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АССОЦИАЦИЯ ПОЛИМОРФИЗМА EAB-СИСТЕМЫ ГРУПП КРОВИ С ЗАБОЛЕВАЕМОСТЬЮ ПЛЕМЕННОГО СКОТА АЙРШИРСКОЙ ПОРОДЫ

POLYMORPHYSM ASSOCIATION OF EAB-SYSTEM BLOOD TYPE WITH INCIDENCE OF AYRSHIRE BREED CATTLE

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Аннотация: Карельский тип айрширской породы крупного рогатого скота выведен в результате более чем 30-летней селекционной работы методом чистопородного разведения с использованием быков финской и отечественной селекции. Главными селекционными признаками при отборе маточного поголовья приняты величина удоя, содержание белка и жира. Дальнейшее совершенствование внутрипородного типа определяет необходимость поиска генетических факторов естественной резистентности для использования их в качестве селекционного признака. Удобную генетическую модель для изучения ассоциации с заболеваемостью представляет кодоминантная форма наследования групп крови. На примере одного из племенных хозяйств Республики Карелия выполнен ретроспективный анализ причин выбытия молочных коров для установления генетической детерминированности заболеваний. Проработку экспериментального материала проводили с привлечением отдельных методов кластерного, факторного и дискриминантного анализов, которые позволили не только сгруппировать многочисленные зоотехнические показатели по однородности их проявления, но и установить структуру связей между изученными переменными (продолжительность жизни, продуктивность молока, содержание жира, живой массы и возраста первого отела, аллели, причина выбытия). Пошаговый дискриминантный анализ на 97,73 % подтвердил достоверность разделения животных на три группы (кластера). В качестве основных дискриминаторов, достоверно разделивших поголовье коров, выделены показатели продолжительности жизни, продуктивности, живой массы и возраста первого отела. С привлечением факторного анализа установлено наличие прямой достоверной связи между аллелем EAB-системы и причиной выбытия животного. Определены наиболее часто встречающиеся аллели EAB-системы у животных, выбывших вследствие наиболее часто встречающихся заболеваний (заболевания конечностей, вымени, обмена веществ). По частоте встречаемости аллелей сделали предположение, что у животных-носителей аллеля $B_1I_1P_1A'_1G''$ вышеуказанные заболевания развиваются на более позднем этапе жизни. Напротив, коровы-носители аллеля $B_1Q'I''$ подвержены им в более ранние периоды жизни. Гипотетически животные-носители аллелей $QA'_1E'_3F'_2$ и I' резистентны к заболеваниям конечностей, $O_2P_1P_2I'_1$, PI’, P_2I', Q, A'_1I'', I’ – обмену веществ, носители аллелей $O_2P_1P_2I'_1$, A'_1I''– к заболеваниям вымени. Предложен селекционный путь совершенствования внутрипородного типа айрширского скота – формирование относительно однородного стада по продолжительности использования высокопродуктивных животных, устойчивых к заболеваниям на основе оптимизации подбора родительских пар с учетом маркерных генов.

Abstract: The Karelian type of the Ayrshire breed of cattle was bred as a result of over 30-year long selection work using the method of purebred breeding using bulls of Finnish and domestic selection. The principal selection indicators when selecting the breeding stock were the volume of milk yield, contents of protein and fat in the milk. Further improvement of the inner breed type determines the necessity of searching genetic factors of natural resistance for using them as a selection indicator. The co-dominant form of inheriting the blood type presents a convenient genetic model for studying associations with disease incidents. At the example of one of the breeding farms of the Republic of Karelia, a retrospective analysis was conducted revealing the causes of dairy cows’ morbidity to establish genetic determination of diseases. Processing of the experimental materials was conducted by using methods of cluster, factor and discriminating analysis, which allowed not only for not grouping the numerous population (441 species) according to homogeneity of manifestations of zootechnical indicators, but also to establish the structure of connections between the researched variables (life longevity, milk production, contents of fat, live weight, and age of the first calving, alleles, and the reasons for disposal). The step-by-step discriminative analysis confirmed by 97,73 % the reliability of dividing the animals into three groups (clusters). Among the principal discriminators dividing the cows reliably were: life expectancy, productivity, live weight and age of the first calving. The use of factor analysis established the direct unidirectional connection between the allele of EAB-system and the reason for the animal withdrawal. The most common alleles of EAB-system in animals removed due to widespread diseases (diseases of limbs, udder and metabolism). By the frequency of alleles, we made an assumption that in animal carriers of allele $B_1I_1P_1A'_1G''$ the aforementioned diseases develop at a later stage of life. On the contrary, cows-carriers of allele $B_1Q'I''$ are subject to them in earlier periods of life. Hypothetically, animal carriers of alleles $QA'_1E'_3F'_2$ and I' are resistant to limb diseases, $O_2P_1P_2I'_1$, PI', P_2I', Q, A'_1I'', I' – of metabolism, carriers of alleles $O_2P_1P_2I'_1$, A'_1I''– to udder diseases. There was a selection method suggested to improve the inner-breed Ayrshire cattle – forming a relatively homogenous stock by longevity of using highly productive animals resistant to diseases on the basis of optimization of choosing parent couples with regard to marker genes.

Ключевые слова: айрширская порода скота, генетические маркеры, факторный, кластерный, дискриминантный анализ, селекция.

Key words: Ayrshire breed of cattle, genetic markers, factor, cluster, discriminating analysis, selection.

Introduction

Using the methods of genetics and immunology, immunogenetics is based on serological differences of erythrocytes in representatives of one species of animals (Stahl, 1973). The outer shell of the erythrocyte includes numerous genetically determined molecules responsible for various functions in the body, which determines the significance of researching blood types in the cattle selection (Tikhonov, 1967; Serdyuk, 2018).

Blood types belong to genetically polymorphous indicators, are determined by serological methods and obey Mendel’ law. The system means factors of blood types or phenotypical groups, which are controlled by alleles of one locus. The blood type formula embraces all the present factors in one given animal (Stahl et al., 1973).

The genetic structure of the Karelian type of Ayrshire breed is studied on the basis of erythrocyte antigens of blood type in hemolysis reactions. Immunological samples are used as markers during certification of breeding animals, verification of their origins, allele fund analysis of stocks, lines, families, evaluation of genetic similarities and differences, study of hereditary specifics and potential capabilities of the breeding cattle. Each herd has a specific distribution of genotypes, which is a reflection of selection work, the principal task of which is to preserve the “successful” gene combinations in the future generations. To preserve the desirable genotype, it is good to use blood types whose inheritance can be traced in a number of generations (Maksimova, Shulga, 2017).

The connection between the genotype and productivity according to the blood type polymorphism was a subject of a number of research (Brum et al., 1968; Rausch et al.(1968); Mather et al., 1977; Gonyon et al., 1987; Haenlein et al., 1987; Rocha et al., 1998; Tkachenko et al., 2015). Brum et al. (1968) researched the connection between the type of polymorphism in nine genetic loci and productivity of cows od Holstein breed, and established that alleles in B-locus of the blood type were reliably tied to the percentage of fat content; at the same time loci A, J, L and Z did not have any notable impact on productivity. Rocha et al. (1998) summarized the results of the forty years’ work on using blood type as genetic markers in the selection process of Holstein cattle and found the influence of M-locus on the milk and protein yield. On the basis of the previous genetic monitoring of farm families of Ayrshire breed, the connection of alleles of blood type EAB-system with productivity indicators was found (Maksimova Shulga, 2017). The research by Tkachenko et al. (2015) established that allele $E'_{3}F'_{2}G'O'G''$ is an immunogenetic marker of the high yield of milk.

Hargrove et al. (1980) studied the connection of blood polymorphism with reproductive capacity and established the significant influence of S-system. When studying the factors of reproduction of breeding cows of black-and-white cattle, it was revealed that using bulls with alleles different from the allele fund of the herd increases the reproductive capacity of cows as well as average daily growth of young animals in the postnatal period (Politkin, 2013).

Results of research of the genotype connection with incidence of mastitis were presented in the work of Larsen et al. (1985), where association of 11 blood types with mastitis was researched. The status of mastitis was traced during three lactation periods. A significant influence of the blood type system M was observed on the frequency of mastitis incidence during the first and second periods of lactation.

Selective value of alleles and genotypes is based on the analysis of mastitis incidents in milk cows, delays of placenta, endometritis depending on the presence in the genotype of certain alleles of EAB- and F-V-systems of blood type. Based on the analysis of incidents and results of research of blood samples of black-and-white cows, complex genotypes were revealed, which can be used as markers for cow resistance to mastitis, endometritis, delays of placenta, as well as disposition to the studied diseases (Skripnichenko, Krovikova, 2014). The data on antigens of EAB-system of blood types can be used as immunogenetic markers of resistance (susceptibility) of Ayrshire cows to endometritis and mastitis. Thus, two antigens were discovered in this system with high frequency of occurrence in cows with endometritis T_1– 0,211 and P’ – 0,155 respectively. On the contrary, presence of antigens I_2, P_2, J_2, J'_2, G’, Q’ in the genotype is connected with resistance to these diseases (Maksimova, Shulga, 2017). The use of genetic markers allows for managing the genetic structure of the herd and increasing the share of animals-carriers of desirable genotypes (Panina, 2009; Silkina, Bukarov, 2012).

Further on, when improving the inbreeding type of Ayrshire breed, the study of genetic factors of natural resistance is of greatest interest, since as a result of targeted breeding for dairy production cows demonstrate increased susceptibility to diseases (Mishchenko, 2008). The data received during the research of Bakharchiev (2010), Vilver (2014) confirm the genetic conditioning of the natural resistance factors. Hereby, summarizing the results of domestic and foreign research it is necessary to mention that immunogenetic monitoring of the herd, being the integral component of selection, can be used for studying genotypical resistance of animals to this or that disease.

The goal of this work is to reveal genetic conditioning for morbidity of breeding dairy cows of Karelian type Ayrshire breed.

Materials and Methods

The object of the research is the group (441 heads of livestock) removed breeding Ayrshire animals from one of the breeding farms of the Republic of Karelia. For analysis, indicators of the primary zootechnical registration for 2016—2017 were used: life expectancy, age of first calving, live weight, milk productivity as well as reasons for animal withdrawal (diseases of limbs, udder, digestive and breathing systems, reproductive organs, malfunction of reproductive function, injuries, withdrawal for old age). Besides, blood types were taken into account (alleles of EAB-system), which were determined in the laboratory of immunogenetics of “Karelian GSHOS” pursuant to the existing regulations (2002).

Preliminarily, the qualitative indicators (reasons for withdrawal, alleles of EAB-system) were ascribed relevant codes, which were not used during interpretation of results of qualitative data processing.

Statistical processing of the aforementioned data of zootechnical registration was conducted in three stages using certain methods of multivariate analysis (Kim et al., 1989; Duke,1997) on a PC using the Excel and StatGraphics Centurion XV software. The first stage included grouping animals by the studied indicators (variables) with the use of cluster (Varde method, Euclid distance) and step-by-step discriminant (method of inclusion) analyses. During the second stage we established the structural connections between the variables with the use of factor (principal component method) analysis. The third stage called for calculation of allele occurrence (Popov et al., 2018) – relation of the allele number to the total number of animals under study.

Results

When grouping the animals by homogeneity of the studied qualitative variables, three clusters were received (Table 1). The step-by-step discriminant analysis confirmed by 97,73 % the correctness (reliability) of dividing the animals into three groups. The main discriminators are the variables in the following sequence: life expectancy, fat content in milk, age of the first calving, and live weight.

Table 1

Animal Grouping by the Complex of Zootechnical Indicators

Indicator	Cluster		
	I	II	III
	Centroids		
Life expectancy, months.	84,5	70,4	50,6
Fat content in milk, %	3,9	4,2	3,9
Maximal productivity, kg	8709,4	7152,4	7057,2
Age of first calving, months.	28,1	29,1	26,0
Live weight, kg	571,8	543,5	515,1

Revealing the connections between the studied variables with bthe use of factor analysis showed presence of three factors (Table 2).

Table 2

Factor Analysis Results

Indicator	Factor loads		
	F_1 (25,9 % of total variance)	F_2 (17,3 % of total variance)	F_3 (14,8 % of total variance)
Alleles	–0,02	–0,31	0,59
Reason for withdrawal	0,03	0,16	0,84
Life expectancy	0,85	–0,01	–0,09
Milk productivity	0,60	–0,61	0,01
Live weight	0,66	0,05	0,16
Age of the first calving	0,45	0,14	–0,05
Fat content in milk	0,26	0,80	–0,05

According to the signs and values of factor loads the known regularities were received: according to the first factor (F_1) — with growing life expectancy of dairy cows their live weight and productivity also grow; according to the second (F_2) — with decrease of milk productivity the fat content of milk increases. The third factor (F_3) established the unidirectional connection between the allele EAB-locus of blood and reason for animal withdrawal, which allows for assuming genetic determination of the diseases under study. Their proportion as principal reasons for animal withdrawal was shown differently in the selected clusters (Table 3). In the studied selection limb diseases dominated. A significant share of animals was removed due to udder diseases and abnormality of the reproductive function, as well as metabolic diseases.

Table 3

The Structure of Allocated Clusters Due to Animal Withdrawal

	Share of animals with different reasons for

Reason for withdrawal	withdrawal according to allocated clusters, %		
	I	II	III
Limb diseases	43,8	23,5	57,4
Udder diseases	21,1	20,8	13,3
Reproductive function disorder	16,2	18,9	15,3
Metabolic diseases	8,1	14,2	9,3
Difficult delivery and complications	4,9	5,7	1,3
Digestive system diseases	1,6	6,6	2,7
Reproductive organs diseases	1,1	0,9	0,0
Respiratory system diseases	0,5	0,0	0,0
Pericarditis	0,0	0,9	0,0
Low yield	0,0	1,9	0,7
Accidents (injuries)	2,7	6,6	0,0

For the clusters under consideration, the most frequent alleles of EAB-system were selected in animals withdrawn due to the prevailing diseases (of limbs, udder, metabolism). The reproductive function disorder occurs due to a number of factors and will be a subject of special study (Table 4).

Table 4

Frequency of Alleles in EAB-system (n = 441)

Allele of EAB-locus	Reason for animal withdrawal								
	Limb diseases			Udder diseases			Metabolic diseases		
	clusters			clusters			clusters		
	1	2	3	1	2	3	1	2	3
$B_1I_1O_1P_1P'_1F'_2G''$	0,0084	0,0024	0,0012	0,0060	0,0024	0,0024	-	0,0012	-
$B_1I_1P_1A'_1G''$	0,0012	-	-	0,0048	-	-	0,0024	-	-
$B_1Q'I''$	-	-	0,0048	-	-	0,0012	-	-	0,0024
BYA'E'3G'P'Q'	0,0060	-	0,0024	0,0132	0,0036	-	0,0048	0,0024	-

$B_1Y_2E'_3G'G''$	0,0108	0,0024	0,0252	0,0156	0,0012	0,0036	0,0036	0,0024	0,0072
$B_2G_2O_1Q'I''$	0,0036	0,0012	0,0132	0,0024	0,0024	0,0024	0,0012	0,0012	0,0012
$B_2G_2O_1G''$	0,0024	0,0012	-	0,0048	0,0012	-	-	-	-
O_1	0,0012	0,0060	0,0024	0,0108	0,0012	-	-	0,0012	-
$O_2P_1P_2I'_1$	-	0,0012	0,0012	-	-	-	-	-	-
PI’	0,0048	0,0012	-	0,0036	0,0024	0,0012	-	-	-
$P_1A'_1G'G''$	0,0084	-	0,0084	0,0024	-	-	-	-	0,0024
P_2I'	0,0060	-	0,0012	0,0022	0,0036	-	-	-	-
Q	0,0012	0,0024	0,0036	0,0048	0,0012	0,0012	-	-	-
$QA''_1E'_3F'_2$	-	-	-	-	-	0,0036	-	-	0,0012
$Y_2A'_2$	0,0048	-	0,0012	0,0060	-	0,0012	0,0012	0,0012	-
A'_1	0,0182	0,0048	0,0096	0,0108	0,0024	0,0024	0,0048	0,0024	0,0012
$A'_1E'1$	0,0072	0,0036	0,0132	0,0072	0,0012	-	-	-	0,0012
A'_1I''	0,0012	-	0,0096	-	-	-	-	-	-
E'_3Q	0,0012	-	0,0024	0,0048	-	-	0,0012	0,0012	-
I’	-	-	-	-	0,0012	0,0024	-	-	-

Alleles $B_1I_1O_1P_1P'_1F'_2G''$, $B_1I_1P_1A'_1G''$, $B_1Q'I''$, BYA’E’3G’P’Q’, $B_1Y_2E'_3G'G''$, $B_2G_2O_1Q'I''$, O_1, $P_1A'_1G'G''$, $Y_2A'_2$, A'_1, $A'_1E'1$, E'_3Q were revealed in animals withdrawn for the reasons of the aforementioned three diseases. Allele $B_1I_1P_1A'_1G''$ is typical for the animals of the first cluster with maximal life expectancy, allele $B_1Q'I''$, on the contrary, for the third cluster. Animals withdrawn due to limb diseases did not have allele $QA''_1E'_3F'_2$ or I’, due to udder disease – allele $O_2P_1P_2I'_1$, metabolic diseases – $O_2P_1P_2I'_1$, PI’, P_2I', Q, A'_1I'', I’.

Discussion

In the considered selection (441 heads of livestock) by the variable set, the animals were divided into three groups, which distinctly differ by life expectancy, productivity, fat content in milk, age of first calving and live weight. On the basis of the detailed analysis of the indicators it was established that the first cluster covers 41,9 % of dairy cows and is characterized by maximal values of two variables.

For the animals of the second (24,0 %) and third (34,1 %) clusters, reduction of the life period is related to decrease of milk productivity. The third cluster shows the lowest life expectancy as well as minimal indicators of productivity, live weight and age of first calving. Early withdrawal of least resistant animals does not allow for revealing their genetic productive potential; therefore, the task of selection is in forming relatively homogeneous livestock of dairy cows with productive longevity typical for the animals of the first group.

The use of factor analysis confirmed the regularities between animal life expectancy, milk productivity, fat content, and hypothetically established the connection between the allele of EAB-system of blood and reasons for animal withdrawal. The most frequent alleles of EAB-system were determined in animals withdrawn due to diseases of limbs, udder, metabolism in all received clusters. According to allele incidence, we made an assumption that animal carriers of allele $B_1I_1P_1A'_1G''$(cluster 1) develop diseases of limbs, udder and metabolism at a later stage of life. On the contrary, cows-carriers of allele $B_1Q'I''$(cluster 3) are subject to these diseases during earlier periods of life. Hypothetically, animal carriers of alleles $QA''_1E'_3F'_2$ and I' are resistant to limb diseases, $O_2P_1P_2I'_1$, PI', P_2I', Q, A'_1I'', I' – to metabolic diseases, and allele $O_2P_1P_2I'_1$, A'_1I''– to udder diseases.

The study of genetic factors causing susceptibility to diseases will allow for revealing the probability of disease development from the inherited alleles of EAB-system. The results of the presented assessment with the use of a set of methods of multifaceted statistical analysis showed feasibility of selecting parent pairs with regard to marker genes for the sake of forming a highly productive livestock resistant to diseases.

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