High prevalence of human papillomavirus DNA detected in cervical swabs from women in Southern Selangor, Malaysia.

ABSTRACT

Persistent high-risk human papillomavirus (HPV) infection is known to play an important role in the genesis of cervical cancer. Since new screening and prevention strategies, namely improved HPV testing and HPV vaccination have been aggressively promoted recently, it is crucial to investigate the HPV distribution in Malaysia in order to maximize their costeffectiveness. This study was therefore conducted to assess the HPV type distribution in the most populous region, the state of Selangor. A total of 200 cervical swab samples were collected in two health-screening campaigns, and also from women attending obstetrics and gynecology clinics in several hospitals in Selangor. DNA extraction was performed and HPV DNA was detected via nested PCR using MY09/MY11 as outer primers and GP5+/GP6+ as inner primers which target the L1 gene of the viral genome. The purified PCR products were subjected to automated DNA sequencing to determine the HPV genotype. Out of 180 βglobin positive samples, 84 (46.7%) were positive for HPV DNA. The most common HPV type found was high-risk oncogenic type 16 (40%), followed by HPV type 18 (3.3%), HPV 33 (1.7%), HPV 31 (0.6%), and low-risk HPV 87 (0.6%). Our study confirmed that nested PCR method is highly sensitive in detecting HPV DNA even in low risk patients. Since a relatively high prevalence rate of HPV infection was found in this population, prompt healthcare policy changes to bring about implementation of early HPV vaccination program is desirable to prevent a high incidence of cervical cancer.

Keyword: Human papillomavirus (HPV); Cervical cancer; Malaysian women; Nested PCR.