minimum of 98.4% similarity between variants. Among the 62 reverse sequences, five different variants of the mtDNA D-loop sequence fragment were also identified.

The MEGA programme (Tamura, K. et al., 2021) was used to determine the genetic distance between individuals and to create phylogenetic trees for the studied group of dogs. Phylogenetic trees created on the basis of the analysed forward and reverse D-loop mtDNA sequences of the Polish Lowland Sheepdog breed individuals, in both cases divided the investigated group of animals into five haplogroups. Both the analysis of forward and reverse sequences determined the genetic distance between individuals to be 0.01. The low value of the coefficient indicates very low genetic variability among PLS.

Five mitochondrial DNA D-loop haplogroups were distinguished among the analysed group of Polish Lowland Sheepdog breed individuals. Low variability of mtDNA D-loop sequences and low genetic variability in the studied population of Polish Lowland Sheepdog was demonstrated.

Many dog breeds have been shown to be adversely affected by inbreeding, which contributes to homozygosity that increases the incidence of hereditary disorders. Low genetic variability and accumulated health problems can endanger the breed and, in extreme cases, lead to extinction. Therefore, it is important to carry out research on the genetic variability of the breed in order to control the possibility of hereditary disorders, to make the proper breeding decisions and to prevent the deterioration of animal health jeopardising the future of the breed.

SECONDARY CONSTRICTIONS ON THE CHROMOSOMES OF AGRICULTURAL ANIMALS: DIFFICULTIES OF DETECTION AND STUDY

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Introduction. For the proper functioning and division of cells, the synthesis of ribosomes is important, which is carried out by the dynamic structure of the nucleus – the nucleolus. It implements the synthesis of rRNA by RNA polymerase I, its maturation, and the assembly of ribosomal subparticles. In addition, proteins involved in these processes are localized here in high concentrations. The formation of the nucleolus occurs on a specific region of the chromosome – the nucleolar organizer (NO), containing RNA genes (rRNA). More often this happens on secondary constrictions of chromosomes, where genes encoding the synthesis of ribosomal RNA are located.

The nucleolus is the densest part of the nucleus and is easily stained with basic dyes. The size of the nucleolus and its constituent components change depending on the activity of the cell and the stage of the mitotic cycle. In the prophase of mitosis, when the activity of NO decays, the nucleoli disappear, that is, they pass into the cytoplasm as granular and then fibrillar components. But the material of the fibrillar center associated with regulatory acidic proteins is preserved. At the same time, it becomes compact and is redistributed between rDNA clusters, that is, regions of NOs of chromosomes. Residual nucleolar material, which consists of acidic proteins, can be detected by histochemical methods. In particular, these proteins are selectively stained with silver nitrate and in a light microscope they appear as dark lumps (precipitated silver).

Individual chromosomes contain a nucleolus organizing region (NOR). The number of nucleoli in a cell can vary, but their number per nucleus depends on the gene balance of the cell. It has been established that certain places on some chromosomes are involved in the formation of

nucleoli. Such chromosomes, as a rule, have secondary constrictions, the zones of which represent the places where the development of the nucleolus occurs.

Through staining in various ways, researchers are able to examine and determine the structural elements of chromosomes. But they still face certain difficulties both in determining the structural elements of cells and in carrying out the staining itself.

Purpose. Comparison the number of NORs in different species of farm animals and clarifying the complexity of their detection and study.

Materials and Methods. Chromosomes and NOs of farm animals. Histochemical methods: staining with silver nitrate, detecting in a light microscope.

Results. The number and location of NORs in agricultural animals are shown in Table 1.

The data of Table 1 show that the most polymorphic chromosome loci that form NORs are found in Korean and Friesian cattle, swamp and especially B. bubalis and Bubalus arnee bubalis.

The results showed that in cattle of the genus Bubalus in Thailand, NORs are located on the same pairs of autosomes as in swamp buffalo (B. bubalis) and river buffalo (B. bubalis). The presence of NOR in chromosome 6 of the river buffalo has been the subject of much debate. But research results confirmed its presence. The number of nucleolus-forming chromosomes in River buffalo is unstable and rarely reaches its maximum value of 12. These results that in the cattle population there is significant intercellular and individual polymorphism in the number of active NORs, that is, their significant variability.

AgNOR-banding was used to identify NORs. In these regions of chromosomes, genes involved in the formation of the nucleolus are localized. There are several modifications of this coloring. In general, the essence is to treat chromosome preparations with silver salts at a certain temperature. After treatment with the drug, the chromosomes turned yellow, and dark brown or black dots were clearly visible in NORs of the chromosomes. Various differential stains to G- and Ag-banding made it possible to study the polymorphism of organisms based on NORs.

Table 1. The number and location of NORs in different species of farm animals

Animal species	Numbers of chromosome pairs with secondary constrictions	Location of NORs	Number of NORs
Korean cattle Bos taurus L.	2, 3, 4, 11, 28	Telomeres	5
Holstein friesian cattle breed Bos taurus L.	2, 3, 6, 11, 27	Telomeric regions of autosomes	5
Bos indicus L.	2, 3, 4, 28	Autosomes	4
Thailand cattle Bos taurus L.	≈ 4, 8, 23	Autosomes	3
Buffalo swamp B. bubalis	4, 8, 20, 22, 23	Autosomes	5
Buffalo river B. bubalis	3, 4, 6, 8, 21, 23, 24	Autosomes	7
River buffalo Bubalus arnee bubalis	3, 4, 8, 21, 23, 24 (3, 4, 6, 21, 23, 24)	Autosomes	6
Domestic horse	1, 27, 28, 31	Autosomes	4
Domestic pig	8 10 14	Pericentromeric regions Secondary constriction regions Autosome	3
European rabbit Oryctolagus cuniculus	13, 16, 20, 21	Autosomes	4

The difficulties lie in the fact that, first of all, the biochemical mechanisms of Ag-banding chromosomes are not yet known. However, it has already been established that with this method it is not the DNA of ribosomal genes or rRNA that is stained, but acidic proteins. It is assumed that these proteins are part of the structure of the nucleolus and are associated with rRNA. This is why not every NO exhibited Ag-banding, but only those functioning in interphase, in the previous mitosis in which the chromosomes were fixed. Regarding the chromosomes of the domestic horse, which carry NORs, they do not always respond positively to the Ag-NOR technique. So, just 5, and in several cases only 4, active NORs were identified. Chromosomes of the 28th pair react variably to the technique.

The European rabbit – Oryctolagus cuniculus – is a cytogenetically very useful model animal – each chromosome is easily distinguished from the rest due to its size and morphology. So, even with the routine method of chromosome staining, it was possible to identify chromosomes that are positively stained with silver.

Conclusions. Secondary constrictions, unlike the primary constriction, do not serve as a site for attachment of spindle threads and do not determine the angle of bending of chromosomes during their movement. Some secondary constrictions are associated with the formation of nucleoli, these are NOs. The genes responsible for rRNA synthesis are localized in such secondary constrictions. The synthesis and maturation of rRNA occur in the nucleoli.

Even today, with sufficiently developed technologies, there are various difficulties in recognizing the structural elements of chromosomes. Firstly, due to the microscopic dimensions of the materials. Secondly, there is variability in interpretation. Thirdly, due to the difficulty of detecting NOs during different stages of cell division and, finally, choosing the right angle for shooting. And also – the complexity and inaccuracies of the research itself and the mechanism of coloring with some dyes. In most cases, NO is a secondary constriction, but sometimes these areas are found on short arms. Therefore, these studies need to be continued.

THE TOPOGRAPHIC AND MACROSTRUCTURAL CHARACTERISTICS OF SOMATIC LYMPH NODES IN LABORATORY RATS RECEIVING A HIGH-FAT DIET.

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Introduction. Currently, there is a significant amount of literature in the scientific community that extensively discusses the anatomy of laboratory rats, describing the structure of muscles, bones, nerves, and the circulatory system. Special attention is paid to publications that describe experimental interventions on the systems and organs of these animals. Lymph nodes occupy a special place among other organs of the hematopoietic and lymphopoietic system, as they simultaneously perform drainage and immune functions. The morphofunctional status of lymph nodes is often considered as a general indicator of the internal environment under the influence of various factors, including environmental and age-related aspects. Rat lymph nodes are numerous organs of various sizes and shapes. They are scattered throughout the body in close connection with lymphatic vessels. Data on the topography and morphometric parameters of somatic lymph nodes in rats are contradictory and quite limited. In most cases, scientists focus on visceral lymph nodes, as opposed to somatic ones, because they have significant differences depending on the functional