

## Human Papillomavirus Type 16 E4 Gene Variation as Risk Factor for Cervical Cancer

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**Abstract :** HPV16 E4 gene plays an important role in viral genome amplification and release. Therefore, a variation of the E4 gene nucleic acid sequence may affect the carcinogenicity of HPV16. In order to understand the relationship between the variation of HPV16 E4 gene and cervical cancer, this study was to amplify and sequence the DNA sequences of E4 genes in 118 HPV16-positive cervical cancer patients and 151 HPV16-positive asymptomatic individuals. After obtaining E4 gene sequences, the phylogenetic trees were constructed by the Neighbor-joining method for gene variation analysis. The results showed that: 1) The distribution of HPV16 variants between the case group and the control group differed greatly ( $P = 0.015$ ) and the Asian-American (AA) variant was likely to relate to the occurrence of cervical cancer. 2) DNA sequence analysis showed that there were significant differences in the distribution of 8 variants between the case group and the control group ( $P < 0.05$ ). And 3) In European (EUR) variant, two variations, C3384T (L18L) and A3449G (P39P), were associated with the initiation and development of cervical cancer. The results suggested that the variation of HPV16 E4 gene may be a contributor affecting the occurrence as well as the development of cervical cancer, and different HPV16 variants may have different carcinogenic capability.

**Keywords :** cervical cancer, HPV16, E4 gene, variations

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