

Human Papillomavirus Genotype Distribution in Cervical Cancer in India: Results from a Multi-center Study

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Abstract

The prevalence of HPV genotypes in cervical cancer differs in various regions, though types 16 and 18 generally account for the majority. Knowledge of HPV genotypes in cervical cancer covering the diverse Indian population is important in consideration of the potential future impact of HPV prophylactic vaccination and HPV-based screening strategies. To determine HPV genotype distribution in cervical cancers representing different regions a total of 278 cervical cancer cases were enrolled from cancer centers in North, East, Central and South India. Cervical scrape specimens were tested for HPV DNA using the MY09/11 L1 consensus PCR method followed by sequencing for genotyping, as well as for HPV mRNA utilizing the PreTect™ HPV-Proofer assay. In instances of negative or discrepant results between the two tests, biopsy specimens were tested. HPV DNA and/or mRNA were detected in 91.7% of the cases. Genotype 16 was the most common type, detected alone in 59.4% and in association with type 18 in 3.6% of cases. Genotype 18 was detected as a monotype in 13.3% cases. In total, types 16 and 18 alone or in co-infection with each other were detected in 76.3% cases. Genotype 33 was the third most common type. Overall, genotypes 16, 18, 31, 33, and 45 were the five most common types, detected in 87.1% of the total cases. There were no significant regional differences. In conclusion, the currently available HPV prophylactic vaccines targeting types 16 and 18 have the potential to reduce the burden of cervical cancer in India by over 75%.