

Genotyping of human papillomavirus in cervical intraepithelial neoplasia in a high-risk population

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Infection with the human papillomavirus (HPV) is responsible for 99.7% of cervical cancers, the second most prevalent neoplasia in women worldwide and the fifth leading cause of death by cancer in this population. In Chile, the incidence rate is 14.4 cases per 100,000 women per year and it is considered a significant public health problem. The natural history of cervical cancer begins gradually from low-grade and high-grade squamous intraepithelial lesions to an invasive disease. In this study the frequency of HPV types was determined by HPV genotyping with reverse line blot hybridization in 200 cytobrushes of women with preneoplastic lesions in a high-risk population. HPV DNA was found in 89% of the lesions (83.3% of low-grade squamous intraepithelial lesions and 93.6% of high-grade squamous intraepithelial lesions). Multiple HPV infections were found in 14.4% and 15.5% of low- and high-grade lesions, respectively. HPV 16 was the most frequent genotype in single infections, followed b