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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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