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Molecular-Genetic Processes in Animals

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ABSTRACT

The purpose of this work is molecular genetic studies on animals and their analysis and refinement. Modern achievements and problems of molecular genetic processes were covered.

KEYWORDS: gene, molecular, animal, genetic analysis, genome, DNA.

Introduction. Since 1953, when it was shown that the material carrier of a gene is DNA, genetics has received a new impetus for its development. At the forefront are studies at the molecular level of the structural organization of the gene and the genome in general, which made it possible to study the mechanisms of the functioning of genes. The study of the genome by molecular genetic methods has led to rapid progress, primarily in prokaryotes. At the beginning of this study (the end of the 1960s), there was almost no information about the molecular structure of the genome of higher eukaryotes. Progress in the molecular genetic analysis of the eukaryotic genome is hampered not only by their high complexity, but also by the lack of a sufficient number of convenient and informative markers.

It is known that in the genome of higher eukaryotes an important part is made up of repetitive sequences, the function of which is unknown to us, and the genes themselves are strongly intronized, so that most of them (more than 90%) are understandable in the analysis of protein polymorphism. However, functionally significant regions may be included in unanalyzed sequences. Thus, modern ideas about the mechanisms of realization of genetic information play an important role in regulation. Thus, genetic information plays an important role in the implementation of modern ideas about the mechanisms of implementation. However, functionally significant regions may be included in unanalyzed sequences.

The use of polymorphic nucleotide sequences in a DNA molecule as marker systems is more promising, and their effectiveness has been proven for the first time. The genetic variability of the genetic material determines the heterogeneity of DNA segments of the same localization in different individuals. These different nucleotide sequences are called DNA polymorphisms if the percentage of chromosomes carrying a modified nucleotide sequence variant at a given location exceeds 1% in the population. The use of polymorphic DNA sequences as a marker system makes it possible to test genetic polymorphism at the genotype level, rather than at the level of gene expression products. More precisely, at the molecular level, it can be noted that variants of the DNA nucleotide sequence are the main cause of all subsequent phenotypic changes (protein production, morphological or physiological traits, etc.) and are themselves a phenotypic manifestation of the genotype. DNA markers make it possible to solve the problem of saturating the genome with markers and labeling almost any interesting research.

The DNA segment, including the non-coding segment, is the main advantage of DNA markers over traditionally used eukaryotic genetic markers. The characteristic feature of this polymorphism is its ubiquitous distribution, Mendelian inheritance for nuclear DNA and maternal inheritance for DNA of cellular organelles, many alleles and high heterozygosity, codominant expression and inheritance stability, selective neutrality, ease and reliability of testing, and tropical lack of effect. This has led to the widespread use of DNA polymorphism for economically important traits as a next generation

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genetic marker. The use of such a marker system in theoretical and applied research has a number of advantages: the possibility of conducting research on materials of any tissues and at any stage of development (including for prenatal studies), the possibility of conducting retrospective studies. Long-term storage of DNA samples and the possibility of obtaining information about the nature of gene changes. At the same time, it should be noted that the study areas provide an opportunity for retrospective genetic retrospective studies (due to long-term storage of DNA samples) and obtaining information about the nature of gene changes. It should be noted that the study areas provide an opportunity to conduct genetic retrospective studies (long-term storage of DNA samples) and obtain information about the nature of gene changes. It should be noted that the study areas provide an opportunity to conduct genetic retrospective studies (long-term storage of DNA samples) and obtain information about the nature of gene changes.

With the introduction of DNA markers, progress has been made in the molecular genetic analysis of the eukaryotic genome. In the near future, genetic analysis of documents encoded by certain chromosomal loci will rely with accuracy on knowledge of the complete nucleotide sequences of the corresponding loci and knowledge of the allelic variants of these sequences. At the same time, such information has not yet been obtained for the genomes of humans and economically valuable animal species. At this stage, individual sections or individual sections of the genome can be studied to identify polymorphic factors associated with a given locus. To solve the problem of mass distribution, it is still necessary for DNA specialists to obtain the genome of animals (especially in the discovery of genetics and genetic selection) to solve the problem of their labeling.

Literature review. The article was used with reference to the literature used for molecular, animalgenetic processes and their analysis. The necessary sources have been obtained and included in the bibliography.

Research methodology and empirical analysis. Various methodological approaches were used to obtain genetic results. Molecular methods proved to be the most effective, which made it possible to improve the quality of testing of gene products (protein polymorphism), the genetic material of a cell (DNA polymorphism). The most indicative markers are obtained from polymorphisms stored for more than 25 years. With their help, there was a real breakthrough in research.

The purpose of our analysis was the molecular genetic analysis of the human and animal genome at several organizational levels: at the level of the entire genome, at the level of individual chromosomes and regulatory documents, at the level of individual loci (genes), etc. One of the novelties of the work was to see the production of molecules from traditional genetic diseases, for example, the production of genomes, the study of the genetic diversity of populations at the interspecific and species-global levels, the analysis of the entire polymorphism, etc.

Results. Animal genetic engineering has expanded significantly in recent years, and the use of this technology raises ethical questions, some of which are related to animal welfare, which the World Organization for Animal Health describes as "the condition of an animal ... faces its own challenges that can give" ", he describes. These issues should be addressed by all stakeholders, including veterinarians, since all parties can be aware of ethical issues and make an important contribution to the current debate about the creation and use of genetically modified animals. In addition, it is important to try to reflect public values in scientific practices and new technologies, especially those that are publicly funded but may be considered morally questionable.

Several terms are used to describe genetically modified animals: genetically modified, genetically modified, transgenic, and biotechnologically produced, among others. In the early stages of genetic engineering, the main technology was transgenesis, which literally means the transfer of genetic material from one organism to another. However, with advances in this field, new technologies have emerged that do not require transgenesis: recent applications allow the creation of genetically modified animals by deleting genes or manipulating pre-existing genes. To reflect this progress and include strictly non-transgenic animals, guidelines developed by the Canadian Council

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for the Care of Animals have adopted the generic term "genetically modified".

Summary. In the course of these studies, all efforts were properly highlighted and analyzed. Because of the additional challenges posed by genetically modified animals, policy makers often begin to develop appropriate policies requiring increased vigilance and monitoring of potential impacts on animal welfare.

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