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Molecular-genetic monitoring in system of preservation of genetic resources of animals

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The purpose. To develop theoretical approaches concerning expediency of application of modern molecular-genetic methods of probes within the limits of holding genetic monitoring in system of preservation of genetic resources of animals. **Methods.** Dialectic method of scientific knowledge, analysis and systemic generalization. **Results.** It is necessary to consider ndigenous breeds as carrying agents of the unique genetic information which cannot be replicated by modern methods of selection. In some ecosystems economically expediently their growing in purity, and also straight introduction in zones where reproduction of highly productive forms is impossible. From this point of view, study of gene pools of indigenous breeds is important for searching new useful genes of quantitative or other attributes (productivity, resistance to diseases and stresses) which in the further can be used in selection. **Conclusions.** For comprehensive analysis of genetic structure of pedigree resources of breeds development and systematization of methods on determination of the most informative tests for different types of DNA-markers is necessary. Heading of elements of molecular-genetic monitoring will promote detection of carrying agents of valuable genes complexes by deriving molecular-genetic information of features of genetic structure. That will allow identifying and determining optimum content of gene pools and quality of genetic material for backfilling and keeping specimens of biomaterial.

Key words: *molecular-genetic monitoring, genetic resources, polymorphism, DNA-markers.*

As a result of the processes occurring in complex systems of relations between nature and man, the ecological directions of the development of society have become a priority and concentrated on the protection of natural resources. The problem of protecting the gene pool of the planet and the processes of adaptation of different populations to rapidly changing environmental conditions have become the fundamental directions of research in modern science.

At the present time, the problem of preserving the gene pool of rocks and populations of agricultural species of animals, which by the level of productivity can not compete with highly specialized tribal resources, becomes of paramount importance. In a market economy, their breeding does not provide the necessary level of profitability, which forces the owners of the appropriate number of animals to reduce its size or completely stop the direction of their breeding. In particular this applies to local (indigenous) highly adapted to the conditions of the breeding species, leading to a narrowing of the natural diversity and irreversible loss of unique characteristics that are inherent in this species. Such rocks are often characterized by better adaptability to adverse environmental factors have a strong constitution, elevated levels of total resistance, stable high reproductive capacity and a number of other valuable qualities, effective reproduction methods are breeding impossible or costly.

Preservation of species appropriate, in connection with the changing requirements of agricultural species due to competition (new food interaction prices for them), changes in the management and provision of livestock (mechanization, improving production technology), changes in hygiene and Environmental requirements (new types of diseases, vaccines, changes in the environment). Any aboriginal breed is a reserve of hereditary qualities, the use of which does not constitute the necessity of the present, but is a prospect of the future [1].

In the herd of Ukraine, such breeds include gray Ukrainian, white Ukrainian, Lebedinskaya, and Burat Carpathian. They can be qualified precisely those genetic resources of the biosphere, which were created for a long period, and now are on the verge of destruction. As a result of the 2006-2010 survey of livestock breeding resources in Ukraine, the importance of in-depth study of the genetic structure of herds, the identification of the most typical representatives of each of these breeds was noted. Such work is needed to determine the network of gene pool herds and objects, to develop specific measures for the programmatic reproduction of breeding material that can provide support for biodiversity in livestock in Ukraine at the right level. The results of complex research can be used to create the genetic types most adapted to new technologies and to the extreme conditions of reproduction in the future.

Aboriginal rocks should be considered as bearers of unique genetic information that can not be reproduced by modern selection methods. In certain ecosystems it is economically expedient for their breeding to be clean, as well as direct introduction into zones where reproduction of high-yielding forms is impossible. From this perspective, the study of gene pools of native species important to find useful new genes or other quantitative attributes (performance, resistance to disease, stress), which can later be used in breeding [2].

The relatively recent origin of agricultural species (housed) from wild animals indicates their ancestors certain similarities that can be used for complex analysis in genetic mapping [3] and the identification of mutations that underlie phenotypic diversity. Comparison simple genomic sequences shows no clear differences Which can be determined if the mutations do not lie in the areas of gene coding with a well-known function and, in general, the evolution of a single locus can be influenced by selection or drift and not by Must reflect divergences in phylogeny [4].

In addition, the predominant species of animals represent the most valuable model objects for solving the problems of modern medicine. Their use is considered promising for the testing of new drugs, in the study of the functions of genes with monogenic and multifactorial manifestations for various types of diseases [5]. Therefore, a comprehensive analysis of agricultural species is not only important for research and understanding of evolutionary formation processes, but also for the use of the results for applied purposes. This is directly related to the increase in agricultural products received at lower economic costs.

Development of conceptual basis and methodology of conservation programs, regulation and reproduction of biological diversity in livestock Ukraine should be made by taking into account, processing and compilation of international agreements, laws and regulations on the operation of Ukraine and livestock development [6-8].

Based on the data of complex observation of the population under study (breed) it is possible to make reasoned decisions regarding the status of animals and breeds in general, to develop scientifically grounded programs of quality conservation of diversity, taking into account the modeling of the breeding process, and also the choice of its optimal strategy.

Therefore, in the stratification of tribal resources and the implementation of programs for preserving the gene pool of rocks genetic research is becoming increasingly important, and the use of which in gene pool populations creates a system of genetic monitoring, which is designed to solve a wide range of tasks [9, 10].

Genetic monitoring is part of a biological or environmental monitoring that tracks the boundaries of intrapopulation genetic flows. When preserving breeds of domestic species, the internal and intra-breed genetic diversity acts as an object of control, evaluates and predicts its dynamics, determines the optimum and the limits of permissible changes. Genetic polymorphism (structural genes, DNA polylukous sequences, chromosomal and genomic mutations) characterizes the genetic structure of the breed, which is taken as the basis of preserving the gene pool of rare and endangered breeds.

When preserving in situ rocks, the main task is to not lose specific genetic complexes (or a balanced system of genes) that determine the phenotypic genetic characteristics associated with exterior characteristics, productivity, viability, and animal resistance [11].

The basis of genetic monitoring is the feline method (monitoring of fenges and structural genes), monitoring of gene and chromosomal mutations, monitoring of the gene pool using various types of molecular genetic markers (STR, ISSR markers, QTL). The use of molecular methods makes it possible to evaluate, predict and control the population-genetic processes occurring in herds during artificial and natural selection in a qualitative way.

The genetic assessment of the population status of these criteria is based on the implementation of genetic expertise that provides inventory of the allelic composition of rocks and the systematic application of genetic methods to solve the theoretical and practical issues of breeding farm animals. As objective criteria for the diversity of the gene pool of populations take into account the number and frequency of detected alleles and the theoretical and actual level of homozygosity for certain loci. It is believed that a small number of alleles and a high numerical value of the coefficient of homozygosity indicates the homogeneity and consolidation of the population gene pool, and a large number of alleles and relatively low homozygosity - a significant reserve of genetic diversity.

Studies of such a plan have both theoretical and practical significance in determining the genetic status of rocks, the evaluation of the effectiveness of the application of different breeding methods and breeding.

The advantage of molecular genetic methods in the genetic monitoring system lies not only in the possibility of long-term preservation of samples of genetic material, but also in the fact that for the determination of DNA polymorphism there is a real possibility of the use of semen of the pedigrees. This is a prerequisite for the creation of DNA banks through the accumulation of a certain number of doses of semen from predators who have long since left. In particular, for this purpose it is expedient to use sperm banks, in which the semen of the fruit growers of local and small breeds is stored,

Accumulation and storage of genetic material now in cryobank and DNA banks will further facilitate the accumulation of information on structural genes, polyloxine DNA spectra, mutational variability, which can become an indispensable source of information in fundamental gene geographic studies and the choice of genetic strategies for rock conservation programs and Selection of animals with predicted qualities.

The International Program for the Conservation of the Diversity of Genetic Resources of Animals and Plants, developed and implemented under the auspices of the FAO, is intended to sample samples at the level of individual species based on genetic markers, based on 25% of the rocks of their total amount for a particular species of farm animals. In the presence of more than 200 species, at least 50 of them must be examined. Within each breed, it is recommended to investigate 50 unrelated individuals, and to detect the variability of the breed by microsatellite - at least 25 animals. It is recommended that the intestine samples of animals be formed from several herds (at least 3-5, and optimally - 8-10) in such a way that in They were presented by the descendants of different breeders, which were used during the last 6-8 years in herds of cattle, 4-5 years old - in herds of pigs and sheep, 2-3 years - in herds of birds. For a comparative evaluation of gene pools, the minimum sample should be 10-15 head per each herd. If the goal is to identify the specificity of intraformed formations, then the number of animals in the samples should be increased by 3-4 times.

One of the important tasks in determining the most optimal and valuable samples of biomaterials for long-term storage in a DNA bank is to identify the most optimal DNA markers that would enable the molecular genetic characteristics to be determined both at the individual level and to characterize the gene pool of the breed.

In studying genetic variability in natural populations, nucleotide sequences are more informative than electrophoretic variants of proteins, since most DNA does not encode proteins. Genetic variability in non-coding parts of DNA (intron, flanking regions, etc.) is detected only at the level of DNA sequences. DNA sequences also allow you to get detailed information about the causes of genetic variability - due to nucleotide replacements, insertions / deletions, genetic conversions, unequal crossings, horizontal gene transfer, etc. DNA polymorphism makes it possible to proceed from the analysis of the action of individual genes to the integral study of entire genomes.

The degree of DNA polymorphism evaluates differently, but the most common is the number of segregation sites per nucleotide position and nucleotide diversity (or heterozygosity at the nucleotide level).

The size of the polymorphism of DNA, which does not depend on the sample size, is the average number of nucleotide differences in the position between the two sequences (nucleotide diversity).

Compared to the direct sequencing method of nucleotide sequences, this method gives a more rough estimate of the number of nucleotide substitutions. However, it provides accurate results when comparing close sequences, in addition, it is a fast and relatively inexpensive method for detecting the number of nucleotide substitutions. Therefore, it is better to use it in studies of genetic differentiation of intranasal populations or closely related species.

Characteristics at the molecular genetic level are conducted mainly for the analysis of genetic diversity within and between animal populations and for the determination of genetic interactions among such populations, in particular: to determine parameters of variability within and between rocks; To identify the geographical localization of individual populations; To obtain information on evolutionary relationships (phylogeny trees) and to find out centers of origin and migration routes; For carrying out gene mapping, including identification of carriers of known genes; To establish the origin and genetic interactions; For genetic improvement of animal populations using markers; For the creation of DNA repositories for research and development (FAO, 2005).

In our view, the definition of mitochondrial DNA polymorphism is one of the important characteristics of testing tribal resources in terms of biodiversity assessment, which makes it possible to make an objective notion about the contribution to the gene pool of genetic material inherited by the maternal line. One of the most common methods that makes it possible to determine the genotype of animals as QTLs and mtDNAs is the PCR-PDRF method.

The enzymes of restriction recognize the specific combinations of nucleotide pairs (restriction sites), mainly in lengths of 4 or 6 nucleotide pairs, and cut the DNA in these sites. Therefore, if the ring DNA of the animal mitochondria carries n recognition sites (restriction), it will be fragmented into n segments after processing by this enzyme. The number and location of the restriction sites is determined by the nucleotide sequence. The closer the DNA sequences are compared, the greater the coincidence of the distribution of the fragments of the restriction. Thus, by comparing the localization of restriction sites, one can estimate the number of nucleotide substitutions for homologous DNA sequences. The number of nucleotide substitutions can also be estimated by the share of general restriction DNA fragments.

In population genetics, restriction enzymes are often used to detect genetic polymorphism over DNA nuclear loci; In this case, the alleles are fragments of varying lengths after restriction by a certain restriction enzyme. The polymorphism of the lengths of the restriction fragment (PDRF) is used to create genetic mapping maps, however, it is also useful in evolutionary studies. The number of alleles detected for the genetic locus (DNA fragment) is usually small and population differences can be determined in terms of allele frequencies. For a large number of PDRF loci in closely related species, the number of nucleotide substitutions can be estimated from the data of DNA fragmentation by restriction enzymes.

It is assumed that nucleotides (A, T, C, G) are randomly distributed in DNA sequences and the probability of substitution is the same for all sequence positions. These assumptions are not always correct, however, since the enzyme restriction method is used only when the number of nucleotide substitutions on the site (d) is relatively small ($d < 0.2$), the violation of these assumptions does not lead to significant errors [12].

Improved work within biodiversity conservation and improving the selection and breeding work depends on integrated assessment system genotype genetic monitoring, which aims to combine a balanced system of complex genetic tests to comprehensive evaluation of breeding material.

The very definition of the most valuable genotypes at both the individual and the population level for quantitative traits loci (QTL) in conjunction STR, ISSR-markers, mtDNA, in our opinion, is one of the key elements of molecular genetic evaluation of biomaterial.

For a comprehensive analysis of the genetic structure of breeding resources of breeds, it is necessary to improve and systematize the methods for determining the most informative tests for different types of DNA markers. The introduction of elements of molecular genetic monitoring will help identify carriers of genetic systems, by obtaining molecular genetic information genetic structure features that will identify and determine the optimal composition of the gene pool and genetic material as bookmarks and preservation of samples of biological material.

Conclusions

For comprehensive analysis of genetic structure of pedigree resources of breeds development and systematization of methods on determination of the most informative tests for different types of DNA-markers is necessary. Heading of elements of molecular-genetic monitoring will promote detection of carrying agents of valuable genes complexes by deriving molecular-genetic information of features of genetic structure. That will allow identifying and determining optimum content of gene pools and quality of genetic material for backfilling and keeping specimens of biomaterial.

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