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Abstract

Human papillomavirus (HPV) infection is estimated to be the most common sexually transmitted infection and is one of the causal factors in cervical cancer. Understanding the epidemiology of this infection is an important step toward developing strategies for its prevention. Cervical samples from 210 healthy women with normal and abnormal cytomorphology were studied for the detection of HPV DNA by polymerase chain reaction (PCR), utilizing the two most commonly used consensus primer sets. The primers; MY09/MY11 and GP5+/GP6+ located within the L1 region of HPV genome, amplified a broad spectrum of HPV genotypes in a single reaction. The PCR amplification of HPV genomes is a sensitive method that is used for the detection of cervicovaginal HPV. With the aim of identifying the HPV types, samples were also subjected to PCR using specific primers for HPV types 16 and 18. In addition, basic demographic information, sociodemographic characteristics, and sexual behavior were recorded. HPV was detected in 13.8% of the study population aged 18 to 57 years using PCR. HPV16 (6.6%) was more commonly detected than HPV18 (3.8%). The highest prevalence of HPV infection was seen in women below 27 years old, and then, a new increase was seen higher than the age of 48. In conclusion, our study demonstrated that younger age at marriage, economic status, parity, and dwelling are the major risk factors determining HPV infection.

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