

PRELIMINARY RESULTS ON HIGH RISK HUMAN PAPILLOMAVIRUS SUBTYPES IN CERVICAL CANCER SPECIMENS IN HIV+ AND HIV- WOMEN FROM BOTSWANA

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Background

Cervical cancer is the fourth most common cancer in women worldwide and HPV is the primary causative agent. Women with HIV are at a higher risk of persistent HPV infection leading to cervical cancer. However, distribution of HPV subtypes is not well known in invasive cervical cancer.

Objective

To explore the prevalence and distribution of HPV genotypes of women from Botswana and develop a technique for HPV detection using cervical cancer biopsy tissue.

Methods

The HPV DNA was prepared from paraffin-embedded samples (10 µm section) of 52 cervical biopsy specimens. HPV genotyping was performed through Abbott Real-Time PCR and for samples with low DNA concentration nested-PCR (using consensus MY011/09 primer pair followed by GP5/6 primers) applied. The ~150pb PCR products were subjected to direct DNA sequencing to determine HPV subtypes. Statistical comparison among frequencies was done with chi square test.

Results

In 52 specimens tested, HPV genotypes identified were: HPV-16 (n=27, 51.9%), HPV-18 (n=9, 17.3%), other *hr*-HPV genotypes (n=16, 30.8%). HPV-16 was more prevalent in HIV-infected (45.5%) than in HIV-uninfected subjects (36.8%) ($X^2=4.39$, $df=1$, $p=0.036$), no statistical difference was found for HPV-18 by HIV status. Moreover, the carriers of HPV-16 and/or -18 were more likely to be HIV-infected (72.7%) than HIV-uninfected (36.8%) ($X^2=6.45$, $df=1$, $p=0.011$). Majority of our cervical cancer samples had either HPV-16 and/or -18 (86.5%) and the rest had other *hr*-HPV genotypes (13.5%).

Conclusion

We developed a highly sensitive method to provide the spectrum of HPV genotypes in cervical cancer patients from Botswana. Our study demonstrates a high prevalence of HPV-16 and -18 in cervical cancers patients with difference in prevalence according to the HIV status.

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