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HUMAN PAPILLOMA VIRUS GENOTYPES OF THE HIGH RISK IDENTIFIED IN CERVICAL CANCER TISSUES

Background/Aim. Human papillomavirus (HPV) is the most common sexually transmitted virus. About 10.4% of clinically healthy women of reproductive age worldwide are HPV carriers. A proportion of carriers and the frequency of specific HPV genotypes differ significantly depending on the geographical region. HPV of the high risk may cause the cervical cancer. It is very important, to analyse a spectrum of HPV genotype for the future vaccine optimization. **Methods.** To do so, we used the genomic DNA isolated from 28 tissue samples of cervical cancer and Allplex™ HPV HR detection kit, using q-PCR on a Bio-Rad CFX96 machine. **Results.** We observed the multipleinfection of tumor cells, up to 6 genotypes in one sample (in 3.6% of cases). We established that in normal tissue, genotype 51 was found in only approximately 13% of samples, while in all tumors it is found in more than 35% of cases. It is important to note that as tumors progress, the presence of genotype 51 decreases. Thus, in stage I tumors, genotype 51 is found in more than 60% of samples, often with 16 and 18 – (56–66% of samples), while in stage III samples, genotype 51 is found in only 43% of cases. The well-characterized high-risk genotypes 16 and 18 are found in 65–68% of cases in samples of stages I–II and more than 85% of cases of stage III samples, as expected. **Conclusions.** The most common genotypes that were circulating in Ukraine appr. 20 years ago, among women diagnosed with cervical cancer were HPV genotypes 16, 51 and 18. In samples of conditionally healthy cervical tissue opposite the tumor, HPV genotypes 59 and 16 dominated. In cervical cancer tissue samples, co-infections were 71%, with infections with two genotypes prevailing (21%). Among co-infections, the combination of HPV genotypes 16 and 51 were dominated. The frequency of detection of any HPV genotype in cervical cancer samples did not depend on the patient's age, histological type and stage of cervical cancer. An additional study on prospective cohort samples, collected during 2025–2026 is on the way. **Grants/Fundings.** This work was supported by a research program of Ministry of Education and Science of Ukraine "Genetic characterization of high-risk human papillomaviruses in Ukraine and Latvia to inform national policy of cervical cancer prevention" (0125U002954).

Keywords: cervical cancer, human papilloma virus, HPV genotyping, vaccination.

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