

Virology

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Molecular epidemiology and genotype distribution of Human *Papillomavirus* (HPV) among Arab women in the state of Qatar

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Background: Human Papilloma Virus (HPV) infection is the major cause of cervical cancerworldwide. With limited data available on HPV prevalence in the Arab countries, this studyaimed, to identify the prevalence and genotypic distribution of HPV in the state of Qatar.

Methods: 3008 cervical samples, exclusively of women with Arab nationality residing in Qatarwere collected from the Women's Hospital and Primary Health Care Corporation in Doha, Stateof Qatar.HPV DNA detection was done using GP5+/6+ primers based real time-polymerasechain reaction (RT-PCR) assay followed by the usage of HPV type specific primers based RTPCRreactions and Sanger sequencing for genotype identification.

Results: Similar prevalencerates of HPV infection was identified in both Qatari and non-Qatari women at 6.2% and 5.9% respectively. HPV 81, 11 and 16, in decreasing order were the most commonly identified genotypes. HPV 81 was the most frequent low-risk genotype among women with both normal(74.0%) and abnormal (33.3%) cytology. HPV 16 (4.6%) was identified as the predominanthigh-risk HPV genotype among women with normal cytology and HPV 16, HPV 18, and HPV56 (22.2% each) were the most common identified high-risk genotypes in women with abnormalcytology. Conclusions: The overall HPV prevalence in Arab women in Qatar was identified as6.1 % with an increased HPV prevalence seen in women with abnormal cytology results and nosignificant trends seen with age. In contrast to Western countries, we report a varied genotypic profile of HPV with a high prevalence of low-risk HPV genotype 81 among the Arab womenresiding in Qatar.

Keywords: Human Papilloma virus, Qatar, Genotyping, Prevalence, Arab women, Cytology.

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