Common wheat (*Triticum aestivum* L.) is very important widely grown crop used for bread baking, food and animal feed. Wheat yield is the third largest cereal production in the world, after maize and rice [1]. In consequence of methods of modern plant breeding, numerous varieties with increased productivity were obtained. However, due to the recent undesired climate changes and global warming, the selection of drought-tolerant germplasm donors must be constantly monitored to include them in contemporary breeding programs [2]. Marker-assisted selection (MAS) based on DNA markers can be effectively applied in the process of such selection [3–6]. While different types of DNA sequences can be employed for this purpose.

First DNA marker systems to study drought tolerance in plants were based on non-coding DNA sequences — RAPD (Random Amplified Polymorphic DNA) [7, 8], SSR (Simple Sequence Repeats) [9, 10] and ISSR (Inter Simple Sequence Repeats) [8] etc. Presently, attention mostly attracted to target encoding gene sequences, which play a great role in plant response to stress factors. These genes predominantly represented with transcriptional factors (TFs) and dehydrin genes [11].

In present work, our aim was to study DNA polymorphism of preselected gene loci of three transcription factors (*TaNAC2a*, *TaWRKY2*, and *TaWRKY19*) and the Late Embryogenesis Abundant (LEA) proteins dehydrin (*Td29b*) related to wheat drought tolerance. The genes structure and chromosome location were established via bioinformatics tools. It is stated that *TaWRKY2* and *TaWRKY19* genes were comprised of 4 exons and 3 introns located on 2BS and 1DS chromosome arms, respectively; *TaNAC2a* — 2 exons and 1 intron 7AS; *Td29b* — single exon gene 3AS. Using polymerase chain reaction, no polymorphism was observed. Polymorphic bands were detected for *TaWRKY2* locus. The screening of the distribution of the revealed polymorphic loci was carried out for a set of wheat and rye varieties, old landraces and interspecific hybrids. The polymorphism of *TaWRKY2* locus indicated the presence of some other possible alleles of the gene. The obtained data are important for further investigations of wheat drought tolerance.

**Key words:** *Triticum* spp., polymerase chain reaction, transcription factors, *TaNAC2a*, *TaWRKY2*, *TaWRKY19*, LEA, *Td29b*, drought tolerance.
Arabidopsis plants [12]. It was also found out that TaWRKY2 overexpressing plants had enhanced STZ and RD29B gene expressions due to temperate binding to the loci from RD29B STZ-1 and STZ-2 locus of Arabidopsis. As to TaWRKY19 transgenic plants, they had higher expression levels of DREB2A, RD29B, Cor6.6 and RD29A genes [12].

Another TF family that highly introduced in common wheat is represented with proteins containing a highly conserved NAC domain at the N-terminus and a variable transcriptional regulation domain at the C-terminus [16, 17]. Overexpression of different TaNAC responded to enhanced biotic and abiotic tolerance [18, 19]. It was postulated in the [16], that TaNAC2a transgenic plants of tobacco had extremely increased drought tolerance.

Special role in response to dehydration stress relates to dehydrin proteins, which help plant cell cope with osmotic changes. The number of dehydrins were described in wheat [20, 21]. Late Embryogenesis Abundant (LEA) proteins belong to above mentioned group of proteins and can be candidate for wheat improvement [22]. It was reported [23] that LEA proteins accumulation enhanced stress tolerance protecting plant cells against dehydration. It was also described the importance of Td29b dehydrin in common wheat, which synthesis was highly induced by dehydration.

Materials and Methods

The subject of the study was a set of wheat cultivars of Ukrainian and foreign origin (25 and 36, consequently), a set of 52 old wheat species, distant and interspecific hybrids, 4 varieties of rye.

BLAST searches and sequence analyses were implemented by BLASTn on the Triticum aestivum genome (https://blast.ncbi.nlm.nih.gov/ and https://wheat-urgi.versailles.inra.fr). The schemes of exon–intron structures were obtained by employing the online Gene Structure Display Server bioinformatic tools (http://gsds.cbi.pku.edu.cn/) from both coding sequence (CDS) and genomic sequences [24].

Total DNA was isolated from one kernel with the modified CTAB method [25]. Polymerase chain reaction (PCR) of 20 μl included 0.5 μM of forward and reverse primers each (Metabion, Germany), 1× Reaction Buffer B (Solis BioDyne, Estonia), 2 mM MgCl₂, 0.2 μM of each deoxyribonucleoside triphosphate (Thermo Fisher Scientific, USA), 1 unit of FIREPol® DNA Polymerase (Solis BioDyne, Estonia), 30 ng of total plant DNA. Primer sequences for loci TaNAC2a, TaWRKY2, TaWRKY19 and Td29b used in the study and PCR conditions are indicated in the Table 1. The CDS accessions in the GenBank are HM027575.2 (TaNAC2a), EU665425.1 (TaWRKY2), EU665430.1 (TaWRKY19) and AJ890139.1 (Td29b).

The PCR products were separated by means of electrophoresis in 2% agarose gels in lithium borate buffer, 0.1 μg/ml ethidium bromide [26]. Gels were visualized in UV-light with a photosystem Canon EOS 600D. GelAnalyzer 2010 software was applied to identify the size of amplified fragments (http://www.gelanalyzer.com). Frequencies for each combination of amplified fragments were calculated according to [27].

Results and Discussion

As it was denoted above, data on CDS only are available for those three studied transcriptional factors (TaNAC2a, TaWRKY2, and TaWRKY19) and the dehydrin (Td29b). Thus, we managed to predict the exon-intron

| TF gene     | Primer sequences 5′→3′ | PCR conditions     |
|-------------|------------------------|--------------------|
| TaNAC2a     | F: GGTAGTGCCTGCTTCCCAAT R: TGAATGGTTGTGCTGCC [16] | 94 °C — 30 s; 58 °C — 30 s 72 °C — 30 s; 35 cycles |
| TaWRKY2     | F: GGCGCTGCCGACGTCATCTT R: AGCAGAGGAGCCTGACGA [12] | 94 °C — 30 s; 58 °C — 30 s 72 °C — 30 s; 35 cycles |
| TaWRKY19    | F: AGGGAAAGCATACGCTGATGGC R: GGCGAGATCGTTCAGAATGGC [12] | 94 °C — 30 s; 60 °C — 30 s 72 °C — 30 s; 35 cycles |
| Td29b       | F: CGCACCCAGCTGATGTCG R: CCCAGCCAGTATAACCCCAT [23] | 94 °C — 30 s; 53 °C — 30 s 72 °C — 30 s; 35 cycles |
structure and location of their genes by means of alignment via BLAST tools.

Having carried out every CDS alignments in the database of wheat whole genome shotgun contigs, the gene structures and chromosomal location were defined for three studied transcription factors (TaNAC2a, TaWRKY2, TaWRKY19) and the dehydrin (Td29b) (Fig. 1) in accordance with [28]. Hence, TaWRKY2 and TaWRKY19 have similar structure of 4 exons and 3 introns (Fig. 1, A, B), though, they are situated in different chromosomes (TaWRKY2 — short arm of 1D chromosome; TaWRKY19 — short arm of 1B). Both primer pairs applied in the following DNA polymorphism study hybridized at the end of the fourth exon. The gene of TF TaNAC2a comprises of 2 exons and 1 intron (Fig. 1, C) and allocates at the short arm of 7A chromosome. The primer pair for this gene locus annealed at the central part of exon 2. It was established, that Td29b gene might have referred to single exon gene (Fig. 1, D). Its location is the short arm of 3A chromosome.

Molecular genetic study

To study DNA polymorphism of the selected loci of 4 genes (three TF — TaNAC2a, TaWRKY2, TaWRKY19; and the dehydrin gene Td29b) a set of 25 Ukrainian and 37 international wheat accessions from Global Wheat Program of the International Maize and Wheat Improvement Center (CIMMYT) and the Wheat Germplasm Bank was collected. By means of applying primer pairs and PCR conditions indicated in the Table 1, we observed no polymorphism for gene loci TaNAC2a, TaWRKY19 and Td29b. There was one fragment amplified only for each sample — fragment of approximately 227 base pairs (bp) for TaNAC2a gene locus, 160 bp for TaWRKY19, 86 bp for Td29b (Fig. 2).

Following the amplification of total genomic DNA of all common wheat varieties of Ukrainian and foreign origin, there were two fragments detected for each sample. We observed three different genotypes in the studied TaWRKY2 locus. The first one

![Fig. 1. Prediction of gene exon-intron structure:](image)

A — TaWRKY2; B — TaWRKY19; C — TaNAC2a; D — Td29b

![Fig. 2. The electrophoregrams denoting PCR-products segregation of DNA marker systems:](image)

A — TaNAC2a; B — TaWRKY19; C — Td29b

Lanes 1–6 — common wheat varieties (Glenlea, Comanche, Wilbur, Granero Inta, Tobarito M 97, V-17); M — marker of molecular weight GeneRuller™ DNA Ladder Mix
represented amplified fragments of 173 and 188 bp, second — 188 and 200 bp, the third — of 173 and 200 bp (Fig. 3). Moreover, Ukrainian varieties showed greater diversity, than those foreign ones. The frequencies for each allele of amplified fragments among Ukrainian varieties are 0.52 (173+188 bp), 0.28 (173+188 bp) and 0.2 (173 + 200 bp). On the contrast, a set of amplified fragments 188+200 bp was not observed among 36 foreign varieties obtained from the CIMMYT. In addition, only two samples (Milleau Inia and Tobarito M97) possessed 173+200 bp pattern. Thereafter, frequencies for these two allele of amplified fragments among the CIMMYT varieties were 0.944 (173+188 bp) and 0.056 (173+200 bp). The results on the DNA polymorphism study of TaWRKY2 locus are indicated in the Tables 2 and 3.

**Table 2. Detected DNA polymorphism of TaWRKY2 locus in Ukrainian varieties**

| Variety          | Originator                | Amplified fragment, bp | Variety          | Originator                | Amplified fragment, bp |
|------------------|---------------------------|------------------------|------------------|---------------------------|------------------------|
| Astarta          | IPPG NASU                | 173, 200               | Poliska 90       | NSC “IA NAAS”              | 173, 188               |
| Bohdana          | IPPG NASU                | 173, 188               | Shchedrivka Kyivska | IPPG NASU NSC “IA NAAS” | 173, 188               |
| Bunchak          | PBGI NCSCI NAASU         | 173, 188               | Slavna           | IPPG NASU                 | 188, 200               |
| Darunok Podillia | IPPG NASU                | 173, 188               | Smuhlianka       | IPPG NASU                 | 188, 200               |
| Drevlianka       | n.a.                     | 173, 188               | Solomiia         | IPPG NASU                 | 173, 188               |
| Favorityka       | IPPG NASU                | 173, 200               | Sonata           | Institute of Field and Vegetable Crops, Novi Sad, Serbia | 173, 200               |
| Hileia           | IPPG NASU                | 188, 200               | Sotnytsia        | IPPG NASU                 | 188, 200               |
| Kryzhynka        | RMIW NAASU IPPG NASU     | 173, 200               | Spasivka         | IPPG NASU                 | 188, 200               |
| Natalka          | IPPG NASU                | 173, 188               | Vesnianka        | IPPG NASU                 | 188, 200               |
| Novokyivska      | IPPG NASU                | 173, 200               | Yatran 60        | IPPG NASU                 | 173, 188               |
| Odeska 267       | PBGI NCSCI NAASU         | 173, 188               | Yednist          | PBGI NCSCI NAASU           | 173, 188               |
| Pereiaslavka     | IPPG NASU                | 173, 188               | Zolotokolosa     | IPPG NASU                 | 188, 200               |
| Podolianka       | IPPG NASU                | 173, 188               |                  |                           |                        |

*Note: IPPG NASU — Institute of Plant Physiology and Genetics, National Academy of Sciences of Ukraine; PBGI NCSCI NAASU — Plant Breeding and Genetics Institute — National Center of Seed and Cultivar Investigation, the National Academy of Agrarian Sciences of Ukraine; RMIW NAASU — The V.M. Remeslo Myronivka Institute of Wheat, the National Academy of Agrarian Sciences of Ukraine; NSC “IA NAAS” — National Scientific Centre “Institute of Agriculture of the National Academy of Agrarian Sciences of Ukraine”; n.a. — not available. http://www.wheatpedigree.net, State register of plant varieties suitable for distribution to Ukraine of the Ministry of Agrarian Policy and Food of Ukraine http://www.sops.gov.ua/reestr-sortiv-roslin.*

**Fig. 3. The electrophoregram depicting DNA polymorphism of TaWRKY2 locus:** Lanes 1 — Odeska 267; 2 — Poliska 90; 3 — Darunok Podillia; 4 — Podolianka; 5 — Astarta; 6 — Kryzhynka; 7 — Sotnytsia; 8 — Zolotokolosa; M — molecular weight marker GeneRuller™ DNA Ladder Mix.
**Table 3. Detected DNA polymorphism of TaWRKY2 locus in varieties from germplasm collections of the CIMMYT**

| Variety | Locality | Originator* | Year of registration | Amplified fragment, bp |
|---------|----------|-------------|----------------------|------------------------|
| 1       | AC Vista | Canada (Saskatchewan) | Agriculture and Agri-Food Canada Semi-arid Prairie Agricultural Research Centre, Swift Current | 1996 | 173, 188 |
|         | Albis    | Switzerland (Zurich) | Federal Research Station for Agronomy | 1983 | 173, 188 |
|         | Anza     | Mexico, USA (California) | California Agricultural Experiment Station | 1971 | 173, 188 |
|         | Batavia  | Australia (Queensland) | Queensland Wheat Research Institute | 1991 | 173, 188 |
|         | Caribo   | Germany | Heidenreich, Bad-Schwartau | 1968 | 173, 188 |
|         | Cenad-512 | Romania | n.a. | 1958 | 173, 188 |
|         | Comanche | USA (Kanzas) | Kansas Agricultural Experiment Station | 1942 | 173, 188 |
|         | D-12     | Peru | n.a. | 1972 | 173, 188 |
|         | Excalibur | Australia (South-Australia) | RAGT | 1990 | 173, 188 |
|         | Gabo     | Australia (New-South-Wales) | University of Sydney Plant Breeding Institute, Cobbitty | 1942 | 173, 188 |
|         | Glenlea  | Canada (Manitoba) | University of Manitoba | 1972 | 173, 188 |
|         | Grande- Del-Monte | Venezuela | n.a. | n.a. | 173, 188 |
|         | Granero Inta | Argentina | Inta | 1987 | 173, 188 |
|         | Inia-F-66 | Mexico | INIA, CIMMYT | 1966 | 173, 188 |
|         | Iskamish-K-2-Light | Afghanistan | n.a. | 1975 | 173, 188 |
|         | Janz     | Australia (Queensland) | Queensland Wheat Research Institute | 1989 | 173, 188 |
|         | Katunga  | Australia (Victoria) | n.a. | 1992 | 173, 188 |
|         | Ke Feng 2 | China (Heilongjiang) | Keshan WRI | 1979 | 173, 188 |
|         | Kimmo    | Finland | n.a. | 1941 | 173, 188 |
|         | Klein Favorito | Argentina | E. Klein | 1920 | 173, 188 |
|         | Kulin    | Australia (Western-Australia) | Department of Agriculture, W.A. | 1986 | 173, 188 |
|         | Manital  | Italy | Samoggia Luigi, Bologna | 1981 | 173, 188 |
|         | Millaaleau Inia | Chile | INIA, CIMMYT | 1982 | 173, 200 |
|         | Recital  | France | Benoist | 1986 | 173, 188 |
|         | Rokycanska samekta | Czechoslovakia | n.a. | 1899 | 173, 188 |
|         | Safed Lemara | India | Indian Agricultural Research Institute | 1967 | 173, 188 |
|         | Sakha 69 | Egypt | Agricultural Research Center, Giza | 1980 | 173, 188 |
|         | Svenno  | Sweden | W. Weibull | 1953 | 173, 188 |
|         | Talimka | Kyrgyzstan | Kirgizskaya GSS | 1940 | 173, 188 |
|         | Tobarito M 97 | Mexico | CIMMYT | 1997 | 173, 200 |
According to CDS sequence of TaWRKY2 (GenBank ID EU665425.1), the primer pair for this TF locus is likely to amplify the fragment of 188 bp long. Such a fragment was observed through the study; however, not all the wheat samples possessed it. Consequently, there must be an indel mutation, which is likely to form another allele.

The old wheat landraces is the source of potential genes of interest which can be of great value for common wheat improvement in modern breeding programs. Thus, the following screening of a number of wheat landraces and interspecific hybrids was carried out. The data were indicated in the Table 4. As it can be seen from the table, most of them carried fragments of 173+188 bp (46 among 52 samples, frequency — 0.88). On the other hand, all the 3 fragments (173, 188 and 200 bp) were amplified from 2 wheat accessions (*T. spelta* var. *duhamelianu* Baulaender and

Table 4. Detected DNA polymorphism of TaWRKY2 locus in old wheat species, distant and interspecific hybrids

| Species/Hybrid/Cross | Subspecies | Country of originator | Amplified fragment, bp |
|----------------------|------------|-----------------------|------------------------|
| AD                   | *T. persicum*/Ae. tauschii | Japan                | 173, 188               |
| AD                   | *T. dicoccum*/Ae. speltoides | Azerbaijan           | 173, 188               |
| AD                   | *Ae. ventricosa*/T. dicoccum | Russia               | 173, 188               |
| AD                   | *T. aestivum*/Ae. comosa | Russia               | 173, 188               |
| AD 217               | *T. timopheevii*/Ae. umbellulata | Japan           | 173, 188               |
| AD 7                 | *T. ispahanicum*/Ae. cylindrical | Azerbaijan           | 173                    |
| AD 8                 | *T. dicoccum*/Ae. triuncialis | Azerbaijan           | 173, 188               |
| Aegilotricum cylindroaestivum | *Aegilops cylindrica*/T. aestivum | Armenia          | 173, 188               |
| Haynatricum          | *T. dicoccum*/Daspyrum villosum | Russia           | 173, 188               |
| PAH-31               | *T. dicoccum*/T. monococum | Russia               | 173, 188               |
| PEAH                 | *T. dicoccum*/Ae. tauschii | Russia               | 173, 188               |
| *T. dicoccum* Scuebl. | var. *rufum* | Sweden               | 173, 188               |
| 1                     | 2                          | 3                | 4                |
|----------------------|-----------------------------|------------------|------------------|
| *T. dicoccum* Schuebl. | var. *aeruginosum*          | Azerbaijan       | 173, 188         |
| *T. dicoccum*         | var. *aeruginosum* Runo     | Russia           | 173, 188         |
| *T. dicoccum*         | var. *serbicicum* Polba 3   | Russia, Udmurtia | 173, 188         |
| *T. dicoccum*         | var. *dicoccum*             | Ukraine          | 173, 188         |
| *T. dicoccum*         | var. *nigroajar*            | Ethiopia         | 173, 188         |
| *T. dicoccum*         | var. *rufum*                | Ukraine          | 173, 188         |
| *T. dicoccum*         | var. *aeruginosum*          | Russia, Dagestan | 173, 188         |
| *T. dicoccum*         | var. *seminanum*            | Germany          | 173, 188         |
| *T. dicoccum*         | Polba Kokchetavska          | Kazakhstan       | 173, 188         |
| *T. dicoccum Schuebl.*| var. *vasconicum* Crjunella | Spain            | 173, 188         |
| *T. dicoccum*         | var. *rufum*                | Spain            | 173, 188         |
| *T. dicoccum*         | var. *atratum*              | Poland           | 173, 188         |
| *T. dicoccum*         | n.a.                        | Kazakhstan       | 173, 188         |
| *T. dicoccum Schuebl.*| var. *serbicium*            | Belarus          | 173, 188         |
| *T. dicoccum Schuebl.*| var. *dicoccum*             | n.a.             | 173, 188         |
| *T. dicoccum Schuebl.*| var. *serbicium* Chervona krasa | Belarus       | 173, 188         |
| *T. dicoccum Schuebl.*| var. *haussknachtianum* Bolshaia holova | India     | 173, 188         |
| *T. dicoccum Schuebl.*| var. *loganse* Polba Kokchetavska | n.a.        | 173, 188         |
| *T. dicoccum Schuebl.*| var. *volgense* Vernal     | USA              | 173, 188         |
| *T. dicoccum Schuebl.*| var. *aeruginosum*          | Armenia          | 173, 188         |
| *T. dicoccum Schuebl.*| var. *serbicium*            | Russia           | 173, 188         |
| *T. dicoccum Schuebl.*| var. *volgense*             | Russia           | 173, 188         |
| *T. dicoccum Schuebl.*| var. *haussknachtianum*     | Kazakhstan       | 173, 188         |
| *T. dicoccum Schuebl.*| var. *haussknachtianum*     | Azerbaijan       | 173, 188         |
| *T. dicoccum Schuebl.*| var. *aeruginosum* Runo     | Russia           | 173, 188         |
| *T. ispahanicum*      | var. *ispahanicum*          | Iran             | 173, 188         |
| *T. kiharae*          | *T. timopheevii × Ae.tauschii* | Japan       | 173, 188         |
| *T. macha*            | var. *palaeoimereticum*     | Georgia          | 173, 188         |
| *T. sinkajae*         | var. *sinkajae*             | Russia           | 173              |
| *T. spelta*           | var. *album*                | Canada           | 173, 188         |
| *T. spelta*           | var. *caeruleum* CDC Zobra  | Canada           | 173, 188         |
| *T. spelta*           | var. *griseoturanorecens*   | Tajikistan       | 173, 188         |
| *T. spelta*           | var. *duhamelianum*         | Poland           | 173, 188         |
| *T. spelta*           | var. *duhamelianum* Baulaender | Germany      | 173, 188, 200    |
| *T. spelta*           | var. *duhamelianum* Frankenkorn | Germany     | 173, 188         |
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T. vavilovii var. vavilovii) representing frequency 0.04 only. Three wheats (frequency — 0.06) had only one type of fragment (173 or 188 bp). The only sample (frequency — 0.02) (T. hexapolonicum) had fragments of 173 + 200 bp.

Additionally, four rye verities (Avgust, Khmarka, Remington and Stoir) were tested for polymorphism in TaWRKY2 locus. As a result, the only fragment of 200 bp was detected in each sample. This fact shows that other cereal crops might have the TaWRKY2 gene too.

The study of the genes, that impact greatly on drought response, is of great value for wheat improvement in present-day plant breeding programs. The current research reveals knowledge on DNA polymorphism of three transcriptional factors (TaNAC2a, TaWRKY2, TaWRKY19) and the dehydrin (Td29b) genes which can be applied for MAS. During the analysis the gene structure and chromosomal location were established. Thus, TaWRKY2 and TaWRKY19 genes comprised of 4 exons and 3 introns (2BS and 1DS, respectively); TaNAC2a — 2 exons and 1 intron (7AS); Td29b — single exon gene (3AS).

In the result of this study, no polymorphism was observed for gene loci TaNAC2a, TaWRKY19 and Td29b by means of preselected primer pairs. In contrast, polymorphic bands were detected for TaWRKY2 locus that did not correspond to CDS from GenBank. This fact indicated the presence of some other possible alleles of the gene.

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Table 4. End

| 1 | 2 | 3 | 4 |
|---|---|---|---|
| T. spelta | var. caeruleum | Azerbaijan | 173, 188 |
| T. spelta | var. album | Canada | 173, 188 |
| T. vavilovii | var. vavilovii | Armenia | 173, 188, 200 |
| T. hexapolonicum | n.a. | Armenia | 173, 200 |
| Tritordeum 1199/09 | T. durum/Hordeum chilense | Spain | 188 |
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ПОЛІМОРФІЗМ ГЕНІВ ДЕЯКИХ ТРАНСКРИПЦІЙНИХ ФАКТОРІВ, ЩО ПОВ’ЯЗАНИ З ПОСУХОСТІЙКІСТЮ ПШЕНИЦІ

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Метою дослідження було вивчити поліморфізм попередньо відібраних локусів генів трьох транскрипційних факторів (TaNAC2a, TaWRKY2, TaWRKY19) та протеїн пізнього ембріогенеза (LEA) дегидрину (Td29b), пов’язаних зі стійкістю пшениці до посухи. Структуру генів та хромосомну локалізацію було встановлено за допомогою біоінформатичних підходів. З’ясовано, що гени TaWRKY2 та TaWRKY19 складаються з 4 екзонів і 3 інтронів, локалізованих на плечах 2BS та 1DS хромосоми, відповідно; TaNAC2a містить 2 екзони та 1 інтрон 7AS. Ген Td29b містить один екзон 3AS. У результаті використання полімеразної ланцюгової реакції не було виявлено поліморфізму для локусів генів TaNAC2a, TaWRKY19 та Td29b за допомогою попередньо відібраних пар праймерів. Проте для локусу TaWRKY2 виявлено поліморфні фрагменти. Скринінг поширення поліморфних локусів проводили для набору сортів пшениці та жита, давніх пшениць та міжвидових гібридів. Поліморфізм локусу TaWRKY2 свідчить про наявність деяких інших алелей цього гена. Ці дані є важливими для подальших досліджень посухостійкості пшениці.

Ключові слова: Triticum spp., полімеразна ланцюгова реакція, фактори транскрипції, TaNAC2a, TaWRKY2, TaWRKY19, LEA, Td29b, посухостійкість.