The formation of dairy cattle intrabreed type: Macropopulation aspects

I Yu Eremina¹, L A Gerasimova²* and A I Kuklina²

¹ Krasnoyarsk State Agrarian University, 90, Mira Av., Krasnoyarsk, 660049, Russian Federation
² Reshetnev Siberian State University of Science and Technology, 31, Krasnoyarskii Rabochni Av., Krasnoyarsk, 660037, Russian Federation

*E-mail: lyu-gerasimova@yandex.ru

Abstract. The long-term changes in the phylogenetic population characteristics of nine herds of red-and-white dairy cattle of Krasnoyarskii Krai (Russia) in the process of breed formation were estimated. Immunogenetic indicators (erythrocyte antigens) were used. The genetic structure of the population was investigated according to the frequencies of antigenic factors, the frequencies of the phenogroups. The genesis of the formed breed features is outlined by the indicators of the genetic similarity between the crossed breeds and the maternal subpopulations of individual lines. To study polymorphism, the data of the breeding records of the ARM “Selax Molochnyi”, the OOO RC “PLINOR” and hemolytic tests.

1. Introduction

Macropopulation characteristics can be detected by immunogenetic methods widely used as a general biological approach to evaluate micro evolutionary processes for a wide variety of economically useful species, from fish and poultry to cattle [1-11].

The negative genetic-selection aspects are well known: the disappearance of the breed → the narrowing of the gene pool of the species → the reduction of the genetic potential for solving new selection and adaptation problems. In dairy cattle breeding, for example, increasing of productivity leads to deteriorating of reproductive capacity of cows and decreasing of immunity and resistance [5, 12, 13].

To timely adjust the breeding process, one should know the genetic features of the breeding material, the degree of consolidation of breeds and populations or their differentiation in the breeding process. Along with the traditional methods of comparative analysis of populations based on genealogy data, these problems can be solved by methods of immunogenetic analysis, which reveals internal processes that are not always manifested. Immunogenetic characteristics allow not only to evaluate the gene pool of a certain set of individuals as a whole, but also to reveal trends in its change. Recently, the issue of studying genetic similarity and its evolutionary history has been solved by means of more subtle mechanisms of genetic differentiation; in particular, the method of calculating genetic distance is used. In case of use of blood group antigens as population markers for population comparison, it is legitimate to analyze antigenic similarity [4, 14, 15].

In gene pools of many breeds there is a tendency to the reduction of genetic diversity by blood groups [1]. Each animal population has its own genetic structure of phenotypes, genotypes and frequencies of polymorphic systems influenced by the direction of breeding, the composition of breeders, the difference
in the fertility and viability of individual genotypes, the drift of genes, natural and presigotic selection. Integral influence of these factors leads to maintaining the relative stability of frequencies of the main alleles of blood groups with a steady reduction in genetic diversity due to the elimination of rare alleles. It is believed that the loss of at least one allele of a blood group in a herd should be considered as an unfavorable phenomenon, proceeding from the fact that the decrease in diversity of polymorphic forms is associated with a disruption in adaptive properties, especially in the event of stressful situations. Maintaining a stable ratio of frequencies of the main alleles over a long period, despite various selective effects, suggests that the main alleles mark the most "successful" blocks of genes with a much greater frequency [4, 10, 14, 16].

The immuno-genetic approach has been widely used since the mid-20th century to the present to solve breeding problems by specialists from many countries [2, 3, 5, 6, 13].

Thus, genetic markers, being an integral part of a gene pool of a breed of populations, provide valuable information about changes that occur in them in the breeding process. This information can be used in the practice of breeding work to increase its effectiveness.

The research was conducted to establish the fact of formation of a small taxonomic unit - a breed type of dairy cattle, as a factor in the manifestation of macropopulation processes.

Microevolutionary aspects were considered: genetic differentiation of lines of individual herds by antigenic factors; intrabreed genetic consolidation of red-and black-and-white populations.

2. Objects and methods
The objects of the research were breeding herds of the red-and-white root, bred in the territory of Krasnoyarskii Krai.

The formation of populations of Siberian cattle took place on the basis of the Great Russian one, imported by settlers from central Russia. It was spread on the vast territory of Siberia, Buryatia and the Far East.

To create a new Siberian type, a cross was carried out with the Holstein breed, which is known to have the world's highest genetic potential for milk productivity. Currently, in Krasnoyarskii Krai a lot of work is being done to improve livestock, to make it more adapted to specific natural and technological conditions. A new type of Yenisei red-and-white cattle is approved; a strategic program of work with the breed and the lines was developed and is being implemented [9, 10, 17, 18].

Preliminary background passporting of livestock with analysis was carried out in 1987-1989 [6, 15, 18, 19] and was subsequently carried out from 1992-1993 in stages up to 2015.

In total, the analysis used data on 13000 animals from nine breeding populations of red-and-white cattle. The initial material for the research was the results of testing blood samples of animals.

To study polymorphism, the data of the breeding records of the ARM "Selax Molochni", the OOO RC "PLINOR" and hemolytic tests. The tests were carried out by a set of 47 basic reagents, according to nine genetic systems: A, B, C, F-V, M, L, J, S, Z. To assess the state of genetic systems in a population, breed or breeding group of animals, the results were analyzed using statistical and population-genetic methods.

The genetic structure of the population was investigated according to the frequencies of antigenic factors, the frequencies of the phenogroups. The frequencies of the antigens were expressed as a percentage; the comparison of the genetic structure of the population by blood groups was carried out according to generally accepted indicators: the index of genetic (antigenic) similarity of r ± m [16, 20]. Indices of immunogenetic distances were calculated in accordance with the recommendations of Zhivotovsky L.A. and Mashurov A.M. [10, 14, 15, 19].

To illustrate the nature of phylogenetic connections between the studied herds, the method of unweighted pairwise clustering was used to calculate the indices of genetic distances on the basis of which dendrograms were constructed. The possibilities of the "Statistica" program were used, the algorithms of which provide for clustering based on distances and the construction of dendrograms.
3. Research results

Holsteinized red-and-white cattle were formed on the basis of the Simmental breed. The gene pool of individual herds was also replenished with red-and-white animals of high blood, imported from European countries (Germany, Denmark).

A comparative analysis of the gene pools of combined Simmental lines records the presence of both general and specific features inherent in the lines of Fasadnik, Signal, Clover and Mergel. The greatest similarity is defined between the Signal and Facade lines \( r = 0.99\pm0.01 \), and the smallest one between the lines of Clover and Mergel \( r = 0.93\pm0.01 \) (table 1). With the considerable genetic similarity of the Simmental lines analyzed, it should be noted that there is a certain isolation of the Clover line. This is the point of the initial stage of the divergence of lines that share common ecological and genetic roots [16].

| Lines            | Fasadnik       | Signal       | Mergel       |
|------------------|----------------|--------------|--------------|
| Signal 48634C-239| 0.99±0.01      |              |              |
| Mergel 2122 40-266| 0.99±0.06      | 0.97±0.01    |              |
| Clover 68 KEC-4  | 0.95±0.01      | 0.94±0.01    | 0.93±0.01    |

Indices of antigenic similarity fix the similarity between Holstein line. Such similarity is explained by the use of a single mother base in the formation of different lines. The lines Rosafe Citation and Seiling Triune Rocket are the most distant from each other (table 2), that shows the influence of paternal genotypes on the formed gene pool of red-and-white cattle.

| Lines            | Montvic Chieftain | Rosafe Citation | Seiling Triune Rocket |
|------------------|--------------------|-----------------|-----------------------|
| Rosafe Citation  | 0.92±0.01          |                 |                       |
| Seiling Triune Rocket | 0.87±0.01      | 0.89±0.01     |                       |
| Reflection Sovereign | 0.88±0.01     | 0.91±0.01     | 0.86±0.01             |

We compared the results obtained in the calculation of the antigenic similarity index between the groups of Simmental-Holstein hybrids in the populations under study and the patterns of the relationship of these groups (figure 1, 2).

Comparing the results obtained, it should be noted that these dendrograms adequately reflect the processes described in the analysis of indicators of genetic similarity.

Summarizing the available data, it is possible to speak with confidence about a genetic disunity of the crossbreeds, both within the same population and in their totality; about the significant role of the maternal gene pool, ensuring the consolidation of breeding groups of animals of the same population; about the uniqueness of the ecologically-historically established gene pools of each population, which include mechanisms of adaptation to the specific conditions of the given range.

In general, for the studied populations, no linear consolidation was detected. Linear differentiation exists at the intraherd level (figure 1). Hybrids (RedSF1) have more affinity with maternal Simmental Foundation than animals separate lines.
The following populations were analyzed in dynamics: the original Simmental, introduced red-and-white Holstein, the hybrids of the first generation and the populations working to form a new Yenisei type of red-and-white cattle. (EtP1-EtP4 figure 2).

Consolidation of the Yenisei type populations is higher than Holstein and Simmental lines (figure 1, 2).

4. Conclusion
The results of the study of the antigen spectrum characteristics of linear groups with the same name in different herds indicate linear isolation within each specific farm.

In general, interpopulation linear consolidation has not been identified. Interpopulation interlinear differences are unacceptably small and do not justify the predicted heterogeneity parameters, which can lead to negative consequences in the form of genetic abnormalities and decrease in resistance. Interlinear differences within herds, found in representatives of interbreed F1 hybrids, indicate the presence of a
certain genetic polymorphism; linear differentiation was revealed at the intrastage level. It was established that the coefficients of genetic distances as combined indicators calculated on the basis of immunogenetic indicators can serve as a measure of interlinear and intrabreeding differentiation.

The study confirmed the possibility of using the coefficient of antigenic similarity, an indicator of immunogenetic distance (d) to assess the measures of interbreed and intrabreeding differentiation. This method is a method of molecular taxonomy and is of interest from the point of view of improving the methods of animal breeding. Research results can be used to predict heterosis, line differentiation, and breeding programs aimed at rational use of the dairy cattle gene pool.

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