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ANALYSIS OF HUMAN PAPILLOMAVIRUS TYPE-16 AND -18 LINEAGES IN IRANIAN WOMEN BASED ON LONG CONTROL GENE REGION

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Background / Objectives

Both HPV-16 and HPV-18 play a prominent role in the development of cervical cancer and it was suggested that some variants of HPV-16 and HPV-18 might confer differential risk of cervical disease. The genetic lineages of HPV16 and 18 are not known in Iran. The purpose of this study was to analyze variations of HPV-16 and -18 lineages within the LCR region.

Methods

A total of 2756 samples; including 2638 Cervical ThinPrep and 118 vaginal swabs from Iranian females of 12 provinces, were subjected to HPV screening and then genotyping. Totally 56 samples became positive for HPV-16 (41 samples) and HPV-18 (15 samples). To analyze the HPV lineages, a partial nucleotide sequence of LCR region was sequenced and phylogenetic and SNP analysis were performed using MEGA 5.05 software and HPV genome references.

Results

Sequence analysis of HPV-16 showed that sub-lineage NA1 are the major variant (81.6%, n=31). After NA, sub-lineage EP1 (15.8%, n=6) and the only African variant (AFR2a) were followed. 10 new SNPs were observed in studied HPV-16 sequences. Two new SNPs, T7436G and C7782T, were observed in most of isolates under sub-lineage NA. Eu lineage of HPV-18 is the most prevalent variant in Iran (92.3%, n-12), that followed by As-Am. No AF variant of HPV-18 was found in our study.

Conclusion

We now report the distribution of HPV16 and -18 variants in Iran. Despite other Asian countries, Non-Asian HPV-16 and HPV-18 variants are prevalent in Iran. A possible reason of low incidence of cervical cancer in Iranian women could be explained by this observation.