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POLYMORPHISM OF *SCD1* GENE AND ITS ASSOCIATIONS WITH DAIRY PERFORMANCE IN UKRAINIAN RED-AND-MOTLEY CATTLE AND THEIR CROSSBREEDS

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Aim. To investigate the genetic structure of populations of the Ukrainian Red-and-White Dairy cattle (URW) and its crossbreeds based on SNP g.10153G>A at *SCD1* locus and to evaluate the association of this polymorphism with traits of dairy performance and the fat and protein content in milk. **Methods.** The genetic structure of two groups of cows (purebred URW, $n=43$; URM × M crossbreeds, $n=41$) was studied by g.10153G>A polymorphism of *SCD1* gene using the PCR-RFLP method. The performance was assessed using the indicators from the first completed lactation. The correspondence of the distribution of quantitative traits to the normal law was tested using the Shapiro-Wilk test. For normally distributed traits (milk yield), one-way analysis of variance (ANOVA) with Tukey's post-hoc test was used; for non-normally distributed traits (fat and protein content), the Kruskal-Wallis test with Dunn's post-hoc test adjusted for Bonferroni correction was used. **Results.** Certain intergroup differences in allele distribution were observed: in purebred animals, a slight predominance of allele G was observed (0.535 versus 0.465 for allele A), whereas in crossbreeds, a relative increase in the frequency of allele A was noted (0.524 versus 0.476 for allele G). In the crossbreed group, an increased frequency of the heterozygous AG genotype (0.512) was also observed. For milk yield indicators, opposite genotype-associated trends were identified between groups: in purebred animals, the highest mean values were observed in homozygous AA individuals, whereas in crossbreed animals, they were observed in heterozygous AG individuals; however, within individual groups, no statistically significant differences between genotypes were found ($p>0.05$). No statistically significant associations with genotype were found for fat and protein content ($p>0.05$). **Conclusions.** The results obtained indicate the presence of certain genetic differentiation between the study groups at the *SCD1* locus and a possible dependence of the manifestations of the associations on the genetic background of the population. At the same time, no statistically confirmed effects of polymorphism on milk yield, fat content, or protein content were found. Further studies using larger sample sizes are needed to clarify the nature of the identified trends.

Keywords: cattle, *SCD1* gene, PCR-RFLP, dairy performance, milk fat content, marker-assisted selection (MAS).

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INTRODUCTION

Single-nucleotide polymorphisms (SNPs) are currently the most representative group of molecular markers in the field of molecular genetics. Due to their high distribution density in the genome, stable inheritance, and reproducibility of analysis, SNPs serve as a key tool for marker-assisted selection (MAS). This allows for the highly accurate assessment of correlations between specific loci and economically important traits in farm animals, particularly cattle.

In the context of dairy cattle breeding, genes that modulate lipid metabolism are of particular scientific interest. The fatty acid composition of milk, along with milk yield and protein content, determines the overall biological and consumer value of dairy products. Genetic determinants associated with lipid metabolism should be considered as integral factors influencing not only the fat content of milk but also a whole complex of functional traits of the organism related to energy balance and the adaptive potential of animals (Wathes et al., 2012).

The central regulator of the lipid profile in ruminants is the enzyme stearoyl-CoA desaturase (SCD1), also known as Delta 9-desaturase (di Martino et al., 2015). This membrane-bound protein is localized in the endoplasmic reticulum and acts as a limiting factor (a "bottleneck") in the *de novo* biosynthesis of monounsaturated fatty acids (MUFA). SCD catalyzes the insertion of a double bond in the *cis*-configuration between the 9th and 10th carbon atoms in the chains of saturated fatty acids. Typical substrates of the enzyme are stearic (C18:0) and palmitic (C16:0) acids, which transform into oleic (C18:1) and palmitoleic (C16:1) acids, respectively. In addition, SCD1 activity in the secretory epithelium of the mammary gland is critical for the synthesis of rumenic acid — the major isomer of conjugated linoleic acid (CLA) — from vaccenic acid, which directly influences the dietary properties of milk (Taniguchi et al., 2004; Li et al., 2020; Bernard et al., 2013; Livingstone et al., 2012).

SCD1 gene in cattle is located on chromosome 26 (BTA26) (Lengi, Corl, 2007). Its structure spans approximately 17 kbp and includes six exons and five introns, encoding a polypeptide chain of 359 amino acid residues (Campbell et al., 2001; Criado-Mesas et al., 2020). Despite its initial identification in rodent liver, subsequent studies have confirmed the widespread tissue expression of this gene in ruminants. The *SCD1* transcription profile exhibits a distinct tissue-specific pattern: maximum expression is observed in adipose tissue and the mammary gland during lactation, whereas mRNA levels are significantly lower in the heart, skeletal muscle, and nervous tissue (Li et al., 2020). This localization confirms the strategic importance of the gene in shaping the fatty acid composition of exosecretions and stored fat.

The biochemical mechanism of SCD1 action is based on an aerobic desaturation process that requires the presence of molecular oxygen (O_2), reduced NADPH, and the involvement of the microsomal electron transport chain, which includes cytochrome b5 and NADH-cytochrome b5 reductase. By regulating the ratio between saturated and unsaturated fatty acids, SCD1 influences the physicochemical properties of fat, particularly its melting point and the organoleptic characteristics of the final product.

The functional variability of the *SCD1* locus is due to a significant level of genetic polymorphism. A number of SNPs associated with the variability of productive traits were identified within the gene structure (promoter region and exon-intron junctions). Sequencing identified six key substitutions, three of which are located in the 5th exon (g.10153G>A, g.10213T>C, and g.10329C>T). The most extensively studied polymorphism is g.10329C>T, which results in the A293V aminoacid substitution and correlates significantly with the fatty acid desaturation index of milk and carcass tissues (Kulig et al., 2013; Taniguchi et al., 2004; Kgwatalala et al., 2009).

At the same time, the data on the influence of other SNPs on dairy performance traits remain insufficient. In particular, the functional role of SNP g.10153G>A in shaping the phenotype of dairy cattle remains controversial. There are theoretical assumptions that this substitution may modulate the stability of SCD1 transcripts, altering the intensity of enzyme synthesis and, consequently, the lipid profile of milk. However, the direct influence of this marker on such selection traits as milk yield, fat content, and protein content requires further verification at the population level. In the study by Kulig et al. (2016), no significant associations were found between genotypes and breeding values for milk yield and protein. However, it was found that cows of the GA genotype had the highest breeding values for these traits.

Despite a substantial amount of global data on the role of *SCD1* gene in modulating the lipid profile of milk, this locus remains largely overlooked in domestic breeding science, and the data on its impact

on the productive traits of local cattle populations are virtually nonexistent. This necessitates research to establish associations between the g.10153G>A polymorphism and dairy performance traits in Ukrainian breeds and their crossbreeds, which will lay the scientific foundation for the implementation of marker-associated selection (MAS) in Ukraine and the targeted improvement of the quality characteristics of raw milk.

The aim of this study is to determine the specificities of the genetic structure of the population of Ukrainian Red-and-White Dairy caws and their crossbreeds with Montbeliarde cattle at the *g.10153G>A* locus of *SCD1* gene, as well as to determine the associations between this polymorphism and dairy performance traits to justify its use as a breeding marker.

MATERIALS AND METHODS

The experimental part of the study was conducted at the Genetics Laboratory of the M.V. Zubets Institute of Animal Breeding and Genetics of the NAAS and the production facilities of the SE DG "Nyva" of the M.V. Zubets Institute of Animal Breeding and Genetics of the NAAS. The study population consisted of a herd of Ukrainian Red-and-White Dairy cows. To conduct a scientific and practical experiment based on the principle of control groups, two representative samples of animals were formed based on the results of their first completed lactation. The first group consisted of purebred cows of the Ukrainian Red-and-White Dairy breed (URW, $n=43$); the second group — of crossbred animals ($n=41$) obtained by crossing URW cows with Montbeliarde bulls (URE × M). All animals were kept under identical feeding and housing conditions, which minimized the influence of paratypic factors on the expression of productive traits.

For molecular genetic testing, whole blood samples were collected from the jugular vein into vacuum tubes containing an anticoagulant (EDTA). Genomic DNA was isolated using a sorbent-based method with the commercial Quick-DNA Miniprep Kit (Zymo Research, USA), following the manufacturer's protocol. The verification of the integrity and quality characteristics of the extracted DNA was performed by horizontal electrophoresis in a 1% agarose gel (current parameters: 80 mA, duration: 60 min). The concentration and purity of nucleic acids were additionally verified by spectrophotometry.

The identification of g.10153G>A single-nucleotide polymorphism in exon 5 of the *SCD1* gene was performed using the polymerase chain reaction followed by restriction fragment length analysis (PCR-RFLP). The amplification of the specific gene fragment was performed using oligonucleotide primers designed by Taniguchi et al. (2004):

F: 5′-GTG TCC TGT TGT TGT GCT TCA TCC TGC C-3′;

R: 5′-AAT ATT CTC TCG GGG GTT GAT GGT CTT G-3′ (Taniguchi et al., 2004)

The g.10153G>A single-nucleotide polymorphism in exon 5 of *SCD1* gene was identified by amplifying a specific fragment. **Figure 1** shows the scheme of localization of the investigated SNP and the hybridization sites of primers.

The reaction was performed in a 25 µL volume containing Master Mix, 1.25 µL of each primer (final concentration 0.5 µM), and 2.0 µL of template DNA (total mass approximately 100 ng). The amplification temperature-time profile included: initial denaturation (95°C, 3 min); 30 cycles: denaturation (94°C, 30 s), primer annealing (66°C, 50 s), elongation (72°C, 30 s); final synthesis (72°C, 8 min). The hydrolysis

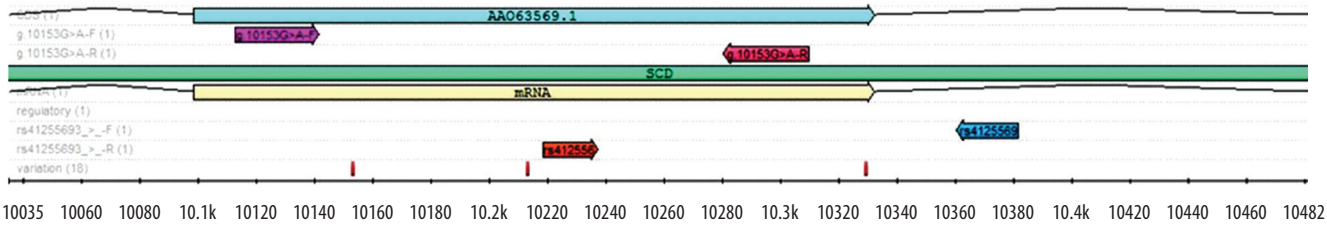

Fig. 1. The scheme of localization of SNP g.10153G>A and the hybridization sites of primers in the coding sequence (CDS) of *SCD1* gene: The top tracks show the positions of the forward and reverse primers relative to exon 5; the scale indicates the coordinates of the genomic sequence (bp); the red markers at the bottom represent the sites of polymorphic variations, including the locus of interest

of the resulting amplicons was performed using the specific restriction endonuclease *NcoI*. The restriction products were fractionated in a 3% agarose gel with the addition of ethidium bromide, followed by visualization under ultraviolet light using a gel documentation system.

The evaluation of dairy performance of the experimental animals was based on data from zootechnical records. The main indicators were as follows: milk yield (kg), fat content (%), and protein content (%) in milk over the first 305 days of completed lactation.

The statistical analysis of the obtained data was performed using the methods of variational statistics and population genetics. Allele and genotype frequencies, as well as the observed and expected genotype distributions were calculated; the correspondence of the population to the genetic equilibrium was tested according to the Hardy-Weinberg law using the χ^2 criterion. The genetic diversity was assessed using the effective number of alleles (Ne), expected (He) and observed (Ho) heterozygosity, and the polymorphism information content (PIC).

Methods of statistical data analysis. The conformity of the distribution of quantitative traits to the normal distribution was tested using the Shapiro-Wilk test. For traits in which normality of distribution was confirmed (milk yield), the intergroup comparisons were performed using the analysis of variance (ANOVA) followed by Tukey's HSD post-hoc test. The results for these traits are presented as the mean and standard error (M ± m).

For traits in which a significant deviation from the normal distribution was established (fat and protein content), the nonparametric Kruskal-Wallis H-test was used, along with a post-hoc Dunn's test and the Bonferroni correction to minimize type I errors in multiple comparisons. The results for these traits are presented as medians and quartiles (Q25–Q75).

RESULTS OF THE STUDIES

Molecular genetic identification of g.10153G>A polymorphism. The genotyping of the study population at the *SCD1* locus (g.10153G>A) was performed using the PCR-RFLP method. The specific amplification of the target region of exon 5 yielded amplicons of 204 bp. The hydrolysis of the PCR products with the restriction endonuclease *NcoI* identified two allelic variants: allele G, characterized by the absence of a restriction site (uncleaved 204-bp fragment), and allele A, in the presence of which the amplicon is cleaved into two fragments of 165 bp and 39 bp.

The electrophoretic visualization allowed for the differentiation of three genotypes: homozygous AA (165 bp and 39 bp fragments), homozygous GG (204 bp), and heterozygous AG, characterized by the presence of all three fragments (204, 165, and 39 bp) **(Fig. 2)**.

The genetic structure of the studied populations at this locus is presented in **Table 1**.

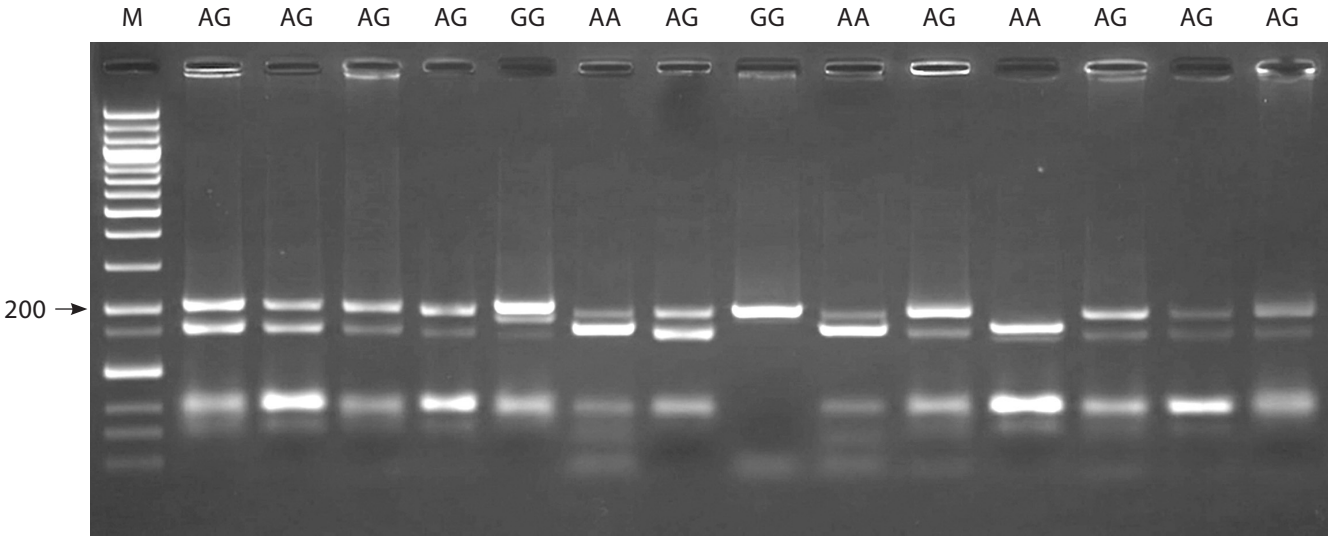

Fig. 2. The electrophoregram of genotyping results for cows at the SCD1 locus (g.10153G>A): M — molecular weight marker (100 bp DNA Ladder); AA — homozygous genotype (165 bp and 39 bp fragments); GG — homozygous genotype (uncleaved 204 bp amplicon); AG — heterozygous genotype (204 bp, 165 bp, and 39 bp fragments)

Table 1. The genetic and population characteristics of the studied groups of animals at the *SCD1* locus (g.10153G>A)

Breed	*n*	Frequencies of genotypes			Frequency of alleles		Genetic parameters				Deviation from Hardy-Weinberg equation	
		AA	AG	GG	A	G	He/Ho	Ne	PIC	Fis	χ^2	*p*-value
URW	43	0.279	0.372	0.349	0.465	0.535	0.499/0.372	1.990	0.374	0.253	2.740	0.098
URW × M	41	0.268	0.512	0.220	0.524	0.476	0.499/0.512	1.996	0.375	–0.026	0.030	0.864

Note: Ho — observed heterozygosity; He — expected heterozygosity; Ne — number of effective alleles; PIC — polymorphic information content; Fis — fixation index; χ^2 — Hardy-Weinberg criterion.

The analysis of the allele pool indicates the presence of specific intergroup differences in frequency distribution. In the group of purebred animals of the Ukrainian Red-and-White Dairy (URW) breed, a slight prevalence of allele G (0.535) over allele A (0.465) was observed. In the genotype structure of this group, heterozygotes GA (0.372) accounted for the largest proportion, although the proportion of homozygotes GG was also high (0.349).

For crossbred animals (URW × M), the opposite trend was observed: allele A was predominant, with a frequency of 0.524 compared to 0.465 in purebred counterparts. A distinctive feature of the genetic structure of the crossbred group is the high prevalence of heterozygous AG genotypes (0.512), whose frequency was nearly twice that of homozygous AA (0.268) and significantly exceeded that of GG (0.220). This distribution may result from a shift in the genetic balance toward heterozygosity due to the crossbreeding effect.

The assessment of the conformity of the actual genotype distribution to the theoretically expected distribution according to the Hardy-Weinberg law confirmed that both studied samples were in a state of genetic equilibrium ($p > 0.05$). At the same time, the URW group showed a significantly higher χ^2 value (2.74) compared to crossbred animals (0.030). Although the obtained value did not exceed the critical threshold ($\chi^2 = 3.84$ for df=1), it demonstrated a clear tendency toward a deficit of heterozygous individuals in the purebred population: the actual number of animals with the AG genotype was 16, while the theoretically expected value was 21.40. In the hybrid group (URW × M), the χ^2 value approached zero, indicating a high level of genetic consolidation and an almost perfect match between observed frequencies and theoretical expectations.

The expected (He) and observed (Ho) heterozygosity indices in both study groups ranged from 0.372 to 0.512. This indicates the maintenance of a consistently high level of genetic polymorphism at the *SCD1* locus, which is a favorable condition for further breeding work. The high saturation of populations with both alleles is also confirmed by the effective number of alleles (Ne), which in both cases approaches its theoretical maximum (1.990–1.996), indicating the absence of locus monomorphism.

The value of the polymorphic information content (PIC = 0.374–0.375) allows for classifying *SCD1* locus as a moderately informative genetic marker. This justifies its use for monitoring the genetic potential of animals, although its resolution is somewhat lower compared to highly polymorphic microsatellite loci.

The analysis of the fixation index (Fis) deserves special attention, as its values in the studied groups show a mixed pattern. In purebred URW animals, the positive value of the Fis index (Fis = 0.253) confirms the observed deficit of heterozygotes, which may be the result of intense breeding pressure or limited use of bulls within the herd. On the contrary, in crossbred animals, the negative value of the fixation index (Fis = -0.026) indicates a slight excess of heterozygotes, which is a characteristic feature of biological heterosis when crossing different gene pools.

Further analysis was aimed at establishing a relationship between *SCD1* gene polymorphism and the quantitative and qualitative indicators of dairy performance in the experimental animals.

The results for the economic traits of cows of different genotypes are summarized in **Table 2**.

The effect of the SCD1 locus (g.10153G>A) on milk fat content. The analysis of fat content did not

Table 2. The dairy performance in cows depending on the genotype regarding *SCD1* gene (g.10153G>A)

Breed	Genotype	*n*	Milk yield, kg	Fat content, % Median (Q25–Q75)	Protein content, % Median (Q25–Q75)
URW	AA	12	6762.0 ± 108.51	3.71 (3.69–3.80)	3.37 (3.34–3.40)
	AG	16	6476.6 ± 187.40	3.75 (3.72–3.80)	3.36 (3.31–3.42)
	GG	15	6329.6 ± 201.30	3.68 (3.66–3.72)	3.35 (3.31–3.38)
URW × M	AA	11	6711.0 ± 144.80	3.70 (3.69–3.72)	3.35 (3.34–3.37)
	AG	21	6931.5 ± 91.48	3.70 (3.68–3.80)	3.35 (3.33–3.36)
	GG	9	6875.7 ± 171.90	3.71 (3.69–3.80)	3.34 (3.32–3.38)

Note: For traits with a confirmed normal distribution (milk yield), the results are presented as the mean and standard error (M ± m); statistical analysis was performed using ANOVA with Tukey's post-hoc test. For traits deviating from a normal distribution (fat and protein content), the results are presented as the median and quartiles (Q25–Q75); the statistical analysis was performed using the Kruskal-Wallis test with a Dunn post-hoc test and Bonferroni correction. A difference was considered statistically significant at a probability level of $p < 0.05$.

reveal statistically significant differences between genotypes ($p > 0.05$).

At the same time, a trend toward higher fat content was observed in heterozygous AG URW animals compared to homozygous GG individuals. From a physiological and biochemical perspective, the observed effect may be associated with changes in the activity of the enzyme stearoyl-CoA desaturase, which are caused by different allelic variants of the gene. This, in turn, could potentially influence the intensity of fatty acid metabolism in heterozygotes. However, the mechanisms underlying this phenomenon require further investigation.

The effect of the SCD1 locus (g.10153G>A) on milk yield. According to the results of a two-way analysis of variance (ANOVA), no statistically significant effect of genotype or breed on milk yield was found ($p > 0.05$). At the same time, a tendency toward a "genotype × breed" interaction was detected ($p < 0.1$). In particular, in purebred URW cows, a decrease in milk yield was observed from the AA to the GG genotype, which may indicate an additive effect of allele A, whereas in crossbred animals (URW × M), the highest values of the indicator were observed in AG heterozygotes, indicating a possible change in the nature of the genetic effect depending on the genetic background (breed).

The effect of the SCD1 locus (g.10153G>A) on protein content. Protein content in milk remained relatively stable (within the range of 3.35–3.41%) across the studied *SCD1* locus genotypes; no statistically significant differences were found ($p > 0.05$). This indicates the absence of an association between this genetic marker and milk protein content in the studied sample.

At the same time, no convincing evidence of a negative effect of allele A on protein content was found, suggesting its neutral effect regarding this trait within the scope of the study.

To assess the breeding value of allele A, further studies on larger samples are necessary, as the associative effects regarding other dairy performance traits remain inconsistent or not statistically confirmed.

DISCUSSION

In the studied populations of URW and crossbreeds, the frequency of allele A (0.46–0.52) is slightly lower than or comparable to that observed in leading European dairy breeds, where it often reaches 0.56–0.66 (Moioli et al., 2007; Macciotta et al., 2011). The increased frequency of allele A in highly intensively bred dairy breeds is traditionally associated with selection for dairy performance traits and milk quality composition.

The literature shows that *SCD1* gene polymorphism may be associated with variations in milk fatty acid composition and the desaturation index (Schennink et al., 2008; Orrù et al., 2011, Rezamand et al., 2014); however, the effects on total fat content are inconsistent and depend on the population and housing conditions. Similar results were obtained by Li et al. (2020), who showed that the influence of *SCD1* gene variants can modulate the fatty acid profile not necessarily altering the total fat content.

In our study, no statistically significant differences in fat content were found between genotypes ($p > 0.05$). At the same time, in some comparisons, a slight tendency toward an increase in this indicator was observed in AG heterozygotes, which may indicate possible genotype-associated variability; however, this requires confirmation in a larger sample.

Certain (statistically insignificant) differences in milk yield were observed between genotypes, with the nature of the association depending on the genetic background of the population. In the purebred URM group, higher average milk yields were observed in animals with the AA genotype compared to those with the GG genotype, which may correspond to an additive effect. In the crossbred group (URW × M), the highest milk yield values were observed in AG heterozygotes, which may indicate a change in the nature of the genotype-associated effect depending on the genetic background and a potential "genotype × breed" interaction. At the same time, such conclusions require further confirmation using specialized interaction models.

Protein content remained stable regardless of genotype ($p > 0.05$), indicating no association between the *SCD1* polymorphism and milk protein content in the study sample. This is consistent with the functional specificity of the enzyme, which is primarily involved in lipid metabolism.

Thus, the results obtained indicate the variability of *SCD1* genotype-phenotype associations depending on the genetic background of the population and the type of trait. At the same time, the most consistently significant effect was observed for milk yield, whereas associations for fat and protein content were not statistically significant.

CONCLUSIONS

The studied populations of Ukrainian Red-and-White Dairy cattle and their crossbreeds are characterized by genetic diversity at the *SCD1* locus (g.10153G>A). No statistically significant differences between genotypes were found in terms of milk yield ($p > 0.05$); however, opposing population trends in the distribution of mean values were observed. No statistically significant effect of genotype on fat and protein content was detected either ($p > 0.05$).

The results indicate that in the studied sample, allelic variants of the *SCD1* gene do not have a stable associative effect on the main traits of dairy performance. Further research should focus on increasing the sample size and analyzing "genotype × breed" interactions to clarify possible population-specific effects.

Adherence to ethical principles. All the studies were conducted in accordance with the requirements of the Council Directive 98/58/EU dated July 20, 1998, regarding the protection of animals, kept for farming, "General ethical principles of experiments involving animals", approved by the First National Bioethics Congress (Kyiv, September 20, 2001) and the Law of Ukraine "On Protection of Animals from Cruelty", 2021.

Statement about the conflict of interests. Being the corresponding author, I declare the absence of any conflicts of interests between the co-authors of this article.

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ПОЛІМОРФІЗМ ГЕНА *SCD1* ТА ЙОГО АСОЦІАЦІЇ З МОЛОЧНОЮ ПРОДУКТИВНІСТЮ УКРАЇНСЬКОЇ ЧЕРВОНО-РЯБОЇ ХУДОБИ ТА ЇЇ ПОМІСЕЙ

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Мета. Дослідити генетичну структуру популяцій української червоно-рябої молочної породи та її помісей за SNP g.10153G>A локусу *SCD1* та оцінити асоціативний зв'язок даного поліморфізму з ознаками молочної продуктивності та масовою часткою жиру і білка в молоці. **Методи.** Генетичну структуру двох груп корів (чистопородні УЧеРМ, $n = 43$; помісі УЧеРМ × М, $n = 41$) досліджували за поліморфізмом g.10153G>A гена *SCD1* методом ПЛР-ПДРФ. Оцінку продуктивності проводили за показниками першої завершеної лактації. Відповідність розподілу кількісних ознак нормальному закону перевіряли за критерієм Шапіро-Вілка. Для ознак із нормальним розподілом (надої) застосовували однофакторний дисперсійний аналіз (ANOVA) з post-hoc тестом Тьюкі, для ознак із відхиленням від нормальності (масова частка жиру та білка) — критерій Краскела–Уолліса з post-hoc тестом Данна з поправкою Бонферроні. **Результати.** Встановлено певні міжгрупові відмінності у розподілі алелів: у чистопородних тварин спостерігалося незначне переважання алеля G (0,535 проти 0,465 для алеля A), тоді як у помісей відзначено відносне зростання частоти алеля A (0,524

проти 0,476 для алеля G). У помісній групі також спостерігалася підвищена частота гетерозиготного генотипу AG (0,512). Для показників надою встановлено різноспрямовані генотип-асоційовані тенденції між групами: у чистопородних тварин найвищі середні значення відзначено у гомозигот AA, тоді як у помісних — у гетерозигот AG, однак у межах окремих груп статистично значущих відмінностей між генотипами не встановлено ($p > 0,05$). Для масової частки жиру та білка статистично значущих асоціацій із генотипом не виявлено ($p > 0,05$). **Висновки.** Отримані результати свідчать про наявність певної генетичної диференціації між досліджуваними групами за локусом *SCD1* та можливу залежність прояву асоціацій від генетичного фону популяції. Водночас статистично підтверджених ефектів поліморфізму на показники надою, жирності та білковомолочності не встановлено. Для уточнення характеру виявлених тенденцій необхідні подальші дослідження на розширених вибірках.

Ключові слова: велика рогата худоба, ген *SCD1*, ПЛР-ПДРФ, молочна продуктивність, жирномолочність, маркер-асоційована селекція (MAS).