BIOLOGIJA. 2014. Vol. 60. No. 4. P. 175–182


# Differentiation between Lithuanian White-Backed and Lithuanian Black-and-White (old genotype) cattle using blood groups

**Edita Kristina Kaurynienė*,**

**Rūta Šveistienė,**

**Virginija Jatkauskienė**

*Institute of Animal Sciences,*
*Lithuanian University of Health Sciences,*
*R. Žebenkos St. 12, LT-82317 Baisogala,*
*Radviliškis District, Lithuania*

The aim of the study was to carry out a genetic analysis of Lithuanian White-Backed (LWB) and old genotype Lithuanian Black-and-White (LBW) cattle within breeds, and to make pairwise comparisons. The blood samples were taken from 164 LWB and 89 old genotype LBW cows. The EAB and EAC blood type systems were analysed, the allele frequency was calculated, and the degree of homogeneity Ca% and genetic distance r between the breeds were measured. In the EAB system, out of 36 studied alleles, 25 were identified in the population of LWB cattle and 21 in the old genotype LBW cattle. In the EAC blood type system, out of 25 studied alleles, 19 were identified in the population of Lithuanian White-Backed cattle and 20 in the old genotype Lithuanian Black-and-White cattle. The research showed that in the EAB system 5 alleles that were found in previous data of LWB cattle are more characteristic of the present population of LWB cattle. $I_2$ allele was most characteristic of the old genotype LBW cattle, whereas $G_2Y_2E'_2Q'$ allele was most characteristic of LWB cattle. In the EAC genetic system only four alleles, $R_2$ ($C_2$"), $WR_2$, $WX_2$, $X_2$($C_2$"), with a high frequency were found in the population of LWB cattle. $C_2ER_2$, $C_2X_2$, $C_2EC$, WE, $R_2C'$ alleles were discovered in the population of old genotype LBW cattle. In the EAB system the degree of homogeneity of LBW was two times higher than that of LWB cattle. The genetic similarity between LWB and old genotype LBW cattle was r = 0.60.

**Key words:** genotype, genetic similarity, blood group, allele

## INTRODUCTION

Cattle blood types were discovered almost at the same time as those of humans. In the last sixty or seventy years, blood types have been intensively studied by numerous scientists, namely, by Royal (1952), Humble (1957), Stortmont (1962), Bouw (1964, 1977), Miller (1966), Tucher (1986), Honberg, Larsen (1992), Bitzmann (2009).

Lithuanian scientists have also contributed to the studies of blood groups, namely, Vagonis, Meškauskas (1975), Kuosa, Tušas, Boveinienė (1999), Tušas (2001), Šveistienė, Jatkauskienė (2008) and others. In 2003, Paulauskas indicated that quantitative genetic variability characteristics and research methods should meet the following requirements: phenotypic variation found in a separate allelic locus should be determined in different individuals; allelic changes in one locus should be distinguished from the changes of

* Corresponding author. E-mail: editakristina@gmail.com

alleles in another locus; most allelic changes in a separate locus should be discerned; the studied loci should reflect the gene sample by the physiological expression and variability. Only part of allelic changes results in morphological changes (Paulauskas et al., 2003).

Farm animal blood erythrocytes contain numerous antigenic factors that make up bloods groups which are hereditary and do not change throughout the whole life of the animal (Vagonis, 1975; Boveinienė et al., 1990; Gaidžiūnienė et al., 2007). Cattle have eleven different blood type systems. Every system has a different number of blood group factors (Stormont, 1962; Bitzmann, 2009; Miller, 1966; Penedo, 2000). Therefore, a blood typing method was widely applied for a cattle parentage analysis. This method is the basis for making up the gene pool of animals, for determining the relationship between different alleles and animal productivity, between blood groups and animal reproduction traits and healthiness (Gaidžiūnienė et al., 2007; Vagonis, 1975). In Lithuania, the parentage of native cattle breeds, which are subsequently entered in herd-books, are tested by immunogenetic methods with all inherited diseases recorded as well. Immunogenetic methods are used for the parentage control of all breeding bulls, bull dams and 5% of heifers born (Directive by the Ministry of Agriculture of the Republic of Lithuania on "Stud Book Regulations" No. 220 of June 29, 2001; preamble changes No. 3D-1025, 2009, 2010, No. 1-39, 2010).

Native cattle with a white longitudinal dorsal stripe and black or brown pigment sides is an indigenous breed currently mostly found in the south eastern regions of Lithuania and called Lithuanian White-Backed cattle. Cattle similar to Lithuanian White-Backed cattle can also be found in north-eastern regions of Poland, Scandinavian countries and some regions of Russia (Litwincziuk, 2002; Šveistienė et al., 2008). More data on the old genotype of Lithuanian Black-and-White cattle are found in the sources from 20th century. These are described as animals of solid build that originated from various native and imported cattle and accounted for about 8% on peasant farms in 1912–1913 (Kuosa, 1980).

In 2006, the genetic analysis of Lithuanian White-Backed, Lithuanian Ash-Grey, Lithuanian Black-and-White and Lithuanian Red cattle indicated that the highest and lowest frequency of allele by PRL gene was detected in Lithuanian White-Backed and Lithuanian Red cattle breeds, respectively. There PRL genotypes AA, AB and BB were identified in the analysed breeds (Miceikienė et al., 2006). In 1994–1998, blood groups of Lithuanian Red, Lithuanian Black-and-White and Lithuanian Ash-Grey cattle were analysed by prof. J. Kuosa and S. Tušas. The study revealed differences between the breeds in the EAB system. Seven and ten different alleles were detected in LBW and LWB cattle populations, respectively. In the EAC blood group system 7 different alleles were found, and allele C2R2WC was found only in several LWB cattle (Kuosa et al., 1999).

Cattle in Lithuania originated from *Bos taurus* (Piličiauskienė, 2008). *Bos taurus* blood peculiarities were thoroughly analysed by Bitzmann who found that blood multi-structural, immunochemical and glucohistochemical qualities are same in both adult and young animals, between male and female cattle (*Bos taurus*). Immunocytochemical blood analysis indicated that antibody CD28 was more distinguished in *Bos taurus* (Bitzmann, 2009).

From 2001 to 2012, the number of LWB cattle changed due to breed restoration with the aim to make the breed more pure (Šveistienė, 2011). The genetic changes in the populations under restoration and most typical alleles of every breed can be determined by comparing research data from several years and blood group antigen frequencies.

The purpose of the study was to carry out the genetic analysis within Lithuanian White-Backed and old genotype Lithuanian Black-and-White breeds and make within-breed comparisons. The progeny parentage is ascertained by using the sire parentage and blood group data accumulated in the laboratory data bank from all breeding enterprises. It was also possible to determine the changes in the population

of LWB cattle by comparing the data of the present restored population with the data recorded 10 years ago.

## MATERIALS AND METHODS

Blood typing studies were carried out by using blood samples collected during expeditions organized by the Coordinating Centre for the Conservation of Animal Genetic Resources. The blood from 89 old genotype Lithuanian Black-and-White cattle was taken in 2011–2012, the blood from 164 White-Backed cattle in 2001–2012 and compared with population data of Lithuanian White-Backed cattle, published by Kuosa, Tušas (1999). The results, which were received after the comparison of the population data of LWB cattle (years 1991–1998 and years 2001–2012), revealed the change in the genetic diversity, based on blood types. The blood samples from every individual animal were taken using a separate needle. The ratio of the preserving solution and blood was 1 to 4. The blood from *v. jungularis* was collected into sterile test-tubes with a preserving solution (*Na citrate* – 3.8% EDTA IK31).

The blood from White-Backed and old genotype Lithuanian Black-and-White cattle was analysed by the blood group method when erythrocyte antigenic factors are determined using a hemolysis reaction. Blood samples were used to prepare 2.5% erythrocyte suspension, 20 µl of specific reagent testserum and 10 µl of erythrocyte suspension were poured into the hollows of serological plates. After 15 min storage, complement was poured and incubated in a thermostat at 28–30 °C. Hemolysis reaction is tested twice on a 0–4 point scale after 2 and 4 hours following complement pouring. Cattle blood typing was carried out at the Institute of Animal Science of the Lithuanian Health Sciences University. Forty eight reagents – testserums (National Research Institute of Animal Production, Poland) in compliance with the requirements of International Society for Animal Genetics (ISAG) were used for cattle blood typing. The data were analysed by genetically most informative EAB and EAC genetic systems (EA – erythrocyte antigen system). The allelic frequency *q* was calculated by the formula $q = n/2n$, where *q* is allelic frequency, *n* is the number of animals with the mentioned allele (Zhyvotovskii, Mashurov, 1974; Matoushek, 1967).

The significance of the differences between allele frequencies was calculated using $\chi^2$ (Vagonis, 1975; Zhyvotovskii, Mashurov, 1974; Matoushek, 1967). The homogeneity degree Ca% and genetic distance *r* were calculated by Vagonis (1975), Zhyvotovskii, Mashurov (1974), Matoushek (1967).

## RESULTS AND DISCUSSION

The EAB system allelic frequencies of Lithuanian White-Backed and old genotype Black-and-White cattle are presented in Table 1.

The studied group of LWB cattle had by three alleles more in the EAB system than the animals ten years ago. The EAB system allelic analysis indicated that LWB cattle population had the same 14 alleles detected in earlier studies and 10 new alleles not detected earlier. Ten years ago, White-Backed cattle population had 22 alleles in the EAB system, whereas the current population numbered 25 alleles. In the EAB system, 21 alleles were identified in the old genotype Black-and-White cattle population. There are more than 50 alleles in the EAB system (Vagonis, 1975; Viinalass, 1999, 2000, 2002). All studies indicated lower number of alleles. According to the data from the years 1994–1998, in the EAB system $I_2$ (0.1488), $B_2Y_2A'_2G'P'Q'G''$ (0.0655), $G_2Y_2E'_2Q'$ (0.0833) alleles were found as typical of the LWB cattle. This is in agreement with the studies of White-Backed cattle by Tušas (2001) and Šveistienė et al. (2008).

From 1994 to 1998, the blood groups of Lithuanian White-Backed and Ash-Grey cattle were genetically analysed by Kuosa et al. (1999) and Tušas (2001). The immunogenetic characteristics of these cattle indicated that some of the alleles in the EAB system were typical of only native cattle and not found in Lithuanian Black-and-White and Lithuanian

**Table 1.** Comparative analysis of EAB system allelic frequency changes in Lithuanian White-Backed and old genotype Lithuanian Black-and-White cattle

| Allele | Lithuanian White-Backed cattle population in 1994–1998, Kuosa, Tušas (1999), n = 84 | Lithuanian White-Backed cattle population, n = 164 | Old genotype Lithuanian Black-and-White cattle population, n = 89 |
|---|---|---|---|
| $B_2O_2$ | 0.0238 | 0.0305* | 0.0056* |
| $B_2O_2B'$ | 0.0357 | – | 0.0281 |
| $B_2O_2Y_2D'$ | 0.0178 | 0.0274 | – |
| $B_2G_2Y_2A'_2O'$ | 0.0060 | 0.0061**** | 0.0506**** |
| $B_2G_2T_1B'$ | 0.0060 | – | – |
| $B_2Y_2A'_2G'P'Q'G''$ | 0.0655 | 0.0701 | – |
| $B_2Y_2O_2$ | – | – | 0.0056 |
| $B_2P'$ | – | 0.0091 | 0.0056 |
| $B_2Y_2P'G'$ | – | – | 0.0169 |
| $B_2G_2P'Q'$ | – | 0.0030** | 0.0169** |
| $B_2G_2Y_2$ | – | 0.0061 | 0.0056 |
| $D'O'G'$ | 0.0595 | 0.0274** | 0.0730** |
| $I_2$ | 0.1488 | 0.0701 | 0.1854 |
| $I'$ | 0.0298 | 0.0244 | 0.0056 |
| $I_2QI'Q'$ | – | – | 0.0056 |
| $I_2Q'$ | 0.0238 | – | – |
| $I_2E'_2QQ'$ | 0.0655 | 0.0671 | – |
| $Y_2$ ($A'_2$) | – | 0.0183 | – |
| $Y_2Y'$ | 0.0060 | – | – |
| $Y_2G'G''$ | 0.0238 | – | – |
| $Y_2Y'G'G''$ | 0.0119 | – | – |
| $Y_2P_2$ | 0.0119 | – | – |
| $G''$ | – | 0.0335 | – |
| $G'G''$ | 0.0119 | 0.0122 | – |
| $G_3B'B''T_2$ | – | 0.0305 | – |
| $G_2I_2$ ($Q'$) | – | 0.0122***** | 0.0843***** |
| $G_2Y_2$ ($O_2$) | 0.0060 | 0.0091**** | 0.0506**** |
| $G_2Y_2E'_2Q'$ | 0.0833 | 0.1341 | 0.1011 |
| $G_2E'_2Q'$ | – | 0.0030***** | 0.0730***** |
| $O_2(A'_2)$ | 0.0178 | 0.0091 | 0.0112 |
| $O_2G'G''Q'$ | – | – | 0.0112 |
| $O_2J'_2K'O'$ | 0.0119 | 0.0427* | 0.0899* |
| $OxY_2D'E'_2O'$ | – | 0.0030 | 0.0169 |
| $P_2$ | – | 0.0854 | – |
| $P_2I'$ | 0.0178 | 0.0274 | – |
| $Q'$ | 0.0476 | 0.0793* | 0.0337* |
| $B^-$ | 0.0952 | 0.1585 | 0.1236 |
| Na | 22 | 25 | 21 |
| Ca% | 5.81 | 7.97 | 16.34 |

* $P \leq 0.05$; ** $P \leq 0.025$; *** $P \leq 0.01$; **** $P \leq 0.001$; ***** $P \geq 0.001$

Red cattle populations (Kuosa et al., 1999). When the immunogenetic analysis of Lithuanian White-Backed cattle was included in the studies of 1994–1998, similarities and differences were clearly observed.

Alleles $B_2G_2T_1B'$, $I_2Q'$, $Y_2Y'$, $Y_2G'G''$, $Y_2Y'G'G''$, $Y_2P_2$, that were detected in White-Backed cattle ten years ago, were no longer identified in the present day White-Backed and old genotype Black-and-White cattle populations. The current LWB cattle population did not retain allele $B_2O_2B'$ which was earlier found with a low frequency of 0.0357, yet it was identified in the old genotype LBW cattle population (0.0218), though other researchers indicated it as typical of Lithuanian Red cattle tested in the last decades (Jatkauskienė et al., 2012). Allele $Y_2Y'$ is indicated by the same authors as more typical of the current Red cattle population (Jatkauskienė et al., 2012). By the data from 2011–2012, alleles $G_2Y_2E'_2Q'$, $B_2Y_2A'_2G'P'Q'G''$, $I_2$, $P_2$ and Q' are more typical of LWB cattle population. The blood typing analysis of old genotype LBW cattle revealed alleles most typical of this population, i. e. $D'O'G'$, $I_2$, $G_2I_2(Q')$, $G_2Y_2E'_2Q'$, $G_2E'_2Q'$, $O_2J'_2K'O'$.

Significant differences between Lithuanian White-Backed and old genotype Black-and-White cattle breeds were determined after a statistical analysis of the blood groups. The analysis indicated that EAB system alleles $G_2I_2(Q')$ and $G_2E'_2Q'$were more frequent in the old genotype LBW cattle than in LWB cattle ($P \geq 0.001$). Our study showed that alleles $B_2Y_2A'_2G'P'Q'G''$ and Q' were most predominant in LWB cattle and corresponded to the LWB cattle characteristics determined by Tušas (2001) in 1994–1998. Moreover, significant differences between White-Backed and Lithuanian Black-and-White cattle were found for the alleles $B_2G_2Y_2A'_2O'$, $G_2Y_2E'_2Q'$, $G_2I_2(Q')$ ($P \leq 0.001$).

The studies of the degree of homogeneity indicated a significant difference in the variables of White-Backed (7.97) and old genotype Black-and-White (16.34) cattle in the EAB system. Ten years ago, the homozygosis of White-Backed cattle was two degrees lower. The comparison of LWB and old genotype LBW cattle populations indicated that the degree of homogenity was twice (16.34%) higher in LBW than in LWB cattle. On the average 23 alleles or 50% lower number than indicated by Vagonis (1975) and Viinalass et al. (2002) were identified in the studied populations. By the degree of homogenity, Black-and-White cattle are closer to each other, while White-Backed cattle are less homozygous.

EAC genetic system alleles $C_2ER_2$, WE, $X_2R_2$ found during earlier studies in White-Backed cattle were no longer detected in the current population. Alleles $C_2X_2$, $R_2C$ ($q=0.0955$, 0.0112) were identified in the population of old genotype Black-and-White cattle (Table 2).

In 164 currently tested Lithuanian White-Backed cattle, 19 alleles in the EAC system were identified ten years ago. The LWB cattle population gained $C'C''_2$, $C_2C'$, $C_2WEX_2$, $C_2WR_2$, $ER_2$ alleles (frequency from 0.0152 to 0.0884). In the EAC system, the old genotype LBW population numbers 20 alleles 15 of which are also found in the LWB population. Alleles $R_2(C_2'')$, $WR_2$, $WX_2$ could be ascribed as typical of the White-Backed population due to their comparatively high frequency (0.1128–0.1524).

The frequency of allele $C_2R_2WC'$ (0.0730) in the population of the old genotype LBW cattle was significantly higher ($P \leq 0.001$) than that of LWB cattle. In the Black-and-White cattle population, the frequencies of alleles $C_2EX_2$ ($P \leq 0.01$) and $C_2WX_2$ ($P \leq 0.05$) were higher and those of alleles $C_2WE$ ($P \leq 0.05$), $C_2WEX_2$ ($P \leq 0.05$), $WR_2$ ($P \leq 0.025$), $WX_2$ ($P \leq 0.001$), $X_2$ ($P \leq 0.05$) were significantly lower as indicated in Table 2. However, the significance of these changes was low.

The degree of homogeneity in the EAC system was 9.36 for the Lithuanian White-Backed and 9.29 for the old genotype Black-and-White cattle populations. Ten years ago the homozygosis of LWB cattle (10.41) was close to the current LWB cattle population (9.36). Currently, the population of LWB cattle has only by one allele lower number of alleles in the EAC system than the population of the old genotype LBW cattle. The average degree of homogeneity in both populations Ca was 9.33.

**Table 2.** Comparative analysis of EAC system allelic frequency changes in Lithuanian White-Backed and old genotype Lithuanian Black-and-White cattle

| Allele | Lithuanian White-Backed cattle population in 1994–1998, Kuosa, Tušas (1999), n = 84 | Lithuanian White-Backed cattle population, n = 164 | Old genotype Lithuanian Black-and-White cattle population, n = 89 |
|---|---|---|---|
| C”C”$_2$ | – | 0.0213 | – |
| $C_2$E | 0.0476 | 0.0274 | 0.0393 |
| $C_2ER_2$ | 0.0238 | – | 0.0056 |
| $C_2EX_2$ | – | 0.0030*** | 0.0337*** |
| $C_2$WE | 0.0655 | 0.0366* | 0.0056* |
| $C_2WER_2$ | 0.0238 | 0.0305 | 0.0337 |
| $C_2R_2$WC’ | 0.0298 | 0.0061***** | 0.0730***** |
| $C_2WX_2$ | 0.0595 | 0.0549* | 0.0955* |
| $C_2$C’ | – | 0.0061 | – |
| $C_2X_2$ | – | – | 0.0955 |
| $C_2C_2$” | – | 0.0061 | – |
| $C_2$EC’ | – | – | 0.0056 |
| $C_2WEX_2$ | – | 0.0884* | 0.0393* |
| $C_2WR_2$ | – | 0.0244 | 0.0112 |
| E | 0.0833 | 0.0274 | 0.0449 |
| $EX_2$ | 0.0060 | 0.0091 | – |
| $ER_2$ | – | 0.0152 | 0.0056 |
| WE | 0.0476 | – | 0.0169 |
| $R_2$($C_2$”) | 0.0119 | 0.1128 | 0.0730 |
| $R_2$C’ | – | – | 0.0112 |
| $WR_2$ | 0.0833 | 0.1128** | 0.0562** |
| $WX_2$ | 0.0119 | 0.1524**** | 0.0674**** |
| $X_2$ ($C_2$”) | 0.1845 | 0.0732* | 0.0337* |
| $X_2R_2$ | 0.0238 | – | – |
| $X_2$L’ | 0.0476 | 0.0457 | 0.0393 |
| C$^-$ | 0.1964 | 0.1463 | 0.2135 |
| Na | 15 | 19 | 20 |
| Ca% | 10.41 | 9.36 | 9.29 |

* P ≤ 0.05; ** P ≤ 0.025; *** P ≤ 0.01; **** P ≤ 0.001; ***** P ≥ 0.001

The comparison of White-Backed cattle with the old genotype Black-and-White cattle indicated the genetic similarity r = 0.60.

## CONCLUSIONS

The results, which were received after the comparison of the population data of Lithuanian White-Backed cattle (years 1991–1998 and years 2001–2012), revealed the change in the genetic diversity based on blood types. The genetic diversity in the EAB system decreased by 7 and increased by 10 alleles, in the EAC system it decreased by 3 and increased by 4 alleles. These changes in the population might have been influenced by the reconstruction within the population.

In the EAB system, out of 36 studied alleles, 25 were identified in the population of LWB cattle and 21 in the old genotype LBW cattle. In the EAC blood type system, out of 25 studied alleles, 19 were identified in the population of White-Backed cattle and 20 in the old genotype Black-and-White cattle.

The research showed that in the EAB system $B_2G_2Y_2A'_2O'$, $B_2Y_2A'_2G'P'Q'G''$, $I_2E'_2QQ'$, $G'G''$, $P_2I'$ alleles, that were found in the 1994–1998 population of White-Backed cattle, are more characteristic of the present population of White-Backed cattle. In the population of the old genotype Black-and-White cattle, the predominance of $B_2Y_2O_2$, $B_2Y_2P'G'$, $I_2QI'Q'$, $O_2G'G''Q'$ alleles could be detected. $I_2$ allele was the most characteristic of the old genotype Black-and-White cattle (q = 0.1854), whereas $G_2Y_2E'_2Q'$ allele was characteristic of White-Backed cattle (q = 0.1341).

In the EAC genetic system only four $R_2$ ($C_2''$), $WR_2$, $WX_2$, $X_2$ ($C_2''$) alleles with high frequency (0.1128–0.1845) were found in the population of LWB cattle. $C_2ER_2$ (0.0056), $C_2X_2$ (0.0955), $C_2EC$ (0.0056), WE (0.0169), $R_2C'$ (0.0112) alleles were discovered in the population of old genotype LBW cattle.

In the EAB system the degree of homogeneity of Black-and-White was two times higher (16.34) than that of White-Backed cattle (7.97).

The genetic similarity between White-Backed and old genotype Black-and-White was r = 0.60.

Received 27 October 2014
Accepted 1 December 2014

**References**

1. Bitzmann D. Ultrastructural, immunohistochemical and glucohistochemical studies of bovine blood cells [Ph. D. Thesis]. Munich; 2009. p. 45–50. German, with English Abstract.
2. Bouw J. Present status of animal blood group research. Vet Sci Commun. 1997; 1: 105–10.
3. Boveinienė B, Kriščiūnas B. Determination and practical use of animal blood groups. Vilnius, Lithuania; 1990. p. 3–16. Lithuanian.
4. Gaidžiūnienė N, Meškauskienė S. Selection of dairy cattle. Vilnius, Lithuania: Ogamas; 2007. p. 119. Lithuanian.
5. Honberg L, Larsen B. Bovine monoclonal antibodies to blood group antigens prepared by murine × bovine or (murine × bovine) × bovine interspecies fusions. Anim Genet. 1992; 23: 497–508.
6. Humble R. Blood types in cattle. Can J Comp Med Vet Sci. 1954; 18: 379–89.
7. Jatkauskienė V, Petrakova L, Razmaitė V. Immunogenetic characteristics of different genotype bulls from Lithuanian Red cattle. Baisogala, Lithuania; 2012. p. 18–28. Lithuanian, with English Abstract.
8. Kuosa J. Lithuanian Black-and-White cattle. Vilnius, Lithuania: Mokslas; 1980. p. 236. Lithuanian.
9. Kuosa J, Tušas S, Boveinienė B. Immunogenetic characteristics of Lithuanian indigenous cattle (Light-Grey and White-Backed). Anim Husb. Scientific Articles. 1999; 35: 117–23.
10. Litwinczuk Z. Programme of protection of Polish Whitebacks cattle resources. Lublin, Poland; 2002. p. 25.
11. Matoushek I. Animal blood groups. Kiev, Ukraine; 1964. p. 45. Russian.
12. Meshkauskas ChP. Blood group genetic analysis of Lithuanian animal breeds, and its use in animal breeding. Kaunas, Lithuania; 1967. p. 24. Russian.
13. Miceikienė I, Pečiulaitienė N, Baltrėnaitė L, Skinkytė R, Indriulytė R. Association of cattle genetic markers with performance traits. Biologija. 2006; 1: 24–9.
14. Miller WJ. Evidence for two new systems of blood groups in cattle. Genetics. 1966; 54: 151–8.
15. Paulauskas A, Slapšytė G, Morkūnas V. Methods and exercises of general genetics analysis. Vilnius, Lithuania; 2003. p. 197. Lithuanian.
16. Penedo MCT. Red blood cell antigens and blood groups in the cow, pig, sheep, goat, and llama. In: Feldmann BF, Zinkil JG, Jain NC, editors. Schalm's Veterinary Hematology. Lippincott Williams and Wilkins; 2000.
17. Piličiauskienė G. The osteological analysis of bones of bovine animals from the territory of

the lower castle in Vilnius and the age determination by dental structure [Ph. D. Thesis]. Kaunas, Lithuania; 2008. p. 125. Lithuanian.

18. Royal GC, Ferguson L, Sutton T. Bovine erythrocyte antigens III. The isolation of blood-group specific substances from erythrocytes. J Immunol. 1952; 71: 22–5.
19. Stormont C. Current status of blood groups in cattle. Ann N Y Acad Sci. 1962; 97: 251–68.
20. Šveistienė R, Kaurynienė EK. Studies of Lithuanian White-Backed cattle population. Gyvulininkystė. 2011; 58: 3–15. Lithuanian, with English Abstract.
21. Šveistienė R, Jatkauskienė V. Analyses of the genetic diversity within Lithuanian White-Backed cattle. Veterinarija ir zootechnika. 2008; 44(66): 67–72.
22. Tucker E, Metenier L, Grosclaude J, Clarke S, Kilgour L. Monoclonal antibodies to bovine blood group antigens. Anim Genet. 1986; 17: 3–13.
23. Tušas S. The variety analysis of Lithuanian local cattle and the preservation of their genetic pool [Ph. D. Thesis]. Kaunas, Lithuania; 2001. p. 55–61. Lithuanian, with English Abstract.
24. Vagonis Z, Meškauskas Č. Animal blood group genetics. Vilnius, Lithuania; 1975. 320 p. Lithuanian.
25. Viinalass H, Vaerv S, Boveinienė B, Bekere R. Characterisation of cattle breeds in Baltic countries by genetic markers. Biologija. 2002; 3: 16–9.
26. Zhivotovskij LA, Mashurov AM. Methodological recommendations for making animal selection based on statistical analysis of immunogenetic data. Dubrovica, Ukraine; 1974. p. 29. Russian.

**Edita Kristina Kaurynienė, Rūta Šveistienė, Virginija Jatkauskienė**

## LIETUVOS BALTNUGARIŲ IR LIETUVOS SENOJO GENOTIPO JUODMARGIŲ GALVIJŲ GENETINIS PALYGINIMAS PAGAL KRAUJO GRUPES

*Santrauka*

Tyrimo tikslas – atlikti Lietuvos baltnugarių ir senojo genotipo Lietuvos juodmargių galvijų genetinę analizę veislių viduje ir jas palyginti tarpusavyje. Tyrimui naudoti 164 Lietuvos baltnugarių ir 89 senojo genotipo Lietuvos juodmargių galvijai. Ištirtos EAB ir EAC kraujo grupių sistemos, nustatytas alelių dažnis, apskaičiuotas homozigotiškumo laipsnis Ca% ir genetinė distancija r tarp veislių. EAB genetinėje sistemoje iš 36 tirtų alelių baltnugarių galvijų populiacijoje identifikuoti 25 aleliai, o senojo genotipo juodmargių – 21. EAC kraujo grupių sistemoje iš 25 tirtų alelių baltnugarių populiacijoje identifikuota 19, senojo genotipo juodmargių galvijų populiacijoje – 20 alelių. Ištirtai dabartinei baltnugarių populiacijai EAB sistemoje būdingesni 5 aleliai, rasti tirtoje baltnugarių galvijų populiacijoje. Senojo genotipo Lietuvos juodmargių galvijų populiacijoje išryškėjo 4 aktualesni aleliai. $I_2$ alelis būdingiausias senojo genotipo juodmargiams, alelis $G_2Y_2E'_2Q'$ – Lietuvos baltnugariams galvijams. EAC genetinėje sistemoje tik keturi $R_2$ ($C_2$"), $WR_2$, $WX_2$, $X_2$($C_2$") aleliai dideliu dažniu (0,1128–0,1845) nustatyti baltnugarių galvijų populiacijoje. $C_2ER_2$ (0,0056), $C_2X_2$ (0,0955), $C_2EC$ (0,0056), WE (0,0169), $R_2C'$(0,0112) aleliai rasti Lietuvos senojo genotipo juodmargių galvijų populiacijoje. EAB sistemoje senojo genotipo juodmargių homozigotiškumo laipsnis du kartus didesnis nei baltnugarių galvijų. Genetinis panašumas tarp baltnugarių ir senojo genotipo Lietuvos juodmargių buvo r = 0,60.

**Raktažodžiai:** genotipas, genetinis panašumas, kraujo grupės, alelis