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Topical Issues of Clinical and Theoretical Medicine

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During the microscopic investigation of the experimental animals' thyroid, it was found that the major area of the organ in occupied by lobules of small sizes without clear division into center and periphery. The overall histological picture depicts tiny structure of the follicles. In the lumens of the majority of the follicles, there is an inconsiderable amount of desquamated epithelium. There are some lobules, which are separated from each other by interlayers of the hydropic stroma that has visually empty slots. In-between collagen interlayers of the interfollicular stroma there are found numerous flattened cells. In the other zones there are lobules, which are demarcated by the hydropic stroma to a lesser extent; the follicles vary in size: central lobules are tiny and those at the periphery are larger. In the tiny follicles and cellular aggregates, light-colored cells with vacuolated cytoplasm are prevailing. The inner contours of the tiny follicles are unclear in some areas. The lumen of the tiny follicles is filled with dimly eosinophilic colloid. Large follicles are generally filled with a colloid pink in color, some contain interfollicular epithelial outgrowths.

Thus, on the preparations of the experimental animals, we note evidences of the enhancement of the thyroid functional activity, which is indicated by vacuolated cytoplasm, rarefaction of the colloid and the increased formation of follicles. In the peripheral areas, folliculogenesis is implemented by follicle fragmentation with liberation of smaller "daughter" follicles.

GLOBAL METHYLATION STATUS IN MALIGNANT BRAIN TUMOR TISSUE.

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The DNA methylation is one of the main epigenetic inheritance form, which contributes in the regulation of gene expression. Abnormalities in DNA methylation processes can provide information about many pathophysiological conditions, including tumorigenesis. DNA hypomethylation was the initial epigenetic abnormality recognized in human tumors. Glioblastoma (GB) is the most common and the most aggressive primary brain tumor in adults and therefore is considered one of the major issue in modern medicine. The aim of our study was to compare global methylation status of DNA in peripheral blood cells and in biopsy tumor tissue from patients with diagnosed GB using Imprint® Methylated DNA Quantification Kit. Results of our study show global hypomethylation DNA status of GB tissues compare to global methylation DNA status of peripheral blood cells. Quantification of global methylation status confirm DNA hypomethylation in malignant brain tumor tissue, which may contribute in deregulation process of gene expression and subsequent tumor cell survival. Furthermore, detection of specific DNA methylation changes in GB tissue can subsequently help in understanding of specific genes activation and silencing through epigenetic events in tumor cells.

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STRUCTURAL CHANGES OF RED BLOOD CELLS UNDER THE CONDITIONS OF VIOLATION OF WATER-SALT BALANCE

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Erythrocytes are important cells in your body that travel in the blood. They are involved in a gas exchange that is essential to human life. Erythrocytes – unique cells in our body, which lose their nucleus and other cytoplasmic organelles in the period of growth.

There are a lot of references about the influence of various factors of external and internal environment on the erythrocytes on the red blood cells. For example, a popular topic of research is the effect of smoking and tobacco smoke, as well as medications that affect the structural and qualitative changes in erythrocytes.

The basis our research is the impact of dehydration erythrocytes - a new trend in the development of histology, physiology and anatomy.

For the studying we take 18 white laboratory male rats, which were divided into two groups: control and experimental. In its turn the experimental was divided into 2 subgroups: the rats with moderate and severe stages of dehydration. The study was performed using scanning electron microscope (SEM). This method makes it possible to study the three-dimensional image at high resolution of red blood cells.

In the study in intact rats percentage groups of erythrocytes it was found that the functionally full erythrocytes constitute the biggest amount – diskocytes. Also it was found echinocytes, stomatocytes, eleptocytes, kodocytes. Diskocytes remain the overwhelming majority of erythrocytes while the influence on the rat's organism of experimental group of general dehydration of average degree. Their proportion has decreased, in comparison with the control group. Increasing of inversely deformed cells is as follows: the number of echinocytes increased in 6 times, the number of stomatocytes has not changed. Significant changes of microrelief of erythrocytes take place with the advent of accurate grooves on the surface of erythrocytes and vesicular formations. This indicates to the cell metabolism, which is manifested of outer transformation of erythrocyte's plasma membrane.

The heavy degree of dehydration is also characterized by a decrease in the number of diskocytes and a significant increase of inversely deformed cells and irreversibly deformed cells in comparison with the control group.

MOLECULAR ANALYSIS OF APOPTOSIS RELATED GENES DNA METHYLATION STATUS IN ENDOMETRIAL CARCINOGENESIS

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Aberrant methylation in the promoters of genes associated with apoptosis was observed in many human cancers, but in the context of endometrial cancer only few publications have described the DNA methylation status of these genes. Apoptosis is a program cell death to maintain a tissue homeostasis in normal menstrual cycle. Disturbances in this pathway can promote cancer cell survival and furthermore are associated with resistance to therapy in endometrial cancer. Despite a high curability of this cancer type, prognosis of patients with advanced disease is still poor. One of the major mechanism of resistance to therapy is the aberrant DNA methylation pattern. Analysis of aberrant DNA methylation status can reveal early biomarkers in endometrial tumorigenesis and reflect apoptosis resistance development. In our study we used a specific methylation array, EpiTect® II PCR Array, with the aim to analyze methylation status of regulatory regions in apoptosis related genes (n = 22) in endometrial cancer tissue compared with normal tissue. We first observed a significantly higher DNA methylation in promoter regions of specific genes regulated extrinsic and intrinsic apoptosis signaling pathways in cancerous endometrial tissue compared with controls. Products of investigated genes can regulate other signaling pathways including lipid metabolism and inflammatory processes. We suggested that epigenetic inactivation of these genes can thus support endometrial cancer progression and malignant phenotype.

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