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SNP ANALYSIS OF UKRAINIAN MAIZE INBREDS WITH ALTERNATIVE STATE OF MOLECULAR CAROTENOGENESIS MARKER *crt*RB1-3′TE

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Aim. SNP analysis and estimation of genetic relations in maize inbreds with the alternative state of β-carotene hydroxylase 1 gene (*crt*RB1) by the molecular marker *crt*RB1-3′TE. **Methods.** SNP analysis, statistical methods. BDI-III panel with 384 SNP markers was used for comparative research of 35 maize inbreds developed and adopted in the northern Steppe of Ukraine. **Results.** SNP analysis of investigated inbred set showed that the part of dimorphic markers was 98.2 %, the average minor allele frequency (MAF) was 0.3040, the average polymorphism information content (PIC) was 0.3064, and the average shift of genetic diversity of markers was 0.3898. There was no significant difference between genetic SNP distances within both groups of inbreds with favourable/unfavourable alleles and between these groups by *crt*RB1-3′TE. The SNP distances were used to build a dendrogram of genetic relations between maize inbreds with an alternative state of the *crt*RB1-3′TE marker. **Conclusions.** The relationship between the allelic state of the β-carotene hydroxylase 1 gene and single nucleotide polymorphism markers for maize inbreds is presented. The alleles of SNP markers BDI-III-130A, BDI-III-15A, BDI-III-60C, BDI-III-61C, BDI-III-116G, BDI-III-128A, and BDI-III-129A were found to be most frequent in the inbreds, which are carriers of the favourable allele of 543 bp of *crt*RB1 gene by the *crt*RB1-3′TE marker. The random distribution of alleles of this gene among maize inbreds developed in the northern Steppe of Ukraine was demonstrated.

Key words: *Zea mays* L., β-carotene hydroxylase 1, single nucleotide polymorphism, molecular markers, carotenoids.

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INTRODUCTION

Maize has a relevant position in the diet of humans and animals due to a rather high content of valuable substances, including carotenoids, in the grain (Nuss E, Tanumihardjo S, 2010). Carotenoids play an important role in the functioning of the digestive and immune systems, vision, and skin; they are antioxidants required for growth and development (Crupi P et al, 2023). The prevailing carotenoids in maize grain are lutein, zeaxanthin, α- and β-carotenes, and α- and β-cryptoxanthins, their number and ratio may vary depending on the maize genotype, environmental conditions, the genotype × environment interaction, the stage of grain maturity, and the degree of substance decomposition during storing (Šimić D et al, 2023;

Djalovic et al, 2024). The amount of digestible individual carotenoids in an animal organism increases in the following direction: β-carotene → α-cryptoxanthin → β-cryptoxanthin → lutein → zeaxanthin (Zurak et al, 2024). The degradation rate for individual carotenoids in the maize grain increases in the following direction: lutein → zeaxanthin → α-cryptoxanthin → β-cryptoxanthin → β-carotene (Gunjević et al, 2024). The most valuable carotenoid is β-carotene, because two molecules of vitamin A instead of one, notable for other predecessors, are formed out of one molecule of this substance in the organism of humans and animals (Diepenbrock et al, 2021; Chandrasekharan et al, 2022; Sun et al, 2022).

A higher content of carotenoids is common for maize genotypes with harder grain than for genotypes with softer grain (Saenz et al, 2020). Grain with a flint structure has a higher content of β-carotenoids (zeaxanthin, β-cryptoxanthin, and β-carotene), and genotypes with dent grain mainly accumulate α-carotenoids (lutein, α-cryptoxanthin, and α-carotene), as a result flint grain contains twice as much provitamin A (Saenz et al, 2021).

The regulation of carotenoid metabolism is complicated and includes transcriptional, post-transcriptional, post-translational, and epigenetic regulation (Sun et al, 2022).

One of the key genes in the biosynthesis of carotenoids is the β-carotene hydroxylase 1 gene (*crt*RB1), which, along with lycopene-ε-cyclase gene (*lcy*E) and phytoene synthase gene (*psy*1) is the most responsible for the content of provitamin A in mature maize grain (Diepenbrock et al, 2021; Băcilă et al, 2022). It was shown that maize inbreds with favorable alleles of gene *lcy*E had the highest content of carotenoids, which were not predecessors of vitamin A, whereas the inbreds with a favourable allele of gene *crt*RB1 had a high level of carotenoids-predecessors of vitamin A (Maazou et al, 2021). The Romanian inbreds with the favorable allele of gene *crt*RB1 demonstrated a high level of β-carotene and β-cryptoxanthin, and the inbreds with a favourable allele of gene *lcy*E – a high level of β-cryptoxanthin, first of all. In the inbreds with favorable alleles of both genes the level of β-carotene was 60 % higher than the inbreds with two unfavorable alleles of these genes (Băcilă et al, 2022). According to (Satarova et al, 2019), the maize inbreds of Ukrainian selection, which have the allele of 543 bp by the *crt*RB1-3´TE marker, contain almost twice as much β-carotene in mature grain than the inbreds with the alleles of 296 bp and 296+875 bp.

The enzyme β-carotene hydroxylase 1 catalyzes the transformation of β-carotene into β-cryptoxanthin. The mutations of this gene lead to slower disintegration of β-carotene (Duo et al, 2021). Molecular DNA markers, which permit to determine the allelic state of *crt*RB1 gene are *crt*RB1-3′TE, *crt*RB1-5′TE, and *crt*RB1-InDel4 (Singh et al, 2021). Among these, one of the most frequently used markers is *crt*RB1-3′TE. PCR with primers specific to *crt*RB1-3′TE yields three amplification fragments of different lengths: 296 bp, 296 + + 875 bp and 543 bp (Yan et al, 2010), with which in fact three different alleles of gene *crt*RB1 can be identified. Very favorable for the accumulation of β-carotene in mature maize grain is a chromosomal rearrangement, which leads to blocking the enzymatic transformation of β-carotene into β-cryptoxanthin and results in the occurrence of the amplification fragment of 543 bp (Yan et al, 2010; Duo et al, 2021). Among the investigated inbreds of Ukrainian selection, the ratio of genotypes with favorable (543 bp) and unfavorable (296 bp, 296 + 875 bp) allelic state of the β-carotene hydroxylase 1 gene by the *crt*RB1-3′TE marker is about 1 : 3 (Satarova et al, 2023b).

The analysis of global high- and low-carotene maize inbreds was conducted either by classical PCR markers, such as *crt*RB1-3′TE, *crt*RB1-InDel4, *lcy*E-5′TE (Duo et al, 2021; Chandrasekharan et al, 2022; Singh et al, 2023 and others), or by SNP markers, usually used for genome-wide genotyping (Azmach et al, 2018; Diepenbrock et al, 2021; Kebede et al, 2021), but the information about the relevance of these types of markers is limited. SNP analysis of Ukrainian elite inbreds was made depending on the germplasm origin (Derkach et al, 2017), but there was no previous compared SNP research of maize inbreds developed in the northern zone of the Steppe of Ukraine with different allelic states of the β-carotene hydroxylase 1 gene. Therefore, our study aimed at a SNP analysis and estimation of genetic relations of maize inbreds with the alternative allelic state of the β-carotene hydroxylase 1 gene on marker *crt*RB1-3′TE from the above-mentioned area.

MATERIALS AND METHODS

Research material consisted of 45 maize (*Zea mays* L.) inbreds with perspective for maize breeding developed at the State Enterprise the Institute of Grain Crops of NAAS of Ukraine, city Dnipro (with the index DK) and three (MS252, MS381, and PHT60), by the private breeding company, the Scientific and Production Farming Enterprise "Company Mais" (Dnipropetrovsk region). The inbreds used by us represent common types

of maize germplasm, namely Iodent, Lancaster, Reid, BSSS, and Mixed.

The inbreds under investigation were divided into two groups by the allelic state of the β-carotene hydroxylase 1 gene according to the results of our previous research (Satarova et al, 2023b). The first group, marked as $Inb_{296,296+875}$, included thirty-five inbreds, characterized by the allelic state of the *crt*RB1 gene by the *crt*RB1-3′TE marker (296 bp or 296 + 875 bp), unfavorable for the accumulation of β-carotene in the mature grain, viz: DK2, DK5, DK216, DK231, DK232, DK236/680, DK239, DK247MV, DK272, DK272/273MV, DK276, DK296, DK301, DK305, DK365, DK367, DK370, DK377, DK-517MV, DK680MV, DK742, DK744, DK777, DK959, DK2323, DK2442, DK3044, DK4173, DK4538, DKK1874, DKV3151, DKV3451, MS252, MS381and PHT60. The second group (marked as Inb_{543}), the genotypes of which had the allelic state of the *crt*RB1 gene by the *crt*RB1-3′TE marker (543 bp), favorable for the accumulation of β-carotene in the mature grain, included ten inbreds, viz: DK200, DK253/129-4, DK267, DK273, DK315, DK366M, DK366S, DK366zM, DK714/195 and DK7337.

The above-mentioned maize inbreds were analyzed for single nucleotide polymorphism of the DNA using the panel BDI-III, including 384 SNP-markers. This panel was developed by BioDiagnostics, Inc. (USA), based on Illumina VeraCode Bead Plate (www.biodiagnostics.net). SNP markers of this panel were selected as highly polymorphic (PIC > 0.25) for modern maize inbreds of the temperate zone. They are biallelic, located on all ten chromosomes, and characterized by a designability rank score >0.6 (Venkatramana et al, 2010). The SNP analysis was conducted using GoldenGate test and the system of result reading Illumina VeraCode (Chao and Lawley, 2015) based on Eurofins BioDiagnostics, (USA) using the method described in detail in (Satarova et al, 2023a).

The results in **Table 1** are presented in the form of x ± SE, where x is the average value, SE – the standard error at the significance level of 0.05. To determine the SNP markers specific for both groups of maize inbreds, we used a chi-square test (χ^2 test, Ewens and Brumberg, 2023). While using the χ^2 test, the initial group $Inb_{296,296+875}$ was considered as the initial group , and Inb_{543} as its derivative A significant disequi-

Table 1. **SNP analysis of Ukrainian maize inbreds with alternative state of molecular carotenogenesis marker crtRB1-3′TE**

Index	Group $Inb_{296,\ 296+875}$	Group Inb_{543}
Number of analyzed inbreds	35	10
Homozygosity, %	100	100
Index of genetic diversity of the inbreds, fractions of a unit		
average	0.1798 ± 0.0067a	0,1776 ± 0,0125a
min-max	0.1701–0.1944	0.1675–0.1834
range	0.0243 ± 0.0027a	0.0159 ± 0.0041b
Genetic distance between the inbreds of the same group, fractions of a unit		
average	0.4378 ± 0.0288a	0.4320 ± 0.1044a
min-max	0.0526–0.7053	0.0456–0.5263
range	0.6527 ± 0.0509a	0.4807 ± 0.1053b
Genetic distance between the inbreds of different groups, fractions of a unit		
average	0.4386 ± 0.0530	
min-max	0.1158–0.7053	
range	0.5895 ± 0.0526	

Note. Inb296, 296+875 – a group of inbreds with the state of the crtRB1-3′TE marker, unfavorable for the accumulation of β-carotene in the mature grain; Inb543 – a group of inbreds with the state of the crtRB1-3′TE marker, favorable for the accumulation of β-carotene in the mature grain. The results are presented in the form of x ± SE, where x – the average value, SE – the standard error at the significance level of 0.05. When two groups are compared, the average values with the same letters are not different at the level of significance 0.05.

Table 2. **The frequencies of seven SNP alleles of the panel BDI-III in the two groups of maize inbreds defined by their allelic state of the crtRB1 gene**

SNP marker*		Group $Inb_{296, 296+875}$	Group Inb_{543}	D	*P*
Number, alternative alleles	Chromosome number	Major allele frequency	Frequency of the allele, major in group $Inb_{296, 296+875}$		
130AG	3	G = 0.74	G = 0.10	0.64	0.0005
15AG	1	G = 0.71	G = 0.25	0.46	0.0216
60AC	2	A = 0.71	A = 0.30	0.41	0.0300
61AC	2	A = 0.71	A = 0.30	0.41	0.0300
116AG	3	A = 0.79	A = 0.40	0.39	0.0251
128AG	3	G = 0.79	G = 0.40	0.39	0.0441
129AG	3	G = 0.79	G = 0.40	0.39	0.0441
Average	–	0.75	0.31	0.44	0.0279

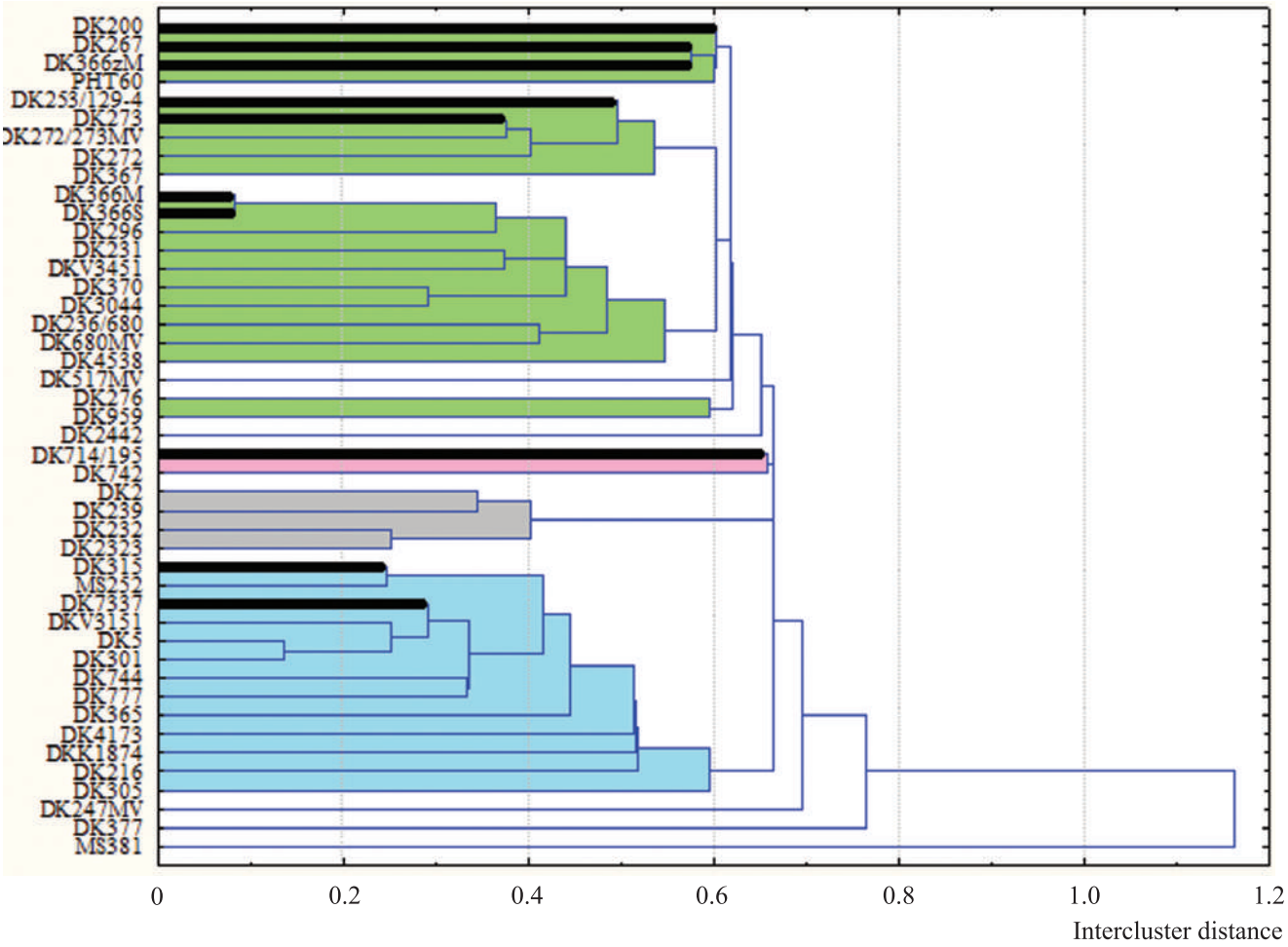
Note. * The number of the SNP marker of the panel BDI-III and its alternative alleles are presented; the names of deoxyribonucleotides are given by the shortened names of nitrogenous bases: A – adenine, T – thymine, G – guanine, C – cytosine; the chromosome number where the SNP marker is located. $Inb_{296, 296+875}$ – a group of 35 inbreds with the states of the *crt*RB1-3′TE marker, unfavorable for the accumulation of β-carotene in mature grain; Inb_{543} – a group of 10 inbreds with the state of the *crt*RB1-3′TE marker, favorable for the accumulation of β-carotene in mature grain. D – the difference between the frequency of the major allele for each SNP marker in the initial group and the frequency of the allele with the same name for the same marker in the derivative group. P – the probability by Fisher's exact test.

librium in the major allele frequencies for the initial and derivative groups by χ^2 at a significance level of 0.05 was determined; the markers were selected from $\chi^2_{observed} \geq \chi^2_{Table\ 0.05}$. The difference between the frequency of the major allele in the initial group of inbreds and the frequency of the same allele in the derivative group was determined for each marker, by which the disequilibrium of allelic frequencies was detected. This difference was indicated as "D" and presented by an absolute value. **Table 2** presents seven SNP markers with the highest D values; the relevance of the disequilibrium alleles ratio by these markers for two groups of inbreds was confirmed by Fisher's exact test at the significance level of 0.05 (Ewens and Brumberg 2023). The dendrogram was built using single linkage clustering in Statistica 7 software (StatSoft Inc., "Statistica," Data Analysis Software System, version 7, 2004).

RESULTS

The genotyping by 384 SNP markers of panel BDI-III for two groups of maize inbreds, $Inb_{296,296+875}$ (35 inbreds) and Inb_{543} (10 inbreds), demonstrated the nucleotide content of 34,560 marker sites. The homozygosity of all 45 investigated inbreds by these sites was 100 %; heterozygous SNP sites were absent. The identification of the allelic state of the investigated SNP markers was successful in 33,039 marker sites (95.6 %). Eleven markers were characterized by a frequency of missing data of > 20 % and removed from further analysis. The part of monomorphic markers was 1.8 %, and of dimorphic markers 98.2 %, respectively. The average frequency of the minor allele (MAF) was at a level of 0.3040 ± 0.0071 while MAF > 0.2 was noted for the prevailing majority (76.4 %) of dimorphic markers. The average polymorphism information content of the used markers in the investigated inbreds demonstrated a high PIC level of 0.3064 under the potential range of values 0–0.3750. The average shift in the gene diversity of markers was 0.3898 ± 0.0075 under the potential range of values 0–0.5000. Thus, the values of the key indices of single nucleotide polymorphism in the investigated inbreds for the used set of SNP markers were within the acceptable range, which enabled direct analysis of the obtained data.

The SNP comparison of two groups of maize inbreds, alternative on the allelic state of the *crt*RB1 gene, demonstrates the specificities of each group (Table 1). For instance, the average genetic diversity of the inbreds in the group $Inb_{296, 296+875}$ was 0.1798, and lower for Inb_{543}, 0.1776, of a considerably smaller range and transferred to the area of lower values. The average genetic SNP distance (pairwise genetic distance) between



The dendrogram of genetic SNP relations of 45 maize inbreds, by single linkage clustering. The inbreds of Inb_{543} group (with the state of the β-carotene hydroxylase 1 gene by the *crt*RB1-3′TE marker, favorable for the accumulation of β-carotene) are marked with bold lines; the light blue lines are referred to the group $Inb_{296,\ 296+875}$ and have the state of this gene by this marker, unfavorable for the accumulation of β-carotene.

the inbreds of group $Inb_{296,\ 296+875}$ was 0.4378. Between the inbreds of the group Inb_{543}, it was lower, 0.4320, with a considerably smaller range, and also transferred to the area of lower values as compared to the initial group. The genetic SNP distances between the inbreds of groups $Inb_{296,\ 296+875}$ and Inb_{543} were within limits 0.1158–0.7053. Thus, the minimum intergroup SNP distance was 2–3 times higher than the minimum values of genetic distances inside the groups. A higher maximum intergroup SNP distance was also noted as compared to the maximum SNP distance between the inbreds of group Inb_{543}. No significant difference was found between the average values of intragroup and intergroup SNP distances.

The disequilibrium in the frequency of the allele, major in the initial group $Inb_{296,\ 296+875}$, was registered for 259 SNP markers (69.4 %); among these, a significant impairment at the significance level of 0.05 was found for 45 SNPs (12.1 %). Therefore, there is some statistical relationship between the allelic state of β-carotene hydroxylase 1 gene by the *crt*RB1-3′TE marker and some SNP markers of the panel BDI-III. To determine the most specific markers, we selected 7 SNP markers, characterized by the highest D values, i.e. the difference between the frequency of the major allele in the initial group and the frequency of the same allele in the derivative group of inbreds according to the Fisher's exact test (Table 2).

The selected markers were located in the non-genic regions of chromosomes 1–3. The major alleles of the markers from the initial group $Inb_{296,296+875}$ were minor for the derivative group Inb_{543}, while the alternative deoxyribonucleotides of each bi-allelic marker were major alleles for Inb_{543}. For the initial group of inbreds, the frequencies of the major alleles were in the range of 0.71–0.79, and for the derivative group, the frequencies

of the same alleles were in the range of 0.10–0.40. Thus, the specific set of SNP alleles, for the group inbreds Inb_{543}, in the pairwise comparison with $Inb_{296,296+875}$ included: BDI-III-130A, BDI-III-15A, BDI-III-60C, BDI-III-61C, BDI-III-116G, BDI-III-128A and BDI-III-129A. The specific set for group $Inb_{296,\ 296+875}$, was: BDI-III-130G, BDI-III-15G, BDI-III-60A, BDI-III-61A, BDI-III-116A, BDI-III-128G and BDI-III-129G.

A dendrogram of genetic SNP relations was built based on SNP distances between the inbreds of the initial and the derivative group (**Figure**). The inbreds of Inb_{543} did not form one definite cluster; they were scattered among five of the 7 clusters of the unfavorable group of inbreds of $Inb_{296,296+875}$, with one to three inbreds of the favorable group present per cluster As seen, among the inbreds represented in group Inb_{543}, some are closer to each other, and some are more distant.

DISCUSSION

The distribution of maize inbreds which carry favorable alleles of carotenoid pathway genes and the relevant variants of molecular markers in a breeding pool in different soil and climatic zones, breeding programs and types of germplasm is an important challenge. The understanding of the patterns of this distribution would allow the prediction of favorable alleles and the content of carotenoids in breeding material. However, the investigations of maize inbreds from the sub-Saharan tropical zone in Africa, (Maazou et al, 2023, Sserumaga et al. 2019, Kondwakwenda et al, 2020), from the Romanian breeding programs (Băcilă et al, 2022), southern European inbreds (Šimić et al, 2023), Serbian inbreds (Djalovic et al, 2024), Ukrainian inbreds (Satarova et al, 2023b) and others did not determine clear regularities in spreading favorable alleles of carotenoid pathway genes. The clustering of the inbreds, conducted in most studies, demonstrated the distribution of favorable alleles of the genes of carotenogenesis among different clusters, which made up the basis for specific breeding programs. Maazou et al (2023) found that the inbreds referred to one heterotic group by the content of vitamin A predecessors and by grain productivity were distributed among three clusters. The clustering of the maize inbreds, which were adopted to the northern zone of Steppe of Ukraine, investigated by us, demonstrated specific grouping into clusters by SNP markers, but the alleles of β-carotene hydroxylase 1 gene were randomly distributed. The intragroup and intergroup genetic SNP distances did not differ considerably, which also suggests a random distribution of maize inbreds with the favorable allele of crtRB1-3´TE-543 bp among the inbred pool of the northern Steppe of Ukraine.

A relevant question, from both a practical and theoretical point of view, is how to apply the information about single-nucleotide substitutions along genomic DNA for marking valuable characters. It was found that some single nucleotide replacements, revealed in genome-wide genotyping, have a statistical association with the allelic state of carotenoid pathway genes and the content of carotenoids in maize grain (Diepenbrock et al, 2021). In some studies, along with classic markers of the allelic state of the β-carotene hydroxylase 1 and lycopene-ε-cyclase genes, namely *crt*RB1-3´TE, *crt*RB1-5´TE, *crt*RB1-InDel14, *lcy*E-3´INDL, *lcy*E-5´INDL, *lcy*E-SNP216, single nucleotide substitutionsin these genes were significant for the same plant (Maazou et al, 2023; Sserumaga et al, 2019; Kondwakwenda et al, 2020; LaPorte et al, 2023; Azmach et al, 2018; Kebede et al, 2021). LaPorte et al (2023) concluded that when genome-wide markers were used, the accuracy of genomic prediction for the carotenoid content in maize grain was higher than when only the markers proximal to two carotenoid-related genes were used. A whole-genome sequencing association study based on 109,937 SNPs (1658 typed) and 130 tropical inbreds of yellow maize (Azmach et al, 2018) detected 13 SNPs, located on chromosome 10, which were related to the content of carotenoids of the ß-branch and such derivative traits as the content of β-carotene, β-cryptoxanthin, their ratio and/or the ratio of β-carotene and zeaxanthin. Another 10 SNPs on chromosome 8 had a considerable impact on the ratio between the content of carotenoids of α- and ß-branches. One SNP from chromosome 5, associated with β-carotene, was also found. Kebede et al (2021) used alleles, favorable for the accumulation of β-carotene, for such specific SNP markers of CIMMYT, Mexico developed panel *crt*RB1-KASP, as snpZM0013, snpZM0014, snpZM0015, snpZM0017, snpZM0018, and snpZM0019 in two maize synthetics. Only marker snpZM0015 was present in the gene; the other six were either higher or lower than gene *crt*RB1. In another study a SNP marker was found as a C/T transition in the first intron of the gene of lycopene-ε-cyclase, by which the investigated inbreds were clearly divided into high and low-carotene containing ones (Maazou et al, 2021). These are examples of correlation of SNP substitutions in non-coding regions for the carotene content. In our study, we found SNP markers of the panel BDI-III, the allelic state of which correlated with the allelic state of the functional marker *crt*RB1-3´TE where the major allele frequen-

cy for a SNP marker changed in average from 0.75 in $Inb_{296,\ 296+875}$ group to 0.31 in Inb_{543} group and from 0.74 in $Inb_{296,\ 296+875}$ to 0.10 in Inb_{543}. The SNP markers identified by us and presented in Table 1 are localized in the non-genic regions of chromosomes 1–3, although the *crt*RB1 gene is located on chromosome 10 (Vallabhaneni et al, 2009).

Summing up the above-presented data, one may assume that the association between the allelic state of the genes *crt*RB1, *lcy* E, the content of ß-carotenoids and single nucleotide substitutions to be localized in non-coding regions of these genes, outside these genes on the same chromosomes or even in non-coding regions on the other chromosomes). The exact nature of such association requires further study and is important for the development of the theoretical basis of marker assisted selection.

CONCLUSIONS

The statistical relationships between the allelic state of the β-carotene hydroxylase 1 gene and markers of single nucleotide polymorphism for maize were established. The following SNP markers for maize inbreds with favorable allelic state of the β-carotene hydroxylase 1 gene by the molecular marker *crt*RB1-3′TE were identified: BDI-III-130A, BDI-III-15A, BDI-III-60C, BDI-III-61C, BDI-III-116G, BDI-III-128A, BDI-III-129A. These SNP markers, especially marker BDI-III-130, are recommended to be used in maize breeding programs for the increased content of β-carotene in mature grain. The SNP analysis of genetic interrelations between inbreds with alternative state of the *crt*RB1-3′TE marker demonstrated their random localization in the investigated pool of maize inbreds developed in the northern Steppe of Ukraine.

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SNP аналіз українських ліній кукурудзи з альтернативним станом молекулярного маркера каротиногенезу *crt*RB1-3′TE

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Мета. SNP аналіз та оцінка генетичних взаємовідносин у ліній кукурудзи із альтернативним станом гена β-каротингідроксилази 1 (*crt*RB1) за маркером *crt*RB1-3′TE. **Методи.** Метод однонуклеотидного поліморфізму ДНК з використанням панелі BDI-III з 384 SNP маркерами, статистичні методи. **Результати.** Проведено SNP аналіз 45 ліній кукурудзи, створених у північному Степу України, залежно від алельного стану гена β-каротингідроксилази 1 за молекулярним маркером *crt*RB1-3′TE. Частка диморфних маркерів становила 98,2 %, середня частота мінорного алеля – 0,3040, середній індекс інформативності маркерів (PIC) – 0,3064, середній показник зсуву генного різноманіття маркерів – 0,3898. Істотної різниці між генетичними SNP дистанціями як в середині груп ліній зі сприятливими/несприятливими алелями за маркером *crt*RB1-3′TE, так і між цими групами не встановлено. Алелі SNP маркерів BDI-III-130A, BDI-III-15A, BDI-III-60Ц, BDI-III-61Ц, BDI-III-116Г, BDI-III-128A, BDI-III-129A визначено як такі, що найчастіше зустрічаються у ліній – носіїв сприятливої алелі 543 п.н. гена *crt*RB1 за марке-

ром *crt*RB1-3′TE. За SNP дистанціями побудовано дендрограму генетичних взаємовідносин між лініями кукурудзи з різним станом маркера *crt*RB1-3′TE. **Висновки**. Встановлено існування взаємозв'язку між алельним станом гена β-каротингідроксилази 1 і маркерами однонуклеотидного поліморфізму ДНК для досліджених ліній кукурудзи. Визначено алельний стан SNP маркерів, який корелює зі сприятливим алельним станом гена β-каротингідроксилази 1 за молекулярним маркером *crt*RB1-3′TE. Показано випадковий характер розподілу алелів цього гена серед ліній кукурудзи, створених в північному Степу України.

Ключові слова: *Zea mays* L., β-каротингідроксилаза 1, однонуклеотидний поліморфізм, молекулярні маркери, каротиноїди.

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Рукописи надсилаються на **конфіденційне** рецензування спеціалістам відповідної галузі.

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