The Modification of Chromatin with Peptides in Breast Cancer Patients

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Breast cancer is genetically determined inherited disease. It is the most common form of cancer in women. There are the data indicating that ductal breast cancer (DBC) (caused by mutation of BRCA1 gene; ~ 85% of all cases) is characterized by genomic instability. There is the reason to assume that chromatin remodeling is prerequisite of genomic instability, which in some cases, it may be reversible. Accordingly, investigations of the means, which will have the ability to correct the altered chromatin and to restore the normal functioning of the genome in DBC, have a paramount importance.

We have examined the genomic mutations (structural and numerical abnormalities) in cells of lymphocyte cultures from individuals infected with DBC and the frequency of sister chromatid exchanges in telomere regions of chromosomes, also the impact of peptide bioregulators on these parameters.

It was found that the cells of patients infected with DBC are characterized by significant reduction of the level of genome stability, which was reflected in high frequency of structural and numerical abnormalities of chromosomes (7.5±1.2 (in control - 1.7±0.3) and 29.5±0.9% (in control – 6.7±1.2%), respectively) and on the other hand, it is possible to correct the altered genetic parameters by influence of peptide bioregulators –Livagen and Epitalon (structural abnormalities: with Livagen - 2.7±0.5; with Epitalon – 3.0±1.1; quantitative disorders: with Livagen – 15.4±3.4; with Epitalon – 8±2.7).

By the results of the study of variability telomeric regions should be noted that, on the one hand, in these individuals there is a chromosome-specific variation of telomere length, shortening, on the other hand, revealed the corrective effect of combinative action with livagen-cobalt, which have also chromosome-specific nature and is revealed by deheterochroamtinization of telomeres.

It was found that the cells of ductal breast cancer patients, on the separate or combinative action of peptide bioregulator and heavy metal, in specific conditions of their usage, have a specific response. This gives a possibility to optimize the selection of a correct exposure for correction of altered genomic parameters.

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