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THE EFFECT OF GENE POLYMORPHISM OF XENOBIOTIC DETOXIFICATION ENZYMES GCLM ON URINE MERCURY CONTENT

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Mercury is removed as conjugated glutathione (GSH). The production of GSH is mediated by glutamylcysteine ligase (GCL) and conjugation using S-transfer as a glutathione (GST). This study was tested if polymorphism in the GCL and GST genes changes mercury retention in people exposed to mercury.

Keywords: mercury, polymorphism

Mercury is an ecotoxicant that causes a wide range of changes in the body and has a harmful effect on human health. It is widely used in industry, agriculture, and medicine. In Kazakhstan, in the city of Temirtau, there is a high level of contamination with mercury from the acetaldehyde plant.

Glutathione-S-transferase (GST) is an important family of enzymes involved in the detoxification of enzymes that are part of the redox cycle of glutathione and are precursors in the synthesis of glutathione also play xenobiotics, including heavy metal ions [1]. GCLM is involved in the synthesis of glutathione playing an important role in protecting against oxidative stress. GCLM contains a polymorphism in the 5'-flanking region (-588C / T) [2]. The inheritance of mutant variants in these detoxification genes can alter the metabolism and elimination of xenobiotics from the body, which may explain the different susceptibility to adverse health effects of various forms of mercury.

The goal of our study was to determine the polymorphisms of xenobiotic detoxification genes to the GCLM of people living in areas contaminated with mercury.

Materials and methods. We surveyed 180 people, 90 of them (main group), living in the mercury-containing territory (Temirtau region), and 90 – healthy people (control group, people living in Vozdvizhenka, Akmola region).

Genomic DNA was isolated from the venous blood of research participants by salting out [3]. The quantitative content of DNA was evaluated on a spectrophotometer (Nanodrop 1000). The concentration of the isolated DNA varied within 10-130 ng / μl. The polymorphism of the GCLM was 329 bp, covering -588C / T determined by PCR methods. The content of mercury in the urine of the examined was determined by stripping voltammetry.

Results. A statistically significant difference was found between the test groups for urine mercury content. Main results are on the frequency of occurrence of genotypes of GCLM genes in the studied groups. The distribution of genotypes did not deviate from the Hardy-Weinberg equilibrium.

The TT, CT, and CC genotypes of the GCLM gene were found in 2 (2.2%), 4 (4.4%), and 84 (94.4%) samples in the main group, respectively, and 0 (0.0%), 1 (1.1%), 89 (98.9%) were present in the control group, respectively. It should be noted that the results of genotyping a part of the GCLM gene were partially confirmed with the results of restriction. According to the results of 31 genotyped samples, only 9 individuals coincided with the results of restriction.

Conclusion. In the study region, the pathological effect of mercury remains on the population. The toxic effects of mercury can be related to the duration of the population's residence in the affected area. The detected elevated levels of inorganic mercury in the urine of exposed individuals indicate that its harmful effects on public health remain.

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DIAGNOSTICS OF HUMAN PAPILLOMA VIRUS WITH PCR-METHOD

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The possibilities of the PCR method for detecting human papillomavirus of oncogenic strains by both qualitative and quantitative methods (Real-Time PCR) as well as a comparative evaluation of the data obtained from the studies with the results and literature data on the frequency of occurrence with different types of HPV in infected women received in Belarus and different countries were studied.

Keywords: human papillomavirus (HPV), oncogene, polymerase chain reaction (PCR), specificity, cytology, cervical cancer.

PCR diagnostics directly reveals the pathogen itself or its parts even in extremely low concentrations, which makes the PCR method more accurate and sensitive. Human papillomavirus (HPV) is a widespread epitheliotropic infectious agent. The PCR method is aimed at identifying carcinogenic strains of HPV, which amount to about 15. The most highly carcinogenic strains 16 and 18 can cause cervical cancer. A person can be infected with several strains at the same time.PCR method can determine how a person is infected with a single subtype of the virus or a number of types, as well as the HPV load can be identified[1].

The purpose of the study is to assess the potential of the PCR method for the early detection of HPV and, in particular, the qualitative and quantitative approach.

The frequency of occurrence of various types of human papillomavirus in 44 infected women was evaluated. The following results were obtained: HPV16 was detected in 24 women; in 9 women – HPV 31,35, 39, 59; and in 11 women – HPV 18,33,45, 52, 58, 67. In addition, 26 women were performed the concomitant determination of the concentration of DNA of HPV 16 and 18 type. Human papillomavirus type 16 was found in 16 (62%) women, 6 (18%) had HPV 18 and 4 (20%) women had human papillomavirus of both types.

According to the literature data on the frequency of occurrence of HPV of oncogenic types in women examined in Belarus with detected HPV in 25% of women HPV type 16 was found, in 25% – HPV 31, 35, 39, 59 types and 50% – HPV 18 , 33, 45, 52, 58, 67 types. In Europe, on the basis of literature data, it was found out that type 16 of HPV occurs in 61.6%; type 18 HPV – in 7%; 33 types of HPV – in 5%; type 45 HPV – in 3.6%; an 31 types of HPV – in 3.3% [2].

Determination of viral load is possible when conducting quantitative PCR analysis. The quantitative method allows to determine the concentration of HPV DNA of highly carcinogenic types, thereby reflecting the severity and prognosis of HPV infection, since an increased load of HPV is associated with an increased risk of developing severe dysplasia and is more common in cervical cancer.

The diagnostic value of the quantitative determination of HPV types 16 and 18 identified by the qualitative method in 26 women. Real time PCR quantitative diagnostics showed that 6 women had <3 Ig copies / 100,000 cells, which indicates that the result was of little clinical significance. In 15 women, the presence of lg copies in the amount of 3–5 indicates the clinically significant result and the risk of developing cervical dysplasia. In 5 women, lg copies of> 5 / 100,000 cells were detected. This indicates a high probability of dysplasia and a high risk of developing cervical cancer.

In conclusion, the study of the structure and properties of functional elements of HPV virion allows to model vaccines with predictable preventive and therapeutic efficacy.

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