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АКТУАЛЬНІ ПИТАННЯ ТЕОРЕТИЧНОЇ ТА ПРАКТИЧНОЇ МЕДИЦИНИ

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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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