

CORRELATION BETWEEN THE HUMAN PAPILLOMAVIRUS TYPE DISTRIBUTION IN MALIGNANT AND PREMALIGNANT CERVICAL LESIONS AT THE UNIVERSITY OF BENIN TEACHING HOSPITAL

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ABSTRACT

BACKGROUND

Cervical cancer is a preventable disease and has continued to constitute a major public health problem. Persistent infection with high risk human papillomavirus (HPV) types is said to play a major role in the causation of the disease. Although, epidemiological studies have established HPV infection as the central cause of invasive cervical cancer (ICC) and its precursor lesions, only a fraction of premalignant lesions progress to ICC. It is important to know whether the HPV type distribution in premalignant lesions is representative of those that go on to cause cancer. This may help in planning more aggressive treatment modalities and more effective follow up measures for premalignant lesions when such virulent HPV types are detected. It may as well help in the evaluation of the potential impact of both existing and future prophylactic HPV vaccines.

AIM

To compare the type distribution of high risk HPVs in women with malignant and premalignant cervical lesions in the University of Benin Teaching Hospital (UBTH).

METHODS

In this case controlled study, sixty women with histologically confirmed ICC and sixty controls with histologically diagnosed cervical intraepithelial lesions (CINs), awaiting treatment at the UBTH were recruited for the study. These had cervical swabs taken for HPV testing using COBAS 4800. All collected specimens were transported to a central laboratory at Access to Basic Medical Care (ABC) foundation, Ibadan, for assay. Data analysis was done using the Statistical Package for Social Students (SPSS) version 20. Relationship between variables was assessed using Chi square test or Fisher exact test where appropriate. Pearson's correlation was used to determine the relationship between HPV types in premalignant and malignant lesions and significant differences between means was determined using Student *t* test. The level of significance was set as $p < 0.05$.

RESULTS

120 subjects who met the inclusion criteria participated in the study: 60 subjects with malignant cervical lesions (ICC) and 60 controls with premalignant cervical lesions (CIN I, CIN II and CIN III). Of the sixty controls, 25 had CIN III, 19 had CIN II while 16 had CIN I. While ninety percent (54) of the 60 subjects with invasive cervical cancer tested positive to at least one hrHPV genotype, only sixty-five percent (39) of the 60 controls with premalignant lesions (i.e. 80%, 57.9% and 50% of those with CIN III, CIN II and CIN I respectively) tested positive to hr HPV testing. This too was statistically significant ($p=0.001$). While HPV-16 is responsible for 63% of the malignant lesions, it is only responsible for 25.6% of their premalignant counterparts. This was statistically significant ($p=0.001$). HPV-16 was more likely to be found in malignant than premalignant cervical lesion ($OR=4.93$, 95%

$CI=1.99-12.20$, $p=0.001$). HPV-18 was less likely to be found in malignant compared to premalignant cervical lesions. However, this association was not statistically significant ($OR=0.32$, $95\% CI =0.08-1.38$, $p=0.158$). Other hrHPV types were also less likely to be found in malignant compared to premalignant cervical lesions. This was statistically significant ($OR=0.32$, $95\% CI= 0.14-0.75$, $p=0.011$).