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Prevalence and type distribution of high-risk human papillomavirus in patients with Cervical Cancer: A population-based study

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Abstract

Background: Cervical cancer is the greater cause of cancer death in women in many developing countries. Persistent infection with human papilloma virus (HPV), primarily high risk types 16 and 18, is recognized as a causal and essential factor for the development of cervical cancer. We aimed to determine the distribution of high-risk HPV genotypes in archival biopsies with cervical carcinoma in patients from Mazandaran Province, Northern Iran.

Methods: A total of 98 paraffin-embedded cervical samples consisted of 63 Squamous Cell Carcinomas (SCC), 4 Adenocarcinomas, 19 Cervical Interaepithelial Neoplasia grade I (CIN-I), 4 CIN-II and 8 CIN-III diagnosed during 2009-2011, were selected to perform high risk HPV genotyping using AmpliSens(R) HPV HCR DNA genotyping kit. The prevalence of HPV infections was assessed in low and high grade cervical lesions by age.

Results: Of the 98 cervical samples analysed by DNA PCR, 78 (79.59%) were positive for HPV DNA. HPV was detected in the 52 of SCC, 4 of Adenocarcinomas, 14 of CIN-I, 4 of CIN-II, and 4 of CIN-III for HPV. From the 78 HPV positive samples, 23 (29.5%) samples were positive for HPV type 16, 32 (41%) were positive for HPV 18, 19 (24.4%) were positive for HPV 45, and 4 (5.1%) of cervical specimens were positive for HPV 39.

Conclusions: This study provides valuable baseline data for future assessment of the impact of current prophylactic vaccination programs that is protective against the two most common oncogenic types of HPV found in cervical cancer, HPV-16 and HPV-18, but not against other high-risk mucosal HPVs, 39 and 45, reported in this population.