

O. I. Metlytska, K. V. Kopylov, A. V. Berezovsky. Modern molecular-genetic approach to increase efficiency of selection process in animal breeding of Ukraine

Evaluation of livestock genomes to identify gene complexes which lead to expression of the quantitative trait desired for breeding is impossible without knowledge of its fine molecular structure and characteristics of "work" of this complex system – the interaction of genes at the level of their protein products, regulation of gene activity, and so on. To address such complex issues focused efforts of leading scientists in the world who have worked within the mapping and sequencing the genomes of the most economically important species of farm animals – "transcript" of the genome of some dog breeds was completed in 2003, the structure of the genome of cattle, pigs, rabbits, horses and turkeys was identified only in 2009, and the notice about completion of international program "Honeybee Genome" appeared only in 2010.

The rapid genesis of methods of molecular genetic analysis of farm animals' genomes is not in vain called "DNA Revolution" and the number of methodological approaches and developments in this field is huge, so we consider it appropriate to be limited to developments of a leading scientific center of Ukraine to address these important issues – Institute of Animal Breeding and Genetics nd. a. M.V. Zubets of NAAS of Ukraine.

The main focus of the institute is developments of scientists which help to solve an important problem of the state – preservation of the existing gene pool of domestic breeds. In this sense, the developments of genetic testing of cattle on the "major" genes of quantitative traits, involved in forming the qualitative indicators of milk and meat productivity (k-Cn, β LG, GH, TG5, CAPN1 530, MSTN), have shown uniqueness of domestic breeds and high frequency of genotypes desired for breeding aimed at improving quality of milk and meat products. For example, k-Cn (kappa-casein) gene can be determined in a herd of animals with genotypes determining the presence of milk protein with desirable properties for cheese-making and selection of animals on some genotypes of β LG, GH, TG5 not only helps to intensify breeding towards milk yield increase, but will increase its fat content. Some mutation, identified in CAPN1 530 (calpain) gene, will provide for its carrier – a representative of beef cattle breeds by expressed marbling of muscle and individuals with abnormalities in MSTN (myostatin) gene will have "double" hypertrophied muscle structure. By the way, convenience to address practical issues of production of molecular genetic markers is that any genetic material (blood, pinched hair from an ear at marking of animals, buccal scrape of mucous membranes, urine, manure, semen, hair with hair follicles and even a few cells of embryos, etc.) can be used for researches at any age of animals. The value of this information is an early assessment of a genotype of an animal, that is, its genetic potential immediately after birth.

Using crossbreeding of different local populations of farm animals with imported ones has helped to improve the genetic potential of productivity of many populations of animals in very short term and the widespread artificial insemination has created conditions for economically useful programmable transmission of genes from parents to offspring. But now, as a result of intensive breeding and breed formation the accumulated reserve of variability has been reduced that can't affect the possibility of strategic breeding. Intensive processes of "holsteinisation" and use of

the limited number of sires of leading lines of this breed at moderate inbreeding and limitation of effective population size have led to the accumulation of "genetic load" in herds of local breeds—mutant variants of gene with lethal and semi-lethal effects.

Determination of hidden genetic abnormalities in cattle (BLAD – Bovine Leukocyte Adhesion Deficiency, CVM – Complex Vertebral Malformation, DUMPS – Deficiency of Uridine Monophosphate Synthase) using DNA diagnostics is carried out to prevent the accumulation of genetic load and reproductive losses. The vast number of spontaneous abortions and reasons of early death of calves with birth defects is caused by gene mutations appearing phenotypically only if carriers of mutant alleles are both parents of a descendant. Identification of animals with heterozygous genotype as carriers of hidden abnormalities, is possible only if using proposed DNA technology.

Another type of testing breeding animals which is obligatory under law "On Livestock Breeding" is a cytogenetic analysis. In the selection and breeding work it is important not only to use methods for assessing the genetic potential of animals on the basis of productivity traits and availability of genetic diseases caused by mutations in specific genes. We must also take into account the sensitivity of animals' genetic apparatus to different mutagenic environmental factors; it makes possible to select animals to improve genetic stability of their offspring and creating genetically stable populations at some farms that will significantly reduce the likelihood of chromosomal or genetic reconstructions in animals.

Reliable ways to assess genetic and population situation, genetic differences at interspecies, within species and individual level include a method of ISSR-PCR. Effective criteria for determining the impact of mutagenic environmental factors and selection factors on the structure of the investigated samples are implemented via this method and it is used as a tool for search of genetic loci associated with expression of the desired quantitative trait. This development is intended for use primarily in pig breeding for obtaining heterosis of offspring with high potential fattening and meat qualities.

As a result of long-term molecular genetic monitoring with use of own-created informative DNA markers in technology ISSR, RAPD, the confirmation of selection achievements in beekeeping was received— creating Khmelnytsky intra-breed type of Ukrainian Steppe bees with construction of unique genetic passport. The basic genetic criteria of "pure breed" of three bee species – Ukrainian, Carpathian and Grey Caucasian Mountain were determined, thus the degree of "pure breed" of bees can be determined accurately on the basis of morpho-metric and molecular genetic indicators. Using ISSR-S4 primer is able to identify the genome fragment of Ukrainian bees with size 950 bp, which is significantly associated with the expression of honey productivity; the research is carried out in this field.

Conducting DNA certification of bees to determine the purebred Ukrainian Steppe bees and Carpathian bees is a necessary part of the breeding work in beekeeping for the prevention and elimination of consequences of undesirable interbreed crossbreeding, linear consolidation, increase of traits of honey productivity.

In 2014, "Guidelines for morphological and genetic evaluation of Ukrainian bees" were formed and approved by the Ministry of Agrarian Policy of Ukraine as a result of long-term comprehensive studies on the genetics of honey bees.

Despite the difficult economic situation, a significant reduction in funding scientific support, reduction of scientific staff, low technological level of existing equipment, the work towards the development of effective technologies for the needs of the agricultural sector is conducted. The unique researches of peculiarities of genetic structure of major histocompatibility complex of cattle and pigs are carried out to identify animals with the best heredity for reproductive capacity and resistance to infectious diseases. Further study of protective and hygienic behaviour of bees, which is currently underway, will enable to improve breeding work in beekeeping with getting environmentally friendly products which can be exported and receive significant foreign exchange earnings to the state budget.

In general, livestock of Ukraine is the most important part of the socio-economic development and food security, as it is a manufacturer of biologically important products in the human diet. It is decidedly, that the progressive development of agriculture which defines export potential, quality of life and prosperity of citizens of Ukraine is impossible without the development of modern technologies and appropriate scientific support.

Keywords: **animal breeding, molecular genetic methods, MAS-selection, immunogenetic markers, genetic abnormalities, ISSR-typing**