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ALLELIC STATE OF THE MOLECULAR GENETIC MARKERS FOR GENES ASSOCIATED WITH SENSITIVITY TO *PYRENOPHORA TRITICI-REPENTIS* TOXINS A AND B AND *STAGANOSPORA NODORUM* TOXIN A AMONG UKRAINIAN COMMON WHEAT CULTIVARS

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Aim. *The study was performed to characterize wheat cultivars of Ukrainian breeding using XBE44541, Xfcp394 and Xfcp623 molecular genetic markers for the Tsn1 and Tsc2 genes conferring sensitivity to the toxins A of the necrotrophic fungi P. tritici-repentis and S. nodorum and toxin B of P. tritici-repentis.* ***Methods.*** *PCR with primers flanking diagnostic markers of the genes and DNA samples of 160 common wheat (T. aestivum L.) cultivars of Ukrainian breeding was used.* ***Results.*** *The frequency of the marker Xfcp394 allele for ToxA insensitivity was extremely high and made up 96.3 %. The frequency of the marker Xfcp623 allele for ToxA insensitivity was lower and made up 60.6 %. The accuracy of the marker Xfcp394 with respect to marker Xfcp623 made up near 59 %. The total amount of the marker XBE444541 for ToxB insensitivity made up 66.8 %.* ***Conclusion.*** *The alleles for the ToxA and ToxB insensitivity of the Tsn1 and Tsc2 genes are common among Ukrainian wheat cultivars and may be used for pyramiding in breeding process.*

Key words: *common wheat, tan spot, S. nodorum blotch, molecular genetic markers.*

Introduction. *Pyrenophora tritici-repentis* (Died.) Drech. is a harmful and worldwide spread phytopathogen of wheat (the genus *Triticum* L.) and causative agent of tan spot. This necrotrophic fungal pathogen is able to reduce the rate of photosynthesis per unit leaf area resulting in reduction of the kernel number per ear. It may be responsible for yield losses of about 5–10 % among susceptible cultivars and more than 50 % under favorable conditions and significantly affect yield quality [1, 2].

P. tritici-repentis races are determined according to their ability to cause necrosis in plants of the wheat cultivar 'Glenlea' and (or) chlorosis in plants of the wheat lines 6B365 and 6B662. There are three main host-selective toxins produced by *P. tritici-repentis*, namely PtrToxA (causes necrosis in plants of the wheat cultivar 'Glenlea'), PtrToxB (causes chlorosis in plants of the wheat line '6B662'), PtrToxC (causes chlorosis in plants of the wheat line '6B365') [3].

PtrToxA is one of well characterized host selective toxins, specific for *P. tritici-repentis* races 1, 2, 7 and 8 [4]. It is a protein of molecular weight 13.2 kDa and length 117 amino acid residues with a globular structure stabilized by disulphide bonds [5, 6].

PrtToxB is also a low molecular, water-soluble, relatively thermostable host-selective protein (6.61 kDa) of 63-64 amino acid residues in length [7]. This toxin is produced by *P. tritici-repentis* races 5, 6, 7 and 8 [3].

Stagonospora nodorum (Berk.) E. Castell. & Germano is also a dangerous phytopathogen of common and durum (*T. turgidum* L.) wheat, causative agent of *S. nodorum* blotch. It affects epiterranean parts of plants and may cause yield losses among susceptible wheat cultivars up to 50 % or up to 100 % in case of rainy weather during grain filling and total aggravation of yield quality [8]. It was shown that *S. nodorum* fungi produce their own toxin A (SnToxA), which is functionally

identical to PtrToxA and lends half or less of *S. nodorum* virulence [9].

PtrToxA and SnToxA sensitivity in wheat plants is governed by the single dominant gene *Tsn1* [9, 10]. The *Tsn1* gene was mapped on the long arm of wheat chromosome 5B [10]. *Xfcp393* and *Xfcp394* were the markers recommended as diagnostic for detection of insensitivity to PtrToxA and SnToxA though according to the literature for the cultivars 'Cheyenne', 'Jagger', 'TAM105', 'Forno', 'Norstar', 'Ben' and 'Langdon' a recombination between the gene and the marker was observed [11].

Lately the *Tsn1* candidate gene was sequenced. On the basis of the obtained sequence, the marker *Xfcp623* was proposed as diagnostic. It was localized in intron 5 of the locus in position 4901…5280 [12].

A single gene localized on the short arm of wheat chromosome 2B and named *Tsc2* is responsible for the sensitivity to PrtToxB [13]. The detailed investigation of the distal part of the chromosome 2B short arm permitted revealing molecular markers flanking the *Tsc2* gene, of which the RLFP marker *XBE444541* was modified into STS one. It was assumed to co-segregate with the *Tsc2* gene so far [14].

The field tests were performed to study *P. tritici-repentis* resistance of Ukrainian wheat cultivars so far [15–17] but the genetic background has not been studied yet.

The aim of our research was to characterize wheat cultivars of Ukrainian breeding using the *XBE444541*, *Xfcp394* and *Xfcp623* molecular genetic markers for the *Tsn1* and *Tsc2* genes conferring sensitivity to PtrToxB, PtrToxA and SnToxA of the necronrophic fungi *P. tritici-repentis* and *S. nodorum*.

Materials and methods

We analyzed DNA samples extracted from wheat seeds of 91 cultivars developed in the Plant Breeding and Genetics Institute (PBGI) of the National Academy of Agrarian Science of Ukraine (NAAS), Odessa and 69 ones developed in the Remeslo Myronivka Institute of Wheat (RMIW) of the NAAS jointly with the Institute of Plant Physiology and Genetics (IPPG), Ukrainian Academy of Sciences (160 in total). The complete list of the cultivars is shown in tables 1 and 2. Besides we analyzed the cultivar 'Bezostaya-1' as it is involved in the pedigree of the majority of modern Ukrainian wheat cultivars. The 'Chinese Spring' cultivar was used as the control for the «tr» allele of the markers *Xfcp394* and *Xfcp623* (associated with the *tsn1* ToxA insensitiveness allele of the gene) and the «tsr» allele of the marker *XBE444541* (associated with the *tsc2* PtrToxB insensitivity allele of the gene), the cultivar 'Katepwa' was used as the control for the «Ts» allele of the markers *Xfcp394* and *Xfcp623* (associated with the *Tsn1* toxin sensitive dominant allele of the gene) and the «Tss» allele of the marker *XBE444541* (associated with the *Tsc2* toxin sensitive dominant allele of the gene). The cultivars for the control were kindly provided by the National Center for Plant Genetic Resources of Ukraine of NAAS (Kharkiv). We extracted DNA from the sample of 25-30 mg. obtained from grinding 5-7 seeds in a ceramic mortar with further use of a Diatom™ DNA Prep100 DNA isolation kit (the sales representative in Ukraine is Neogene® Company) following the standard protocol. PCR was performed using GenPak® PCR Core Kits (the sales representative in Ukraine is Neogene® Company) according to the manufacturer's recommendations. The marker *Xfcp394* has 3 alleles: 383 bp (associated with insensitivity, further – «tr»), 328 bp (associated with sensitivity, further – «Ts»), null-allele (associated with insensitivity, further – «null») [11]. The marker *Xfcp623* has 2 alleles: 379 bp (associated with sensitivity, further – «Ts») and null-allele (associated with insensitivity, further – «tr») [12]. The marker *XBE444541-STS* has 2 alleles: 340 bp (associated with sensitivity, further – «Tss») and 509 bp (associated with insensitivity, further – «tsr», on the agarose gel electrophoresis it is masked by nonspecific bands) [14].

We lowered the annealing temperature to 42°C for the primer pair flanking the marker *XBE444541*. Besides this PCR was performed according the literature condition [11, 12, 14].

PCR results were visualized by electrophoresis in 2–2.5 % agarose gel in 0.5 × TBE buffer with subsequent staining with ethidium bromide and use of the gel- visualization system VISION Gel.

Results and discussion

The data on the allelic state of the analyzed cultivars are presented in tables 1 and 2

As a result of PCR with DNA of the cultivar Bezostaya-1 involved in the pedigree of the majority of Ukrainian wheat cultivars we obtained the «Ts» allele with the primers flanking the marker *Xfcp623* and

Table 1. The allelic state of the molecular markers *Xfcp623* and *Xfcp394* diagnostic for the *Tsn1* locus and *XBE444541-STS* diagnostic for the *Tsc2* locus in common wheat cultivars of the Steppe zone of Ukraine

Accession	Tsn1		Tsc2	Accession	Tsn1		Tsc2
	fcp623	fcp394	BE444541		fcp623	fcp394	BE444541
Albatros-odesskii	tr	tr	tsr	Olviya	Ts	-[2]	tsr
Antonovka	tr	tr	tsr	Otaman	tr	tr	tsr
Bezmezhna[1]	tr	tr	tsr	Panna	tr	-[2]	tsr
Blagodarka-odeska	Ts	tr	tsr	Pelipivka[1]	tr	-[2]	tsr
Borviy[1]	tr	tr	tsr	Pisanka	tr	-[2]	tsr
Bunchuk	tr	tr	tsr	Podyaka[1]	tr	tr	tsr
Dalnitskaya	Ts	tr	tsr	Poklik[1]	tr	-[2]	tsr
Dobrochyn[1]	Ts	tr	tsr	Poliovik	tr	tr	tsr
Dobropolka[1]	Ts	tr	Tss	Poshana	Ts	p/m[3]	tsr
Dyuk	Ts	tr	tsr	Povaga	tr	tr	tsr
Ednist	tr	Ts	tsr	Priboi	Ts	-[2]	tsr
Epokha-odeska	tr	tr	tsr	Prima-odesskaya	tr	-[2]	tsr
Fantaziya-odesskaya	tr	-[2]	tsr	Promin	Ts	-[2]	Tss
Fedorovka	tr	-[2]	tsr	Rozmay[1]	tr	-[2]	tsr
Goduvalnytsya-odeska	tr	tr	tsr	Selena	Ts	-[2]	tsr
Golubka-odeska[1]	tr	tr	tsr	Selyanka	Ts	tr	tsr
Gospodynya	tr	tr	tsr	Sirena-odesskaya	Ts	tr	tsr
Gurt[1]	tr	tr	tsr	Skarbnitsa	tr	tr	tsr
Istyna[1]	Ts	tr	tsr	Sluzhnitsya-odeska	tr	tr	Tss
Kiriya	Ts	p/m[3]	tsr	Strumok	tr	-[2]	tsr
Knyaginya-Olga	tr	tr	tsr	Suputnitsya	tr	tr	tsr
Kosovytsya	Ts	tr	tsr	Tira	tr	-[2]	Tss
Krasunya-odesskaya	tr	-[2]	tsr	Turunchuk	Ts	tr	tsr
Kuyalnik	tr	tr	tsr	Ukrainka-odesskaya	tr	tr	tsr
Kysen[1]	tr	-[2]	tsr	Uzhinok[1]	tr	tr	tsr
Lanoviy[1]	tr	-[2]	tsr	Vatazhok[1]	tr	tr	tsr
Lada	tr	-[2]	tsr	Vdala	tr	tr	tsr
Lastivka-odeska	tr	tr	tsr	Viktoriya-odesskaya	tr	tr	tsr
Lebidka[1]	tr	tr	Tss	Vyhovanka[1]	tr	-[2]	tsr
Lelya	tr	tr	tsr	Yubileinaya-75	Ts	-[2]	tsr
Liona	tr	tr	tsr	Yunnat-odesskii	tr	-[2]	tsr
Lira	tr	-[2]	tsr	Zadumka[1]	tr	-[2]	Tss
Litanivka	tr	tr	tsr	Zagrava-odeska[1]	tr	tr	tsr
Luzanivka-odeska	tr	-[2]	tsr	Zamozhnist	Ts	tr	tsr
Lyubava-odesskaya	tr	-[2]	tsr	Zaporuka[2]	Ts	tr	tsr
Misiya-odeska	tr	tr	tsr	Zastava-odesskaya	Ts	-[2]	tsr
Nebokrai	tr	tr	tsr	Zemlyachka-odesskaya	tr	null	tsr
Nikoniya	tr	tr	tsr	Zhayvir[1]	tr	tr	tsr
Odeska-napivkarlikova	Ts	-[2]	tsr	Zhuravka	tr	tr	tsr
Odesskaya-162	Ts	-[2]	tsr	Zmina	Ts	tr	tsr
Odesskaya-265	Ts	-[2]	tsr	Znahidka-odeska[1]	tr	tr	tsr
Odesskaya-267	tr	tr	Tss	Zorepad[1]	tr	tr	tsr
Odesskaya-51	Ts	-[2]	tsr	Zustrich	tr	tr	tsr
Odesskaya-95	Ts	-[2]	tsr	Zvytiaga[1]	tr	-[2]	Tss
Odesskaya-krasnokolosaya	tr	tr	tsr	Zysk[1]	tr	-[2]	tsr
Oksamitna[1]	tr	tr	tsr				

Here and in Table 2: [1] the cultivars names are given by the transliteration rules from the Ukrainian (the other ones are cited according to http://wheatpedigree.net); [2] no research using a marker was performed; [3] polymorphic samples, both diagnostic bands were obtained

Table 2. The allelic state of the molecular markers *Xfcp623* and *Xfcp394* diagnostic for the *Tsn1* locus and *XBE444541-STS* diagnostic for the *Tsc2* locus in common wheat cultivars of the Forest Steppe zone of Ukraine

Accession	Tsn1		Tsc2	Accession	Tsn1		Tsc2
	fcp623	fcp394	BE444541		fcp623	fcp394	BE444541
Bogdana	tr	tr	tsr	Mironovskaya-66	Ts	Ts	Tss
Demetra	Ts	-[2]	Tss	Mironovskaya-67	Ts	tr	Tss
Dobirna	Ts	tr	tsr	Mironovskaya-68	tr	-[2]	tsr
Dostatok	tr	tr	tsr	Mironovskaya-808	Ts	p/m[3]	Tss
Ekonomka	Ts	tr	tsr	Mironovskaya-rannespelaya	tr	tr	Tss
Ekspromt	Ts	-[2]	tsr	Monotip	tr	tr	tsr
Favoritka	tr	tr	tsr	Natalka	Ts	Ts	tsr
Hurtovina	Ts	Ts	tsr	Oberig-Mironivskii[1]	tr	tr	tsr
Ilichevka	Ts	-[2]	Tss	Palyanitsia	Ts	tr	tsr
Kalinova	Ts	tr	Tss	Pamyati-Remeslo	Ts	tr	tsr
Khazarka	Ts	tr	tsr	Pereyaslavka	Ts	tr	tsr
Kievskaya-ostistaya	tr	-[2]	tsr	Perlina-lisostepu	Ts	-[2]	Tss
Kolos-Mironovshchiny	Ts	tr	Tss	Pivna	tr	tr	tsr
Kolumbiya	Ts	-[2]	tsr	Podolyanka	tr	tr	tsr
Krizhinka	Ts	tr	Tss	Slavna	tr	p/m[3]	tsr
Lasunya	Ts	tr	tsr	Smila[1]	Ts	tr	tsr
Legenda-Mironovska[1]	Ts	tr	Tss	Smuglyanka	tr	tr	tsr
Madyarka	tr	tr	tsr	Snigurka	Ts	tr	tsr
Mirlena	Ts	tr	Tss	Snizhana	Ts	tr	Tss
Mironivska-storichna	tr	tr	Tss	Sonechko[1]	Ts	tr	Tss
Mironovskaya-10	Ts	-[2]	tsr	Svitanok-Mironivskii	tr	tr	tsr
Mironovskaya-11	tr	-[2]	tsr	Svyatkova	Ts	tr	Tss
Mironovskaya-264	Ts	-[2]	tsr	Ukrainka	Ts	-[2]	tsr
Mironovskaya-27	Ts	tr	Tss	Unikum (Yavorina)	tr	tr	tsr
Mironovskaya-28	tr	-[2]	tsr	Vdyachna	tr	tr	Tss
Mironovskaya-29	tr	-[2]	Tss	Vesnyanka	Ts	tr	tsr
Mironovskaya-30	Ts	tr	Tss	Vesta	Ts	tr	Tss
Mironovskaya-31	Ts	-[2]	tsr	Volodarka	tr	tr	tsr
Mironovskaya-32	tr	-[2]	tsr	Voloshkova	Ts	tr	tsr
Mironovskaya-33	tr	-[2]	tsr	Volynskaya-2	tr	-[2]	Tss
Mironovskaya-34	tr	-[2]	Tss	Yasnogirka	tr	tr	tsr
Mironovskaya-35	tr	-[2]	Tss	Yubilyar-mironovskii	Ts	tr	Tss
Mironovskaya-40	tr	-[2]	tsr	Zimoyarka	tr	tr	tsr
Mironovskaya-61	Ts	tr	Tss	Zolotokolosa	tr	tr	tsr
Mironovskaya-65	tr	null	tsr				

the «tsr» allele with the primers flanking the marker *XBE444541*.

The examples of the elecrophoregrams with PCR results are shown in figures 1-3.

The frequency of the «tr» allele of the marker *Xfcp394* for ToxA insensitivity was extremely high and made up 96.3 % (including polymorphic cultivars). Single amplified bands specific for the «Ts» allele were obtained for the cultivars 'Ednist', 'Hurtovina', 'Natalka', and 'Mironovskaya-66'. The cultivars 'Katepwa', 'Kiriya', 'Poshana' and 'Mironovskaya-808' were polymorphic. The frequency of the «tr» allele of the marker *Xfcp623* was lower and made up 60.6 % (97 cultivars of 160 analyzed). For the cultivars developed in the Steppe zone of Ukraine the amount of those with this allele made up 72.5 % (or 66 cultivars of 91 analyzed), for the cultivars developed in the Forest Steppe zone this proportion was about 45 % (or 31 culti-

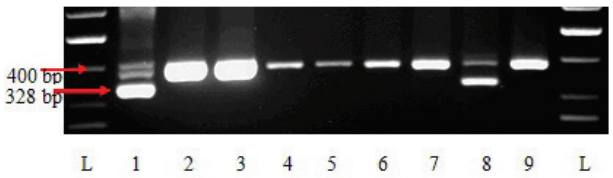

Figure 1. Electrophoregram of the amplification products with the primer pair flanking the marker *Xfcp394* for some cultivars of PBGI breeding in 2 % agarose gel. L – 50 bp ladder; 1 – 'Katepwa'; 2 – 'Chinese Spring' 3 – 'Albatros-odesskii'; 4 – 'Zmina'; 5 – 'Misiya-odeska'; 6 – 'Kosovytsya'; 7 – 'Gospodynya'; 8 – 'Kiriya'; 9 – 'Turunchuk'

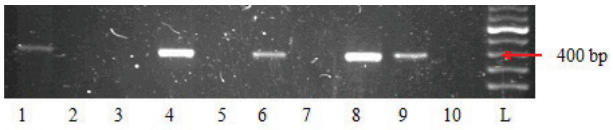

Figure 2. Electrophoregram of the amplification products with the primer pair flanking the marker *Xfcp623* for some cultivars of PBGI breeding in 2 % agarose gel. 1 – 'Katepwa'; 2 – 'Chinese Spring' 3 – 'Albatros-odesskii'; 4 – 'Zmina'; 5 – 'Misiya-odeska'; 6 – 'Kosovytsya'; 7 – 'Gospodynya'; 8 – 'Kiriya'; 9 – 'Turunchuk', 10 – 'Ednist'; L – 50 bp ladder

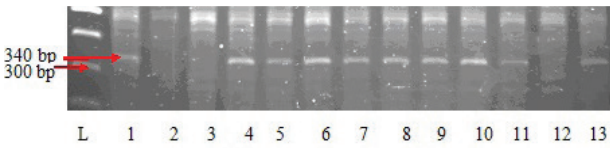

Figure 3. Electrophoregram of the amplification products with the primer pair flanking the marker *XBE444541* of the *Tsc2* gene for some cultivars of the Forest Steppe zone of Ukraine in 2 % agarose gel. L – 100 bp ladder; 1 – 'Katepwa'; 2 – 'Chinese Spring'; 3 – 'Vesnyanka'; 4 – 'Mirlena'; 5 – 'Mironovskaya-66'; 6 – 'Snizhana'; 7 – 'Mironovskaya-61'; 8 – 'Krizhinka'; 9 – 'Mironovskaya-67'; 10 – 'Mironovskaya-rannespelaya'; 11 – 'Mironovskaya-30'; 12 – 'Podolyanka'; 13 – 'Mironovskaya-808'

vars out of 69 analyzed). The accuracy of the marker *Xfcp394* with respect to *Xfcp623* made up near 59 % (the amount of similar data obtained with this marker and *Xfcp623* for the cultivars studied). The total amount of the «tsr» allele of the marker *XBE444541* for ToxB insensitivity made up 66.8 % (or 107 cultivars out of 160 analyzed). The ratio of this allele for the cultivars developed in different climatic zones appeared to be close and made up 70.3 % (or 64 out of 91) for the cultivars of the Steppe zone and 62.3 % (or 43 out of 69) – for the Forest Steppe zone of Ukraine.

We demonstrated rather high frequencies of the «tr» allele of the marker *Xfcp623* of the *Tsn1* gene and the «tsr» allele of the marker *XBE444541* of the *Tsc2* gene among Ukrainian wheat cultivars. On the other hand PCR results on the marker *Xfcp394* may be doubted. This marker showed the same results as *Xfcp623* and indicated sensitivity (insensitivity) to the toxins A according to literature [11, 12] but the possibility of segregation was as well shown [11]. Our study showed a 59 % coincidence between the results with the marker *Xfcp394* and *Xfcp623*, the latter is supposed to be more accurate as it was located in the intron 5 of the locus [12].

Recently the contribution of genetic factors in resistance and susceptibility to necrotrophic fungi was searched for some wheat pathogens in detail [18–20]. It was shown, that many QTLs and yet undiscovered genes take part in interaction between *P. tritici-repentis* and *T. aestivum* [20]. The authors [20] confirmed the role of *Tsn1* and *Tsc2* along with other genes in pathogenesis and revealed additive effects, which suggested the efficiency of resistance gene accumulation in breeding for tan spot resistance.

According to the previous study among the cultivars carrying the «tr» allele of the marker *Xfcp623* and the «tsr» allele of the marker *XBE444541*, 22 cultivars proved to carry the «Lr34+» allele of the marker *cssfr5* [21] and 8 of the markers *caISBP1+caSNP12* of the *Lr34* gene associated with resistance against leaf, stem and yellow rusts, powdery mildew and barley yellow dwarf virus [22]. Those cultivars may be a source of the complex resistance against ToxA-producing races of *P. tritici-repentis* and *S. nodorum* and ToxB-producing races of *P. tritici-repentis* and against rust fungi.

Conclusion

One hundred and sixty common wheat cultivars of Ukrainian breeding were characterized using PCR markers *Xfcp394*, *Xfcp623* and *XBE4444541* diagnostic for the *Tsn1* and *Tsc2* genes associated with sensitivity to PtrToxA, PtrToxB and SnToxA. The frequency of the marker *Xfcp394* allele for ToxA insensitivity was extremely high and made up 96.3 %. The frequency of the marker *Xfcp623* allele for ToxA insensitivity was lower and made up 60.6 %. The accuracy of the marker *Xfcp394* with respect to *Xfcp623* made up near 59 %. The total amount the marker *XBE444541* allele for ToxB insensitivity made up 66.8. The alleles for the ToxA and PtrToxB insensitivity of the *Tsn1* and *Tsc*2 genes are common among Ukrainian wheat cultivars and may be used for pyramiding in breeding process.

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АЛЕЛЬНИЙ СТАН МОЛЕКУЛЯРНО-ГЕНЕТИЧНИХ МАРКЕРІВ ГЕНІВ, АСОЦІЙОВАНИХ ІЗ ЧУТЛИВІСТЮ ДО ТОКСИНІВ А ТА В *PYRENOPHORA TRITICI-REPENTIS* І ТОКСИНУ А *STAGONOSPORA NODORUM* СЕРЕД УКРАЇНСЬКИХ СОРТІВ ПШЕНИЦІ М'ЯКОЇ

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Мета. Дослідження було проведене з метою охарактеризувати сорти пшениці української селекції з допомогою молекулярно-генетичних маркерів *XBE444541*, *Xfcp394* та *Xfcp623* генів *Tsn1* та *Tsc2*, що забезпечують чутливість до токсинів А некротрофних грибів *P. tritici-repentis* та *S. nodorum* і токсину В *P. tritici-repentis.* **Методи.** Було використано ПЛР із праймерами, що фланкують діагностичні маркери генів і зразками ДНК 160 сортів пшениці м'якої (*T. aestivum* L.) української селекції. **Результати.** Частота алеля маркера *Xfcp394*, асоційованого з нечутливістю до ТохА, досить висока і складає 96,3 %. Частота алеля маркера *Xfcp623*, пов'язаного із нечутливістю до ТохА, менша й становить 60,6 %. Точність маркера *Xfcp394* порівняно з *Xfcp623* складає приблизно 59 %. Загальна частка алеля маркера *XBE444541*, асоційованого з нечутливістю до ТохВ, склала 66.8 %. **Висновки.** Алелі генів *Tsn1* та *Tsc2*, пов'язані з нечутливістю до ТохА та PtrТохВ, поширені серед українських сортів пшениці й можуть бути використані для пірамідування в процесі селекції.

Ключові слова: пшениця м'яка, жовта плямистість, септоріоз, молекулярно-генетичні маркери.

АЛЛЕЛЬНОЕ СОСТОЯНИЕ МОЛЕКУЛЯРНО-ГЕНЕТИЧЕСКИХ МАРКЕРОВ ГЕНОВ, АССОЦИИРОВАННЫХ С ЧУВСТВИТЕЛЬНОСТЬЮ К ТОКСИНАМ А И В *PYRENOPHORA TRITICI-REPENTIS* И ТОКСИНУ А *STAGANOSPORA NODORUM* СРЕДИ УКРАИНСКИХ СОРТОВ ПШЕНИЦЫ МЯГКОЙ

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Цель. Исследование было проведено с целью охарактеризовать сорта пшеницы украинской селекции при помощи молекулярно-генетических маркеров *XBE444541*, *Xfcp394* и *Xfcp623* генов *Tsn1* и *Tsc2*, обеспечивающих чувствительность к токсинам А некротрофных грибов *P. tritici-repentis* и *S. nodorum* и токсина В *P. tritici-repentis*. **Методы.** Была использована ПЦР с праймерами, фланкирующими диагностические маркеры генов, и образцами ДНК 160 сортов пшеницы мягкой (*T. aestivum* L.) украинской селекции. **Результаты.** Частота аллели маркера *Xfcp394*, ассоциированной с нечувствительностью к ТохА, достаточно высока и составляет 96,3 %. Частота аллели маркера *Xfcp623*, ассоциированной с нечувствительностью к ТохА, меньше и составляет 60,6 %. Точность маркера *Xfcp394* по отношению к *Xfcp623* составила приблизительно 59 %. Общая доля аллели маркера *XBE444541*, ассоциированной с нечувствительностью к ТохВ, составила 66,8 %. **Выводы.** Аллели генов *Tsn1* и *Tsc2*, связанные с нечувствительностью к ТохА и PtrТохВ, распространены среди украинских сортов пшеницы и могут быть использованы для пирамидирования в процессе селекции.

Ключевые слова: пшеница мягкая, желтая пятнистость, септориоз, молекулярно-генетические маркеры.