

Prevalence of oncogenic human papillomavirus infection in cancerous and dysplastic samples of cervix

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Background and Aim:

Cervix cancer is the most common Cancer in developing countries and the second common cancer in women worldwide. Different studies conducted all over the world have shown a strong correlation between HPV (human *papillomavirus*) and precancerous and cancerous changes in epithelial cells. In this study, the role of specific genotypes of human papilloma virus, especially 16 and 18 genotypes has been evaluated.

Methods:

In this study paraffin- embedded cervical tissue samples obtained of 117 patients with squamous cell dysplasia and carcinoma. After the DNA extraction of samples, papillomavirus was diagnosed by PCR (polymerase chain reaction) method and then was followed by typing procedure of the papilloma virus. Prevalence of different genotypes of papilloma virus genome was studied in analyzed samples.

Results:

DNA of human papillomavirus was isolated in 66.66% of samples. Infection with papilloma virus among the patients with SCC (66 cases) was seen in 55 samples (83/6%) and in 23 samples (45%) of dysplasia group (51 cases). The most prevalent HPV genotypes were 18 (37 samples) equal to 31/62%, 16 (32 samples) equal to 27/35% , and prevalence of genotypes 33 and 31 was 15.38% (18 samples) and 4.27% (5 samples) respectively.

Conclusions:

It was demonstrated that cervix cancer has a high correlation with HPV-16 and -18 in the first line, and genotype 33 in next one. Also data presented in this study show that HPV typing has an important role in screening and vaccination programs of cancerous and precancerous lesions.

Keywords: papillomavirus, cervix cancer, HPV16, HPV18, PCR.

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