

Abstract

Kenya is one of the high endemic zones for hepatitis B virus (HBV) infection. The consensus on prevalence of the HBV genotypes and the existence of their variants have not been fully established in Kenya. Hence, there is a need to further monitor the diversity of HBV. This study aimed to extend the current molecular and epidemiological information about the geographical distribution of HBV genotypes and subgenotypes, as well as to describe the hepatitis B surface antigen (HBsAg) variants circulating in different Regional Blood Transfusion Centres of Kenya. A total of 32 HBsAg positive blood units from five different blood transfusion centers in Kenya were used in the study. The HBV DNA preS/S-gene was amplified and sequenced. Alignments of S gene were applied using reference sequence from GeneBank. Phylogenetic analysis was performed using the MEGA v4.0 software with the neighbor-joining and maximum composite likelihood methods. Twenty-one plasma samples (65.6 %) were DNA positive and were successfully sequenced. Eighteen out of the twenty-one isolates (85.7 %) belonged to subgenotype A1 Afro-Asian: six were from Nairobi, four from Kisumu, two from Embu, and three each from Eldoret and Mombasa. The other three strains (14.3 %, 3/21) belonged to subgenotype D4 from Mombasa. The HBsAg mutations were detected in nine isolates (42.9 %, 9/21). The HBV/A1 and HBV/D4 are dominant among blood donors in Kenya. This demonstrates that continuous monitoring of the HBV diversity would help reveal circulating genotypes and subgenotypes as well as mutants of clinical significance in Kenya.