HIV CO-INFECTIONS WITH CYTOMEGALOVIRUS, HEPATITIS C VIRUS AND HUMAN PAPILLOMAVIRUS IN NORTHERN SOUTH AFRICA

BY

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ABSTRACT

The human immunodeficiency virus (HIV) is responsible for acquired immunodeficiency syndrome (AIDS) affecting millions of people globally. Opportunistic pathogens, such as human papillomavirus (HPV), cytomegalovirus (CMV) and hepatitis C virus (HCV) are associated with HIV infection and AIDS.

Cervical cancer caused by HPV remains a serious public health problem in Sub-Saharan Africa and many other parts of the developing world. The prevalence of HPV is higher in African women with a normal cervical cytology than in women in other regions of the world. Although HPV prevalence data is accumulating in several regions of South Africa, there is no data on the HPV infection in northern South Africa.

Cytomegalovirus is the leading cause of congenital infections. Risk of congenital infection is higher for seronegative women who have a primary CMV infection during pregnancy than it is for seropositive women who experience a reactivation of re-infection. Hepatitis C virus causes liver disease and is a major public health problem for people infected with HIV. Data on HCV prevalence is equally scarce for northern South Africa.

The aim of the study was to determine the prevalence of CMV, HPV and HCV, and also to determine the genotypes of HPV in Northern South Africa in an HIV infected population. The study subjects (n=200) comprised highly active antiretroviral therapy (HAART) naïve and experienced individuals of both genders. The age range was 2-68 years. This was a laboratory based retrospective study. The 200 HIV positive plasma samples were screened for HPV, CMV and HCV antibodies by enzyme-linked immunosorbent assay (ELISA). A group of 50 HIV negative samples was included in the detection of the co-infecting viruses. HPV DNA detection from plasma and peripheral blood mononuclear cells (PBMCs) was done by PCR and genotyped by reverse hybridization using the Linear Array HPV Genotyping Test kit (Roche). Genotyping was further confirmed by phylogenetic analysis of a partial L1 gene.

The antibody prevalence of HPV, CMV and HCV in the HIV infected population was 21% (42/200), 100% (200/200) and 0.05% (1/200) respectively. In the HIV negative population the prevalence was 12% (6/50), 100% (50/50) and 0% (0/50) respectively. Infection with CMV was significantly more prevalent among the unmarried patients than married patients (p=0.000). Infection rate with HPV was not significant in HIV infected females (p=1.000) when compared with the HIV negative group. Similarly, there was no significant difference of HPV infection when age below 15 years and above was considered in the HIV infected and non-infected groups (p=0.983). Forty two (21%) of HIV infected people were found to be co-infected with both HPV and CMV.

Amplification of HPV DNA from HPV plasma could not yield expected DNA fragment (450bp). However expected DNA was obtained from 50% (8/16) PBMCs of the corresponding plasma. Genotyping by Linear Array HPV Genotyping Test was successful for 50% (4/8) of the HPV DNA and all were of the HPV type 16. Ten samples, successfully amplified by conventional PCR out of 16, were shown to be HPV type 16 by phylogenetic analysis.

The study findings show that a low percentage of the study population was infected with HPV, CMV and HCV. In addition, infection with HCV was also low. The limited genotyping showed that HPV type 16 is the more prevalent variant in the studied population. These observations would require confirmation with a larger sample size and HPV genotyping on other specimen type such as cervical cells.