

# Molecular variants of HPV-16 associated with cervical cancer in Indian population

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## Abstract

Human papilloma virus is a causative factor in the etiology of cervical cancer with HPV16 being the most prevalent genotype associated with it. Intratype variations in oncogenic E6/E7 and capsid L1 proteins of HPV 16 besides being of phylogenetic importance, are associated with risk of viral persistence and progression. The objective of this multicentric study was to identify HPV-16 E6, E7 and L1 variants prevalent in India and their possible biological effects. Squamous cell cervical cancer biopsies were collected from 6 centres in India and examined for the presence of HPV 16. Variants of HPV-16 were characterized by full length sequence analysis of L1, E6 and E7 genes in 412 samples. Similar distribution of the variants was seen from the different centres/regions, with the European variant E350G being the most prevalent (58%), followed by American Asian variant (11.4%). Fifty six changes were seen in E6 region, 31 being nonsynonymous. The most frequent being L83V (72.3%), Q14H (13.1%) and H78Y (12.1%). Twenty-nine alterations were seen in E7 region, with 12 being nonsynonymous. The most frequent being F57V (9%). L1 region showed 204 changes, of which 67 were nonsynonymous. The most frequent being 448insS (100%), and 465delD (100%), H228D (94%), T292A (85%). The identified variants some new and some already reported can disrupt pentamer formation, transcriptional regulation of the virus, L1 protein interface interaction, B and T cell epitopes, p53 degradation, and thus their distribution is important for development of HPV diagnostics, vaccine, and for therapeutic purpose. © 2009 UICC