

O. I. Babenko, V. P. Oleshko, V. Y. Afanasenko. The predicted genetic progress in dairy cattle populations using a variety of methods for evaluation and selection of animals

Genetic progress in a herd of animals is due to the selection of four categories of pedigree animals: fathers of sires, mothers of sires, fathers of cows and mothers of cows. Extremely important role in genetic improvement of a herd plays selection of the sires for insemination of breeding stock which become the potential parents of cows. The selection of sires' mothers, sires' and cows' parents provides 90-95% of the effect of selection in animal population, and massive selection of cows' mothers only 5-10%. The main selection trait in a herd is milk production, therefore with the purpose of analyzing the effectiveness of selection by this trait defined pedigree value of 4 categories of pedigree animals, which influenced on the pace of improvement of the populations. Therefore, to accelerate genetic improvement of dairy cattle populations is necessary to increase the magnitude of the genetic benefits of parental animals and reduced generation intervals, which is the aim of our research.

The average annual genetic progress through selection of four categories of pedigree animals in the herd of Holstein breed is 61.2 kg of milk per cow per year and the pace of genetic improvement of the herd – 0.81 %. In the population of Ukrainian Black-and-White Dairy breed, these figures are respectively 43.2 kg of milk and the pace of genetic improvement of the herd – 0.62 %

Much more opportunities in raising the rate of genetic improvement can be achieved through the introduction of genomic (GS) or marker-assisted selection (MAS). Under the terms of the genomic breeding, final estimation of pedigree value of sires is carried out during 2.5 years in the contrast with traditional breeding, which involves the time for 5 years. Experts estimate the cost from the use of GS or MAS compared with conventional breeding are up to 92%, and the efficiency of selection is improved two times.

Taking into account that data of productivity of animals are associated with genes of economically useful traits, the topical issue is the selection of the optimal polymorphic marker systems for their introduction into practice of breeding and assessment of genetic structure of cattle breeds.

On the basis of our results of studies of the effect of QTL – gene, the complex model genotype for the selection of animals for the purpose of increasing milk yield in animals of Ukrainian Black-and-White Dairy breed is like this: CSNS^{AB}, GH^{LL}, β LG^{AB}, Pit-1^{AB}; Holstein – CSNS^{AB}, GH^{LV}, β LG^{AA}, Pit-1^{AB}.

Comparison of model genotypes of Ukrainian Black-and-White Dairy and Holstein shows that there are differences in the combination of genotypes contributing to the best development of traits. Thus, the mass fraction of the protein, the model genotypes are identical at 75% in both breeds: by the yield, quantity of milk fat and protein and total milk fat and protein model genotypes match by 50%.

Due to implementation of genomic evaluation and breeding of dairy cattle, the valuation period of pedigree animals was reduced significantly. Unlike conventional breeding, the introduction of genomic selection will reduce the genetic interval in the

population of Ukrainian Black-and-White Dairy breed of sires' fathers by 4.5 years, sires' mothers by 4.6 years, cows' fathers by 4.6 years and cows' mothers by 2.9 years. In the population of Holstein cattle generation interval of sires' fathers is reduced by 4.3 years, sires' mothers by 4.5 years, cows' fathers by 4.5 years, and cows' mothers by 2.7 years.

The results of our studies show that the rate of genetic improvement of dairy cattle population in the main breeding traits can be improved through the selection of animals by QTL-complexes. Thus, the selection of breeding stock based on a comprehensive model of genotype on yield gave an opportunity to improve pedigree value of the maternal cows at 155 kg compared to traditional breeding, and in the population of Holstein cattle at 246 kg. Only these factors allow genetic progress in milk yield in the population of Ukrainian Black-and-White Dairy cattle by 128.5 kg, which is 2.9 times more than the value of the actual genetic progress and in the population of Holstein cattle – 183.2 kg, which is three times more compared to the actual value of genetic progress for milk yield in this population.

The contribution of the cows' mothers to genetic progress increases. So, if at conventional breeding, the contribution of this category of pedigree animals was negative (-4.9%), selection on QTL complex is 3.2% and in the population of Holstein cattle 12%. If you apply the selection of other categories of pedigree animals (sires' fathers, mothers and parents of sires) on QTL-complexes, which contribution in the genetic improvement of populations is 88.0–96.8%, the rate of genetic improvement of dairy cattle populations will greatly increase.

Conclusion. To accelerate genetic improvement of dairy cattle populations it is necessary to use molecular genetic markers that control metabolic processes in the body.

Keywords: Ukrainian Black-and-White Dairy breed and Holstein breed, pedigree value, genetic progress, genes, genetic markers, genotypes, breeding traits, milk yield