

HPV GENOTYPES COINFECTIONS AND HEALTH RISK- PRELIMINARY STUDY OF THE EAST ROMANIAN POPULATION



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Introduction

HPV are double-stranded DNA viruses that infect the stratified epithelium of the skin and mucous membranes. There have been identified approximately 200 strains with potential for induction of transformations. HPV serotypes are differentiated between one another by the genetic sequence of the external L1 protein capsid. Of these, 15 are classified as having high oncogenic risk (16,18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 68, 73 and 82), 3 with probable oncogenic risk (26, 53 and 66) and 12 with low oncogenic risk (6,11, 40, 42, 43, 44, 54, 61, 70, 72, 81, CP6108) [1]. The infection appears to begin with the virus entering through a site of epithelial disruption (microlesion) that allows viral access to the basal epithelial layer. HPV-16 penetration occurs through clathrin-facilitated endocytosis, although other types of HPV may have other mechanisms of cell penetration [2].

The study aims to identify the degree of infection and co-infection with HPV strains in people of different ages, to assess the risk associated with lack of immunization of the Romanian population.

Materials and Methods

37 cases with suspected HPV infestation were analyzed, in the period 2018-2019, within the Prodiagnostic Analysis Laboratory, from Constanta, Romania. People were between 23 and 64 years old. Endocervical epithelium was taken and analyzed by HPV DNA detection and genotyping in the specialized laboratory of Matei Basarab Medical Center, Bucharest.

Research and Results

Of the total number of people analyzed for the case study, **45.94%** (17 out of 37) tested positive for HPV infection.

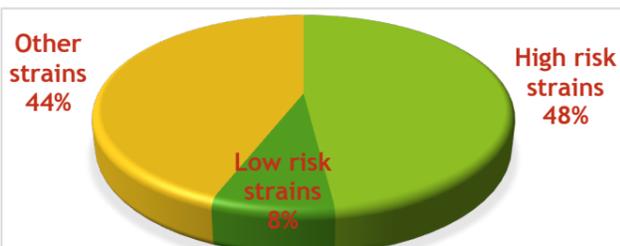


Figure 2 Frequency (%) of HPV strains by risk categories, identified in the case of the analyzed groups

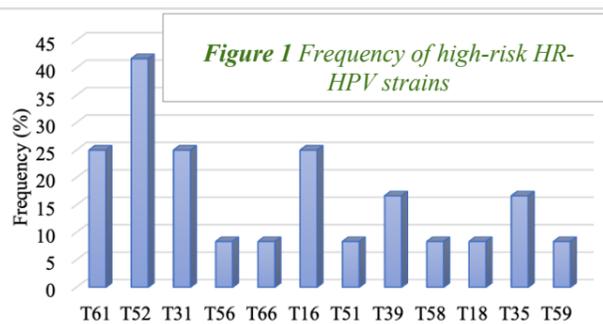


Figure 1 Frequency of high-risk HR-HPV strains

Most cases indicate that there are several associated strains (co-infection) and with different degrees of risk. It should be noted that 6 of the 17 positive cases analyzed (35.29 %) show the association between 2, 3 or 4 high-risk strains. Another 6 cases show co-infection between high-risk strains and other lesser-known strains.

In our study the most common high-risk serotypes were HPV61, HPV31, HPV52, and HPV16. These strains are found with a frequency between 10 - 40%. The most common are HPV52, HPV61, HPV31 and HPV16 having the values of frequency at 25% (HPV61, HPV31, HPV16) and 41% respectively (HPV52)

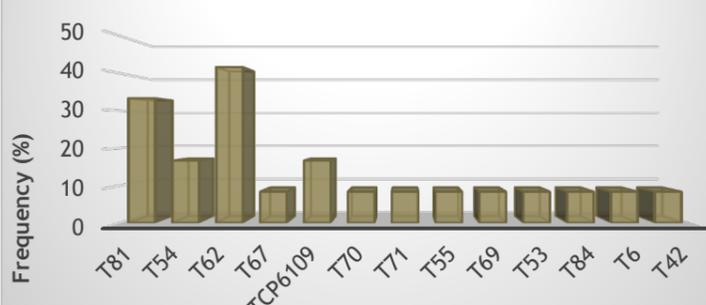


Figure 4 Frequency of low-risk (LR-HPV) or unknown risk HPV strains

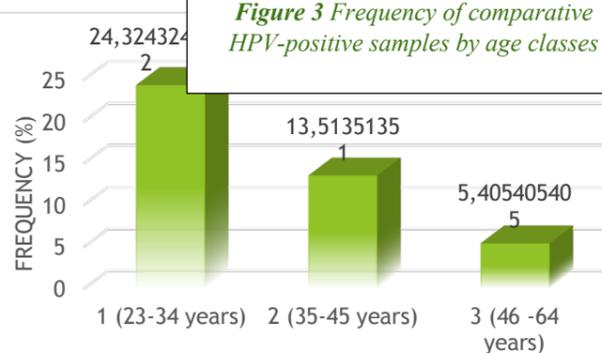


Figure 3 Frequency of comparative HPV-positive samples by age classes

The analyzed batch was divided into three classes of age (Figur. 4), a percentage of 25%, the maximum recorded belonging to the group between 23 and 34 years. This result can be associated with conceptual differences in the relationship between partners and education.

Conclusions

Frequency analysis of strains by risk categories reveals that the largest percentage was recorded in the strains with high risk (48%), followed by the frequency of strains with unknown risk (44%) and that of strains with low risk (8 %).

The association between strains and the 45% frequency indicates an important aspect of the infection as well as important data for diagnosis and treatment and involves a more rigorous monitoring of patients with such associations, the risk increases with the associations. The association between strains and the 45% frequency indicates an important aspect of the infection as well as important data for diagnosis and treatment and involves a more rigorous monitoring of patients with such associations, the risk increases with the associations.

References:

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