MOLECULAR DIVERSITY OF HEPATITIS B VIRUS IN HIV INFECTED PATIENTS AT MBAGATHI DISTRICT HOSPITAL, NAIROBI

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A RESEARCH PROPOSAL SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF DEGREE OF MASTER OF SCIENCE IN INFECTIOUS DISEASES IN THE SCHOOL OF HEALTH SCIENCES OF KENYATTA UNIVERSITY

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DECLARATION

This research proposal is my original work and has not been presented for a degree or award in any other University.

Signature ..... Date 18/09/2013

Samuel Barasa Khaemba

We confirm that this proposal was written under our guidance as the supervisors.

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ABSTRACT

With increasing access to antiretroviral therapy across Sub-Saharan Africa, HIV-infected individuals live longer and the effects of co-infection with chronic viral hepatitis is an emerging critical public health problem. Chronic HBV infection is a leading cause of progressive complications of liver cirrhosis, hepatocellular carcinoma and liver failure in most Sub-Saharan and Asian countries. Patients infected with HIV are at particular risk for HBV infection due to similar transmission routes and up to 10% of patients infected with HIV are also chronically infected with HBV, with 13 times higher risk of death in HIV-HBV dual infection than in mono-infected patients. HIV co-infection accelerates HBV-related liver damage, leading to earlier cirrhosis and end-stage liver disease. Conversely, the presence of HBV co-infection complicates the management of HIV and increases the morbidity and mortality of HIV-infected patients. Both HIV and HBV infections are considered to be hyperendemic in Sub-Saharan continent, with approximately 2% of all annual deaths in Africa resulting from clinical consequences of HBV infection and 25% of all annual deaths resulting from the clinical consequences of HIV infection. Kenya is among the countries that are affected by hepatitis B, with a high HIV burden, leading to frequent HIV/HBV co-infection. Considerable molecular variations are reported to occur throughout the HBV genome and the resultant genetic diversity is correlated with geographical distribution of genotypes and clinical outcome, immunization and antiviral therapy response. This study will assess the molecular genetic variation in HIV infected patients attending Mbagathi District Hospital. The prevalence of HBV in HIV patients will be assessed using SPSS v. 17.0 and Pearson Chi-square test. The data generated will be reported as percentages. Genetic variation will be evaluated using PCR amplification of the S gene and subsequent sequencing of the amplicons. Phylogenetic analysis of the sequences and comparison of identified genotypes with other identified genotypes elsewhere will be carried out using MEGA v 4. Understanding the prevalence and the HBV genotypes will better the knowledge of individual risk factors for hepatocellular carcinoma and form the basis for disease management and for designing preventive strategies.