 19/Msp I.

(Fig. 2). Four different allelic variants were revealed among cultivars in this group. Gli-B1e allelic variant was determined in Hovtva, Schedra Nyva, Liutenka cultivars, Gli-B1f allelic variant was found in Myronivska Slava, Zymoiarka varieties, Gli-B1g and Gli-B1c allelic variants were determined in Gli-B1–4 and L 59/95 wheat lines, respectively (Table 1).

Only one cultivar belonged to the fifth group which was distinguished by *Gli-B1.2* allele with the amplification fragment of 403 bp. The reference cultivars - Ardec (402 bp), Caia (403 bp) and Krasnodonka (401 bp) were used to identify amplification fragment length of cultivar Madiarka (Fig. 2). All the above varieties have Gli-B1h allelic variant (Table 1).

The sixth group was distinguished by *Gli-B1.2* allele with the amplification fragment of 409 bp. We revealed this amplification fragment for the cv. Bilotserkivska Napivkarlykova and line KS 22–04 as in reference cv. Donskaya Polykarlikovaya and Suneca (Fig. 2). Gli-B1d allelic variant of gliadins, which is predominant in Mexico, Canada and Krasnodar (Russia) [18], was detected for all cultivars in this group. Due to the controversial results with Polischuk *et al.* [23], who had pointed out that *Gli-B1.1* allele corresponds to Gli-B1d allelic variant, cultivar Strumok was used to

Table 1. **Polymorphism of *Gli-B1* locus revealed by APAGE and allele-specific PCR**

№	Cultivar (Year of registration)	Allele revealed by PCR		Allelic variant of gliadin (APAGE)
		Gli-B1.1	*Gli-B1.2*	
1	**Albatros** (1990)	369	–	b
2	Anatoliia (2015)	369	–	b
3	Balada Myronivska (2018)	369	–	b
4	**Bezostaya 1** (1959)	369	–	b
5	Bilosnizhka (2006)	369	–	b
6	Blagho (2011)	369	–	b
7	Burghunka (2015)	369	–	b
8	Donetska 48	369	–	b
9	Gli-A1–1	369	–	b
10	Gli-D1–4	369	–	b
11	Gli-D1–5	369	–	b
12	Hratsiia Myronivska (2018)	369	–	b
13	Khaersonska Bezosta (2002)	369	–	b
14	Klarisa (2014)	369	–	b
15	Kokhana (2009)	369	–	b
16	Konka (2014)	369	–	b
17	Koshova (2017)	369	–	b
18	Levada (2005)	369	–	b
19	Lisova Pisnia (2008)	369 + null	–	b+l
20	Mariia (2013)	369	–	b
21	Metalist (2014)	369	–	b
22	MIP Assol (2018)	369	–	b
23	MIP Podolianka (2003)	369	–	b

№	Cultivar (Year of registration)	Allele revealed by PCR		Allelic variant of gliadin (APAGE)
		Gli-B1.1	*Gli-B1.2*	
24	MIP Vyshyvanka (2017)	369	–	b
25	**Mironovskaya 808** (1967)	369	–	b
26	Oberih Myronivsky (2014)	369	–	b
27	Orzhytsia (2013)	369	–	b
28	Ovidii (2009)	369	–	b
29	Pamiati Remesla (2009)	369	–	b
30	Romantyka (2009)	369	–	b
31	Sahaidak (2010)	369	–	b
32	Sonata	369	–	b
33	Sydor Kovpak	369	–	b
34	Tsarivna (2008)	369	–	b
35	Tsarychanka (2013)	369	–	b
36	Ukrainka Poltavska	369	–	b
37	Vezha Myronivska (2018)	369	–	b
38	Vidrada (2010)	369	–	b
39	Yasochka (2006)	369	–	b
40	Gli-B1–12	400	–	o
41	**Federation**	400	–	o
42	Bilotserkivska Napivkarlykova (1999)	–	409	d
43	**Donskaya Polykarlikovaya** (1985)	–	409	d
44	KS 22–04 (2004)	–	409	d
45	**Strumok** (1998)	–	409	d
46	**Suneca**	–	409	d
47	**Ardec**	–	402	h
48	**Caia**	–	403	h
49	**Krasnodonka**	–	401	h
50	Madiarka (2008)	–	403	h?
51	Hovtva	–	397	e
52	Liutenka	–	397	e
53	Shchedra Nyva (2011)	–	397	e
54	**Escualo**	–	397	e
55	L59–95 (1995)	–	397	c
56	**Prinqual**	–	397	c
57	Gli-B1–4	–	397	g
58	Myronivska Slava (2017)	–	397	f?
59	Zymoiarka (2007)	–	397	f?
60	Ariivka (2017)	–	–	l
61	Charodiika Bilotserkivska (2011)	–	–	l
62	Estafeta Myronivska (2018)	–	–	l
63	KS 1 (1995)	–	–	l
64	KS 14 (2005)	–	–	l
65	Kryzhynka (2002)	–	–	l
66	L 41/95 (1995)	–	–	l
67	Ledia (2016)	–	–	l
68	Lybid' (2006)	–	–	l
69	MIP Dniprianka (2018)	–	–	l
70	Myronivska Zolotoverkha	–	–	l
71	**Myronivska 61** (1987)	–	–	l
72	Myronivska 65 (2000)	–	–	l
73	Perlyna Lisostepu (2001)	–	–	l
74	Svitanok Myronivsky (2014)	–	–	l
75	Trudivnytsa Myronivska (2017)	–	–	l
76	Yuviliar Myronivsky (2009)	–	–	l
77	Yuvivata 60 (2013)	–	–	l
78	Vilshana (2010)	–	–	l
79	Vodohrai Bilotserkivsky (2014)	–	–	l
80	Zoriana Nosivska (1998)	–	–	l
81	Gli-B1–3	–	–	l

*Reference cultivars are highlighted in bold. The year of registration in The State Register of Plant Varieties Suitable for Dissemination in Ukraine is indicated in parentheses.

check this. As the result of PCR for Strumok variety, we received *Gli-B1.2* allele with amplification fragment of 409 bp (Table 1).

The results obtained in our research demonstrated wide distribution of two main alleles of *Gli-B1* locus among modern Ukrainian wheat cultivars. The first allele is *Gli-B1.1* with the amplification fragment of 369 bp, according to PCR, which corresponds to Gli-B1b allelic variant of gliadins that has positive impact on dough quality and is present in the majority of bread wheat cultivars in Ukraine and some other countries, such as Bulgaria, Romania and Russia [18]. The second allele is null allele in PCR with allele-specific primers, which corresponds to Gli-B1l allelic variant, linked to some important resistance genes. This allelic variant was predominant in sets of cultivars from The V. M. Remeslo Myronivka Institute of Wheat (MIW) (p=0.474) and Nosivska Selection and Breeding station (p=0.75). According to Kozub *et al.* [29], Gli-B1l became the most frequent (p=0.439) in a set of Forest-Steppe wheat cultivars developed in 1996–2007 in MIW and is the most frequent (p=0.452) in wheat cultivars of MIW created after 2010 [31].

Among Ukrainian breeding centers the highest diversity of *Gli-B1* alleles was revealed in The V. M. Remeslo Myronivka Institute of Wheat (4 allelic variants/19 cultivars) with genetic diversity H=0.57 and Bila Tserkva Breeding Research Station (4 allelic variants/11 cultivars) with genetic variation H=0.6. The Rare for Ukraine allelic variants were introduced by Poltava State Agrarian Academy (Gli-B1e), Nosivska Selection and Research Station (Gli-B1c, Gli-B1d), The V. M. Remeslo Myronivka Institute of Wheat (Gli-B1h, Gli-B1f) and Bila Tserkva Breeding Research Station (Gli-B1d, Gli-B1e). The allelic variants Gli-B1c, Gli-B1g and Gli-B1o were present only in wheat lines.

Gli-B1 loci carry not only important storage protein genes, but also are linked with the resistance and adaptation genes that provide the predominance of certain alleles in the specific environment.

Conclusions

DNA polymorphism of *Gli-B1* locus examined in our research coincided with the diversity of allelic variants of gliadins, which were detected by APAGE method in Ukrainian bread wheat cultivars, and divided all cultivars into six groups at the DNA level.

The predominant (p=0.52) allele of *Gli-B1* locus revealed by PCR was *Gli-B1.1* with the amplification fragment length of 369 bp, also frequent allele (p=0.32) was null allele (1RS.1BL translocation). Thereby the predominant allelic variants of gliadins in modern Ukrainian wheat varieties were Gli-B1b and Gli-B1l that corresponds to earlier studies [29, 31–33]. *Gli-B1.2* allele occurs much less often than *Gli-B1.1* and we revealed three types of different by length amplification fragments with primers specific to *Gli-B1.2*.

Clear correspondence observed in this study allows one to distinguish some important allelic variants of gliadins such as Gli-B1b, Gli-B1l, Gli-B1d, Gli-B1h by the PCR method. However, DNA-analysis applied in this study does not distinguish the Gli-B1c, Gli-B1g and Gli-B1e allelic variants. Nevertheless, at the same time using PCR with *Gli-B1.2* allele-specific primers we revealed polymorphism at *Gli-B1* locus among the cultivars with Gli-B1h allelic variant of gliadins.

The correspondence between allelic variants of gliadins and alleles of *Gli-B1* locus in Ukrainian bread wheat cultivars is retained as in the previously studied [24] "core collection of wheat cultivars".

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Генетична різноманітність *GLI-B1* локусу в українських сортах та лініях пшениці м'якої

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Мета. Дослідити поліморфізм *Gli-B1* локусу в українських сортах та лініях пшениці м'якої, проаналізувати поширення виявлених алелів та порівняти отримані дані із «кор-колекцією сортів пшениці», що була надана Д-р. Є. Метаковським **Методи.** Вісімдесят один сорт та лінія пшениці м'якої з різних селекційно-генетичних центрів України аналізували за допомогою ПЛР з алель-специфічними праймерами до *Gli-B1* локусу, розробленими Zhang *et al.* [2003]. Продукти ПЛР фракціонували у поліакриламідному гелі, після чого фарбували з використанням аргентум нітрату. Алельні варіанти гліадинів аналізували методом електрофорезу в кислому поліакриламідному гелі (кПААГ). **Результати.** Дев'ять алельних варіантів гліадинів було виявлено методом електрофорезу в кислому ПААГ та шість алелів *Gli-B1* локусу знайдено за допомогою ПЛР-аналізу. У 52 % сортів зустрічався алель Gli-B1b, що характеризувався *Gli-B1.1* алелем із довжиною фрагменту ампліфікації 369 п.н. 1RS.1BL транслокація, що несе гени стійкості, також часто зустрічалася в українських сортах пшениці м'якої. Відповідність між алельними варіантами гліадинів та алелями *Gli-B1* локусу обговорюється. **Висновки.** ДНК-поліморфізм *Gli-B1* локусу, виявлений у дослідженні за допомогою ПЛР, логічно збігається з поліморфізмом, що визначається за алельними варіантами гліадинів, проте ПЛР-аналіз із застосованими у роботі праймерами, не дозволив розрізнити алелі, що відповідають Gli-B1c, Gli-B1g та Gli-B1e алельним варіантам гліадинів. Найбільш поширеним для дослідженої вибірки українських сортів пшениці м'якої є алель *Gli-B1.1*, що детектується фрагментом апліфікації 369 п.н. та 1RS.1BL транслокація, яка не дає жодних фрагменів ампліфікації із праймера-

ми до *Gli-B1,* що відповідає алельним варіантам гліадинів Gli-B1b та Gli-B1l, відповідно.

Ключові слова: *Triticum aestivum L.*, *Gli-B1,* гліадини, поліморфізм, ПЛР-аналіз.

Генетическое разнообразие по *GLI-B1* локусу в украинских сортах и линиях пшеницы мягкой

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Цель. Исследовать полиморфизм по *Gli-B1* локусу в современных украинских сортах пшеницы мягкой, проанализировать частоты встречаемости аллелей и сравнить полученные данные с «кор-коллекцией сортов пшеницы» предоставленной Др. Е. Метаковским. **Методы.** Восемьдесят один сорт и линия пшеницы мягкой из разных селекционно-генетических центров и институтов Украины анализировали с помощью аллель-специфических праймеров разработанных Zhang *et al.* [2003]. Продукты ПЦР фракционировали в полиакриламидном геле и окрашивали с использованием нитрата серебра. Аллельные варианты глиадинов анализировали з помощью электрофореза в кислом полиакриламидном геле (кПААГ). **Результаты.** Было выявлено девять аллельных вариантов глиадинов и шесть аллелей *Gli-B1* локуса методом ПЦР. У 52 % украинских сортов пшеницы в исследуемой выборке был выявлен Gli-B1b аллельный вариант глиадинов, который характеризовался *Gli-B1.1* аллелем при ПЦР тестировании (фрагмент амплификации 369 п.н.). 1RS.1BL транслокация, что несет гены устойчивости, также часто встречалась в исследованных сортах пшеницы. В статье обсуждается соответствие между аллельными вариантами глиадинов и аллелями *Gli-B1* локуса, выявленными с помощью ПЦР. **Выводы.** ДНК-полиморфизм выявленный по *Gli-B1* локусу в исследуемых сортах пшеницы, логично соотносится с полиморфизмом аллельных вариантов глиадинов, но ПЦР-анализ с использованными в работе праймерами, не позволил дифференцировать аллели соответствующие Gli-B1c, Gli-B1g та Gli-B1e аллельным вариантам глиадинових белков. Наиболее рапостраненными аллелями в исследованой выборке украинских сортов пшеницы является аллель *Gli-B1.1,* который детектируется фрагментом амплификации 369 п.н., и 1RS.1BL транслокация, при наличии которой фрагментов амплификации с праймерами к *Gli-B1* не выявляется, что соответствует аллельным вариантам глиадинов Gli-B1b и Gli-B1l, соответственно.

Ключевые слова: *Triticum aestivum L.*, *Gli-B1,* глиадины, полиморфизм, ПЦР-анализ ,

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