DETECTION OF HIGH-RISK HPV GENOTYPES BY THE RT-PCR METHOD ON THE TERRITORY OF BELGRADE (OCTOBER 2022-OCTOBER 2023)

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Background: *Human papillomavirus* (HPV) is a small DNA virus, from the family *Papillomaviridae* and genus *Papillomavirus*. The genome is a circular, double-stranded DNA. Over 200 HPV genotypes, that can infect humans, have been identified so far. They are usually transmitted through sexual contact. Based on the consequences they can have on humans, we can classify them into low-risk and high-risk genotypes. High-risk HPV genotypes are also classified as carcinogens, because they cause cancers of the cervix, penis, anus, vagina and oropharynx.

Methods and Objectives: 2154 cervical and urethral swabs have been analyzed. Sampling was carried out at the Institute for Student Health Care and at the Institute of Public Health of Serbia "Dr Milan Jovanović Batut". Samples were collected in Amies (COPAN Diagnostics, Inc.) medium. The molecular method used for detection has been Real Time PCR, and the diagnostic test Viasure *High-Risk Human Papillomavirus* (CerTest Biotec, S.L.). The aim of the paper is to highlight the role and importance of the RT-PCR method in the diagnostics of high-risk HPV genotypes, as well as the consequences of infection with this virus.

Results: Of the 2154 samples tested, 715 (33%) gave a positive result. Of the 715 positives, 384 were samples from the Institute for Student Health Care. Most frequently detected were HPV genotype 16 (21%) and HPV genotypes from a group (31, 39, 56) (32%).

Conclusions: HPV represents one of the most significant and complex targets in molecular diagnostics. The importance of diagnostics stems from its direct connection with the development of cancer. The RT-PCR method is extremely effective in the diagnostics of HPV due to the speed of analysis and the sensitivity of the tests.

Keywords: High-risk HPV, Real Time PCR, Molecular diagnostics, Cancer, HPV genotype 16