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Association of high risk human papilloma virus genotypes with oral squamous cell carcinoma among Pakistani patients

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Background: In Pakistan, oropharyngeal cancer is the second leading malignancy attributed to the extensive use of smokeless tobacco products. In many studies, the high risk genotypes of HPV are proven to play a key role in oral squamous cell carcinoma (OSCC). There is a considerable diversity in the epidemiology of high risk HPV genotypes in different countries.

Aim: The objective of this study was to find out the association between high risks HPV genotype in oral rinse of patients with OSCC and pre malignant oral lesions.

Methods: In this case-control study, 200 samples of oral rinse were analyzed by PCR. A significant association between HPV and OSCC was found (OR=3.14, 95% CI=1.6750-5.8969, P value=0.0004).

Results: There was positive association between presence of both HPV 16/18 and OSCC but it was not significant possibly due to small sample size (OR=3.2381, 95% CI=0.8208-12.7752, P value=0.0934).

Conclusion: As a result of these findings, HPV and predominantly genotypes 16 and 18 may be associated with the development of OSCC in Pakistan.

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Large scale sequencing in samples of individuals recently infected with HIV and those with late diagnosis

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With the advent of Highly Active Therapy (HAART) for the treatment of HIV-infected individuals was the emergence of resistant viral majority and minority populations selected by selective pressure. Despite the monitoring of resistance mutations ARVs, there is insufficient data related to transmitted resistance and polymorphisms caused by drugs used to treat rescue. The aim of this study was to evaluate through large-scale sequencing the occurrence of transmitted resistance mutations (TDRM). Of the 19 sequenced samples were evaluated 10 individuals with late diagnosis and four recent infection of HIV-1. Polymorphisms were found in all sequences evaluated for the protease gene (PR), reverse transcriptase (RT) and integrase (IN). The frequency of mutations can be seen in the chart below. Our results showed that in patients with recent infection (infected at least 180 days) there are viral populations HIV who carry mutations to all classes of drugs particularly the NNRTIs in contrast to those with late diagnosis.

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