

Abstract

Background: Hepatitis B (HBV) and Human Immunodeficiency virus (HIV) are both bloodborne viruses. Markers of either active or past HBV infection are present in many HIV infected patients. Worldwide, HBV prevalence varies geographically and endemicity is classified as low (<2%) or high (>8%). Genotypically, prevalence varies among different populations, with genotype A having a wide distribution. In Kenya, the prevalence of HIV-1/HBV co-infection ranges from 6-53% depending on the sub-population, with genotype A as the most common. **Objective:** To determine the prevalence and characterize HBV in HBV/HIV co-infected injecting drug users (IDUs) from Mombasa, Kenya. **Methods:** Blood samples were collected from HIV-infected IDUs in Mombasa, Kenya. Hepatitis B surface antigen (HBsAg) was tested by enzyme immunoassay (EIA). HBV DNA was extracted by SMITEST R&D kit. Polymerase chain reaction (PCR) was done; followed by population sequencing of HBV preS, core and full genome using specific primers. Analysis was done phylogenetically with reference sequences from the Genbank. **Results:** Seventy two HIV-positive samples were collected from IDUs in Mombasa in February and March 2010. Of these, 10 (13.89%) were HBsAg-positive by EIA. Nine of the 10 samples (12.5%) were PCR positive for HBV in the preS region; from these, four HBV full length sequences were obtained. Phylogenetic analysis showed that all belonged to genotype A1. **Conclusions:** The prevalence of HBV co-infection among HIV-infected IDUs in Mombasa, Kenya was 12.5%. Phylogenetically, sequences obtained from this study showed clusters that were distinct from reported Kenyan reference sequences from the Genbank. The findings point to an existence of a transmission network among IDUs in Mombasa. This further suggests that HBV genotypes in Kenya may be regionally diverse.