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ELEMENTS OF DNA-TECHNOLOGY FORMING QUALITY AND SAFE RAW MATERIALS

Abstract. It is known that cows high milk productivity is associated with decrease in resistance to various diseases, including bovine leukosis, in resistance formation to which the *BoLA-DRB3* gene plays role, whose alleles are associated with resistance (R-alleles *7, *11, *23, *28), sensitivity (S-alleles *8, *16, *22, *24) or are defined as neutral (N) in relation to the disease. Researchers also established association of *BoLA-DRB3*-alleles *8, *11, *23 with an increased milk yield volume, and the *22 allele - with reduced milk yield volume. The aim of research was to study associative communication of servicing bulls *BoLA-DRB3* genotypes groups with their breeding value by female ancestor's dairy productivity indicators. As a result, we studied associative communication of servicing bulls *BoLA-DRB3* genotypes groups with their breeding value by female ancestor's dairy productivity indicators with identification of reduced milk productivity with genetic resistance to bovine leukemia virus infection and bovine leukosis disease relationship, as well as observation of positive correlation between increased milk productivity and genetic predisposition to increased milk yield volumes. The obtained information will be taken into account in breeding during dairy herds reproduction with genetic resistance to bovine leukosis.
Key words: servicing bull, gene, genotype, *BoLA-DRB3*, PCR, SBT, bovine leukosis, milk productivity.

Introduction. The main task in dairy cattle breeding of our country is an objective assessment of genetic potential and improving servicing bull's selection accuracy for herd reproduction, which will serve as a guarantee for industry economic efficiency growth [1-4].

The observed trend towards an increase in cow's milk productivity is closely associated with decrease in resistance to various cattle diseases, which subsequently negatively affects the production process with an increase in output cost [5,6], including due to animals culling and decrease in milk yield average level per herd [7].

In breeding work for formation of highly productive dairy herds populations, screening is carried out for various gene variants of economically significant traits [8-11], including determining resistance to various diseases, including bovine leukosis, the most common in Russian Federation, including Republic of Tatarstan, which is confirmed by studies of causative infection agent - bovine leukemia virus (BLV) [12-15].

The genes of the main histocompatibility complex are considered as a potential molecular marker of cattle resistance to leukosis [16,17], among which *BoLA-DRB3* gene is the most highly polymorphic [18].

Data on *BoLA-DRB3* gene polymorphism [19], which alleles are associated with resistance or susceptibility to bovine leukosis [20,21], make it possible to carry out marker-directed selection in order to obtain disease-resistant animals [22-24].

BoLA-DRB3 gene alleles are divided both into those associated with resistance (R) to bovine leukosis, represented by following alleles: *7, *11, *23, *28, and those related to sensitivity (S): *8, *16, *22, *24 [25], the remaining alleles are defined as neutral (N). Resistance to bovine leukosis is dominant feature, therefore animal carriers of *7, *11, *23 and *28 alleles, even in heterozygous state, will not be susceptible to this disease [26].

Milk, obtained from leukosis dairy cows often leads to decrease in its quality, biological usefulness and safety. At the same time, production of high-quality dairy raw materials is an important task, especially in terms of functional and herodietic dairy products production [27-31].

The researchers also obtained data on different allelic variants of *BoLA-DRB3* gene association directly with milk productivity signs in cattle [32,33]. For example, *BoLA-DRB3* alleles *8, *11 and *23 are associated with increased (I) milk yield, allele *22 - with decreased (D) milk yield.

The aim of this research was to study associative communication of servicing bulls *BoLA-DRB3* genotypes groups with their breeding value by female ancestor's dairy productivity indicators.

Material and research methods. Molecular genetic studies were performed on DNA samples isolated from whole canned blood obtained from 60 servicing bulls of milk production direction, which are cross-breeding and purebred Holstein cattle, belonging to JSC "Head Breeding Enterprise "Elita" of Vysokogorsky District of Republic of Tatarstan. The study was conducted on the basis of interdepartmental laboratory of immunology and biotechnology, Kazan State Academy of Veterinary Medicine named after N.E. Bauman and Research and Production Company "SINTOL" (Moscow).

Nucleic acids were extracted using reagents set for DNA isolation from clinical material "DNA Sorb B" (Central Research Institute of Epidemiology, Russia).

For PCR-amplification of exon 2 locus of *BoLA-DRB3* gene with a length of 319 bp optimized PCR-SBT conditions were used [34] using DRB3FRW (5′-CGCTCCTGTGAYCAGATCTATCC-3′) and DRB3REV (5′-CACCCCCGCGCTCACC-3′) primers and "Encyclo Plus PCR kit" reagent kit (CJSC Evrogen, Russia) under following thermal cycling conditions: preliminary denaturation at 94 °C for 4 minutes; further 40 cycles: denaturation 94 °C - 10 sec., annealing 62 °C - 10 sec., extension 72 °C - 10 sec.; final extension at 72 °C - 5 min.

Electrophoretic detection of resulting PCR fragments was carried out using reagent kit of "EF-genotype 200" (Central Research Institute of Epidemiology) in 2% agarose gel in TBE buffer, containing ethidium bromide, followed by visualization of amplicons in UV-transilluminator (Vilber Lourmat) and fixing result on digital camera (Canon).

For *BoLA* typing by sequencing (SBT), analyzed locus amplicons were sequenced using an "ABI PRISM 3100" genetic analyzer (Applied Biosystems, USA) followed by their alignment in BLAST (https://blast.ncbi.nlm.nih.gov/Blast. cgic) by corresponding partial nucleotide sequences of *BoLA-DRB3* alleles.

The frequency of genotypes occurrence by *BoLA-DRB3* gene was determined by formula [35]:

$$p = \frac{n}{N},$$

where p – genotype frequency; n – number of animal units, having a certain genotype, N – total number of examined animal units.

The calculation of animal unit's frequency alleles was performed according to formula [36]:

$$p = (2N1 + N2)/2n,$$

where $N1$ – number of homozygotes for studied allele, $N2$ – number of heterozygotes, n – sample volume.

When studying the associative communication of servicing bulls *BoLA-DRB3* genotypes groups with their breeding value by female ancestor's dairy productivity indicators, were used data on zootechnical and pedigree accounting of researched farm: pedigree cards (form 1-MOL), pedigree certificates and servicing bulls' catalogs.

The PBI is calculated – the parental bull index according to N.A. Kravchenko, 1963 [37] for each bull by milk yield and buttermilk of their female ancestors.

$$PBI = (2M + MM + MF)/4,$$

where *M* – mothers, *MM* – mothers of mothers, *MF* – mothers of fathers.

The results of research were processed by biometric method using computer and Microsoft Excel. The level of their reliability was determined by Student criterion.

Results and discussion. In assessing servicing bulls of milk productivity direction by origin, the indices of breeding bull's evaluation were used. An analysis of parental bull index (PBI) shows the extent to which offspring can transmit signs of milk production (table 1).

In total, typed sample (n=60) of bulls is divided into six associated groups of *BoLA-DRB3* genotypes: S/S – 25, S/N – 14, N/N – 4, R/N – 4, R/S – 11 и R/R – 2 animals.

Table 1 – Evaluation of servicing bulls of different groups of *BoLA-DRB3* genotypes associated with susceptibility or resistance to leukosis, according to indicators of female ancestor's milk productivity

Associated Genotypes Group		Milk productivity indicators		
		milk yield, kg	fat, %	fat, kg
n=60		Mothers (M)		
S/S	25	8561.0±1956.7	3.82±0.19	327.1±77.1
S/N	14	8800±1454.2	3.90±0.13	344.0±64.8
N/N	4	9918±668.5	4.03±0.18	399.8±41.1
R/N	4	8508±1268.8	3.95±0.22	334.3±35.7
R/S	11	8460±1570.5	3.84±0.18	326.6±71
R/R	2	6803±607.4	4.15±0.45	283.3±55.5
n=60		Mothers of mothers (MM)		
S/S	25	7731±2280.7	3.90±0.38	300.2±88.1
S/N	14	6517±1640.6	3.89±0.22	253.9±69.8
N/N	4	8003±2834.5	3.71±0.17	300.2±119.1
R/N	4	7087±1207	3.96±0.11	279.80±41.2
R/S	11	6736±1644.3	3.85±0.42	261.2±78.8
R/R	2	6347±2045	3.80±0	241.2±77.7
n=60		Mothers of fathers (MF)		
S/S	25	10591±3272.7	3.95±0.22	419.4±131.2
S/N	14	9579±1113.6	3.97±0.34	382.6±71.6
N/N	4	13816±2226.5	4.4±0.69	604.9±133.5
R/N	4	11490±2612.5	3.91±0.07	447.3±92.1
R/S	11	10854±3052.7	4.20±0.51	463.1±170.7
R/R	2	9533±951.8	4.16±0.34	395±7.2
n=60		Parental bull index (PBI)		
S/S	25	9251±2530.3	3.87±0.16	358±94.6
S/N	14	8424±995.5	3.91±0.16	329.4±51.2
N/N	4	10414±825.6	4.04±0.19	420.7±47.1
R/N	4	8898±1403	3.94±0.15	350.6±43.4
R/S	11	8628±1505.5	3.93±0.24	339.1±79.7
R/R	2	7371±1052.9	4.06±0.14	299.3±49
Note: R – alleles associated with resistance to leukosis; S – alleles associated with sensitivity to leukosis; N – alleles neutral to bovine leukosis.				

According to assessment results of parental bull index (PBI), distribution of genotype groups associated with resistance (R) and/or sensitivity (S) and/or neutral (N) state in relation to bovine leukosis had the following configuration in descending order of values:

for milk yield – N/N>S/S>R/N>R/S>S/N>R/R;

for milk fat content – R/R>N/N>R/N>R/S>S/N>S/S;

for milk fat yield – N/N>S/S>R/N>R/S>S/N>R/R.

Evaluation of bulls by parental index showed that highest milk yield (10,414 kg) and milk fat yield (420.7 kg) were observed in bulls of associated N/N genotypes group, and higher milk fat content had bulls of associated R/R genotypes group (4.06%).

At the same time, the smallest milk yield (7371 kg) and milk fat yield (299.3 kg) were observed in bulls of associated R/R genotype group, and the lowest milk fat content (3.87%) had bulls of associated S/S genotypes group.

A comparative analysis of frequency distribution of *BoLA-DRB3* gene alleles associated with cattle milk productivity signs in researched servicing bulls sample is presented in table 2.

Distribution of presented alleles associated with milk productivity signs in decreasing frequency order of occurrence has following configuration: *8>*22>*23>*11.

Table 2 – Occurrence frequency of *BoLA-DRB3* gene alleles, associated with milk productivity signs
in servicing bulls' sample of JSC "Head Breeding Enterprise "Elita" of Vysokogorsky District of Republic of Tatarstan

| Allele number | Number of animal-carriers of certain *BoLA-DRB3* alleles | | Number of specific alleles | Allele frequency, % |
				"Elita" (n=60)
Σ	n=110	100 %	n=120	100 %
Alleles, not associated with milk yield level				
Σ	75	68.19	83	69.18
I-alleles associated with increased milk yield				
*8 (*1201)	14	12.73	16	13.33
*11 (*0902)	5	4.54	5	4.16
*23 (*2701, *2703)	7	6.36	7	5.83
D-alleles associated with decreased milk yield				
*22 (*1101)	9	8.18	9	7.50

The group of I-alleles associated with an increased milk yield volume is represented by three alleles: *8, *11, *23 with occurrence frequency in range of 4.16–13.33%; at the same time, the allele *11 has the lowest occurrence frequency, the *8 allele is the highest. The total proportion of occurrence frequency of this alleles group was 23.32%, with these alleles' presence in genotype of 22.4% of bulls.

The group of D-alleles associated with reduced milk yield is represented by one *22 allele with occurrence frequency of 7.5%. This allele is present in genotype of 8.18% of bulls.

Evaluation of servicing bulls of different groups of *BoLA-DRB3* genotypes associated with milk productivity signs by female ancestor's indicators of the same name is presented in table 3.

Table 3 – Evaluation of servicing bulls of different groups of *BoLA-DRB3*
genotypes associated with milk productivity signs by female ancestor's indicators of the same name

| Associated Genotypes Group | | Milk productivity indicators | | |
		milk yield, кг	fat, %	fat, kg
n=60		Mothers (M)		
I/I	5	8545±2381.8	3.85±0.26	329 ±105.9
D/D	–	–	–	–
N/N	32	8817±1568.2	3.87±0.18	341.2±65.6
I/D	3	6943±2103.8	3.79±0.05	263.1±82.3
D/N	5	8990±564.3	3.9±0.05	350.6±25.2
I/N	15	8462±1792.3	3.89±0.25	336.8±71.7

Continuation of table 3				
n=60		Mothers of Mothers (MM)		
I/I	5	7829±2748.2	3.92±0.35	306.9±129.1
D/D	–	–	–	–
N/N	32	7035±1983.3	3.82±0.27	268.7±78.2
I/D	3	7255±4002.1	3.92±0.29	284.4±137.4
D/N	5	7735±1990.9	4.02±0.62	310.9±78.29
I/N	15	7129±1584.5	3.93±0.32	279.97±66.2
n=60		Mothers of fathers (MF)		
I/I	5	11379±2288.4	4.54±0.64	516.6±160.9
D/D	–	–	–	–
N/N	32	10826±3049.2	3.97±0.31	429.8±129.7
I/D	3	8433±2225.1	4.1±0.29	345.7±118.7
D/N	5	9537±1656.8	3.9±0.05	371.9±67
I/N	15	10816±2797.6	4.03±0.33	435.9±138.5
n=60		Parental bull index (PBI)		
I/I	5	9075±2262.1	4.04±0.32	366.6±118.42
D/D	–	–	–	–
N/N	32	8874±1662	3.88±0.15	349.6±67.8
I/D	3	7394±2556.9	3.9±0.05	288.4±102.4
D/N	5	8813±867.7	3.93±0.18	345.9±37.5
I/N	15	8717±1480.7	3.94±0.22	343.4±67.3

Note: I – alleles associated with increased milk yield; D – alleles associated with decreased milk yield; N – alleles neutral to milk yield.

The typed sample (n=60) of servicing bulls is represented by five associated groups of BoLA-DRB3 genotypes: I/I - 5, N/N - 32, I/D - 3, D/N - 5, and I/N - 15 animals. Moreover, no bulls of associated D/D genotypes group were revealed in the sample under study (Table 3).

According to assessment results of parental bull index (PBI), distribution of genotype groups associated with an increased and/or decreased milk yield volume and/or their neutral (N) state had the following configuration in decreasing order of indicator values:

for milk yield – I/I>N/N>D/N>I/N>I/D;
for milk fat content – I/I>I/N>D/N>I/D>N/N;
for milk fat yield – I/I>N/N>D/N>I/N>I/D.

Evaluation of bulls by parental index showed that bulls of associated of I/I genotypes group were characterized by highest milk yield (9075 kg), as well as milk fat content (4.04%) and milk fat yield (366.6 kg).

At the same time, the smallest milk yield (7394 kg) and milk fat yield (288.4 kg) were observed in bulls of associated I/D genotypes group, and the lowest milk fat content (3.88%) had bulls of associated N/N genotypes group.

Conclusion. According to research results, it was found that the highest PBI in milk yield and milk fat yield was observed in bulls of associated N/N genotypes group, and milk fat content had bulls of associated R/R genotypes group. The lowest PBI in milk yield and milk fat yield was observed in bulls of associated R/R genotypes group, and in terms of milk fat content - had bulls of associated S/S genotypes group. The distribution of genotypes groups, associated with an increased (I) and/or with decreased (D) milk yield volume and/or their neutral (N) state, in decreasing values order of corresponding indicators, showed that the highest PBI indicator for milk yield, milk fat content and milk fat yield was observed in bulls of associated I/I genotypes group. Thus, by researching associative communication of servicing bulls *BoLA-DRB3* genotypes groups with their breeding value by female ancestor's dairy productivity indicators, a relationship was found between reduced milk productivity and genetic resistance to infection with bovine leukemia virus and bovine leukosis disease, as well as a positive correlation between increased milk production and genetic predisposition to increased milk yield.

Researched associative communication of servicing bulls *BoLA-DRB3* genotypes groups with their breeding value by female ancestor's dairy productivity indicators will be taken into account in breeding work in dairy herd reproduction with genetic resistance to bovine leukosis.

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ДНҚ ЭЛЕМЕНТТЕРІ – ШИКІЗАТ САПАСЫ МЕН ҚАУІПСІЗДІГІ ТЕХНОЛОГИЯСЫН ҚАЛЫПТАСТЫРУ КЕПІЛІ

Аннотация. Сиырдың жоғары сүт өнімділігі түрлі ауруға, соның ішінде ірі қара малының лейке-миясына қарсы тұрақтылықтың төмендеуіне, BoLA-DRB3 генінің рөлі аллельдерінің қарсыласуына байланысты екендігі белгілі (У - аллели *7, *11, *23, *28), сезімталдық (Ч -аллели *7, *11, *23, *28) немесе ауруға қатысты бейтарап (Н) ретінде анықталады. Сондай-ақ BoLA-DRB3 аллельдері * 8, * 11, * 23 сүт шығымының ұлғаюы арқылы және сүт шығымы төмен аллель * 22 арасында байланыс орнатылды. Лейкоз сиырдан алынған сүт көбінесе оның сапасын, биологиялық құндылығы мен қауіпсіздігін төмендетеді. Өндірісте әсіресе функционалды және геродиеталық сүт өнімін алу үшін жоғары сапалы сүт шикізатын қолдану маңызды міндет болып саналады. Жалпы, ірі қара малының лейкемияға төзімділігінің генетикалық маркерлерін скрининг жасау жоғары сапалы және қауіпсіз шикізатты құру үшін ДНҚ технологиясының элементі ретінде орналастырылған. Зерттеудің мақсаты – бұқаның BoLA-DRB3 генотиптік тобының асыл тұқымдық құндылығы арқылы аналық ұрпақтарға жақынырақ келетін тегінің сүт өнімділігі тұрғысынан ассоциативті байланысын зерттеу. Молекулярлық-генетикалық зерттеулер генетикалық және асыл тұқымды ірі қара малдың сүт өнімділігі бағытындағы 60 бұқадан өндірілген, консервіленген қаннан оқшауланған ДНҚ сынамаларында жүргізілді. Нуклеин қышқылын экстракциялау ДНҚ-ны оқшаулауға арналған реагенттер кешені арқылы жүргізілді. Ұзындығы 319 п.н. BoLA-DRB3 генінің экзон 2 локусын ПЦР күшейту үшін оңтайландырылған ПЦР -SBT шарттары DRB3FRW және DRB3REV праймерлері арқылы қолданылды. BoLA-ны жүйелеу (SBT) арқылы енгізу үшін талданған локустың ампликондары генетикалық анализаторға реттелді, содан кейін BoLA-DRB3 аллельдерінің тиісті жартылай нуклеотидтік тізбектерімен теңестірілді. Аналық ұрпақтарға жақын тегінің сүт өнімділігі тұрғысынан BoLA-DRB3 бұқалары генотиптерінің асыл тұқымдық құндылықтарының ассоциативті байланысын зерттеу кезінде зерттелетін шаруашылықтың зоотехникалық және тұқымдық тіркелуі туралы деректерді пайдаландық. Сүт өндіруші бұқаларды тегі бойынша өнімділік бағытын бағалау кезінде бұқалардың асыл тұқымдылығын бағалау көрсеткіштері негізге алынды. Бұқаның аталық-аналық индексін (БАИ) талдау ұрпақтарының сүт өндірудің белгілерін жібере алатындығын көрсетеді. Алынған зерттеу нәтижелері биометриялық әдіспен өңделді. Олардың сенімділігі Стьюденттің өлшемі бойынша анықталды. Зерттеу нәтижелері бойынша, сүт өнімі мен сүт майындағы ең жоғары БАИ мөлшері Н/Н генотиптерінің байланысты топ бұқаларында және У/У генотиптерінің байланысты топ бұқаларындағы сүт майының құрамында екендігі анықталды. Сүт мөлшері мен сүт майының шығымы үшін БАИ ең төмен көрсеткіші У/У генотиптерінің байланысты тобының бұқаларында, ал сүт майының мөлшері бойынша Ч/Ч генотиптерінің байланысты тобының бұқаларында байқалды. Сүт шығымының жоғарылауымен (Ж) және/немесе азайтылған (А) көлемімен және/немесе олардың бейтарап (Н) күйімен байланысты генотиптер тобының таралуы тиісті индикатор мәнінің азаю тәртібімен сүт кірісі, сүт құрамы және БАИ үшін ең жоғары көрсеткіш көрсетті, П/П генотиптерінің қауымдастырылған тобының бұқаларында сүт майының шығымы байқалды. Осылайша, аналық ұрпақтарға жақын тегінің сүт өнімділігі тұрғысынан BoLA-DRB3 бұқалардың генотиптік тобының асыл тұқымдық құндылығымен ассоциативті байланысын зерттей отырып, сүт өнімділігінің азаюы мен ірі қара малдың лейкоз вирусымен инфекцияға генетикалық төзімділігі, сондай-ақ көбею арасындағы оң корреляция арасындағы байланыс анықталды. Ірі қара аналықтардың сүт өнімділігі тұрғысынан BoLA-DRB3 тұқымдық бұқалардың генотиптік тобының зерттелген ассоциативті қатынасы ірі қара малдың лейкемиясына генетикалық төзімділігі бар сүтті табын көбейту барысында асыл тұқымды аналық ұрпақтарға жақын тегінің сүт өнімділігі ескерілетін болады.

Түйін сөздер: өндіруші бұқа, ген, генотип, BoLA-DRB3, ПЦР, SBT, ірі қара мал лейкозы, сүт өнімділігі.

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ЭЛЕМЕНТЫ ДНК-ТЕХНОЛОГИИ ФОРМИРОВАНИЯ КАЧЕСТВЕННОГО И БЕЗОПАСНОГО СЫРЬЯ

Аннотация. Известно, что высокая молочная продуктивность коров связана со снижением резистентности к различным заболеваниям, включая лейкоз крупного рогатого скота, в формировании резистентности к которому играет роль ген *BoLA-DRB3*, чьи аллели ассоциированы с устойчивостью (У-аллели *7, *11, *23, *28), чувствительностью (Ч-аллели *8, *16, *22, *24) или определены как нейтральные (Н) по отношению к заболеванию. Также установлена связь *BoLA-DRB3*-аллелей *8, *11, *23 с повышенным объемом удоев, а аллеля *22 – со сниженным объемом удоев. Полученное от лейкозных коров молоко зачастую приводит к снижению его качества, биологической полноценности и безопасности. При этом производство высококлассного молочного сырья является важнейшей задачей, особенно в части выработки функциональных и геродиетических молочных продуктов. В целом скрининг генетических маркеров устойчивости к лейкозу крупного рогатого скота позиционируется как элемент ДНК-технологии прижизненного формирования качественного и безопасного сырья. Целью настоящего исследования являлось изучение ассоциативной связи групп генотипов *BoLA-DRB3* быков-производителей с их племенной ценностью по показателям молочной продуктивности женских предков. Молекулярно-генетическому исследованию были подвергнуты образцы ДНК, выделенные из цельной консервированной крови, полученной от 60 быков-производителей молочного направления продуктивности, представляющих собой помесный и чистопородный голштинский скот. Экстракцию нуклеиновых кислот осуществляли с применением комплекта реагентов для выделения ДНК. Для ПЦР-амплификации локуса экзона 2 гена *BoLA-DRB3* длиной 319 п.н. применяли оптимизированные условия проведения ПЦР-SBT с использованием праймеров DRB3FRW и DRB3REV. Для *BoLA*-типирования методом секвенирования (SBT) ампликоны анализируемого локуса секвенировали на генетическом анализаторе с последующим их выравниванием с соответствующими частичными нуклеотидными последовательностями *BoLA-DRB3*-аллелей. При изучении ассоциативной связи генотипов по гену *BoLA-DRB3* быков-производителей с их племенной ценностью по показателям молочной продуктивности женских предков использованы данные по зоотехническому и племенному учету исследуемого хозяйства. При оценке быков-производителей молочного направления продуктивности по происхождению использованы индексы племенной оценки быков. Анализ родительского индекса быка (РИБ) показывает степень возможной передачи потомству признаков молочной продуктивности. Полученные результаты исследования обработаны биометрическим методом. Уровень их достоверности определяли по критерию Стьюдента. По результатам проведенного исследования установлено, что наибольший показатель РИБ по удою и выходу молочного жира отмечен у быков ассоциированной группы генотипов Н/Н, а по содержанию молочного жира – у быков ассоциированной группы генотипов У/У. Наименьший показатель РИБ по удою и выходу молочного жира отмечен у быков ассоциированной группы генотипов У/У, а по содержанию молочного жира – у быков ассоциированной группы генотипов Ч/Ч. Распределение же групп генотипов, ассоциированных с повышенным (П) и/или со сниженным (С) объемом удоев и/или их нейтральным (Н) состоянием, в порядке убывания значений соответствующих показателей показало, что наибольший показатель РИБ по удою, содержанию молочного жира и выходу молочного жира отмечен у быков ассоциированной группы генотипов П/П. Таким образом, изучением ассоциативной связи групп генотипов *BoLA-DRB3* быков-производителей с их племенной ценностью по показателям молочной продуктивности женских предков наблюдалась взаимосвязь сниженной молочной продуктивности с генетической резистентностью к инфицированию вирусом бычьего лейкоза и заболеванию лейкозом крупного рогатого скота, а также положительная корреляция между повышенной молочной продуктивностью и генетической предрасположенностью к повышенному объему удоев. Изученная ассоциативная связь групп генотипов *BoLA-DRB3* быков-производителей с их племенной ценностью по показателям молочной продуктивности женских предков будет учитываться в селекционно-племенной работе при воспроизводстве молочного стада с генетической устойчивостью к лейкозу крупного рогатого скота.

Ключевые слова: бык-производитель, ген, генотип, *BoLA-DRB3*, ПЦР, SBT, лейкоз крупного рогатого скота, молочная продуктивность.

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