Abstract

Hepatitis B virus (HBV) genotypes are important in both the clinical manifestation of disease and treatment response. Although Kenya belongs to the African Region (AFR-E) characterized by high mortality and hyperendemicity of HBV, there is a paucity of HBV genotyping data. The aim of this study was to molecularly characterize the basic core promoter/precore (BCP/PC) and complete surface (S) regions of HBV isolated from 61 HBsAg-positive liver disease patients attending Kenyatta National Hospital in Nairobi. HBsAg, HBeAg and viral loads were determined. HBV DNA was amplified and sequenced from 58/61 patients. In addition to the complete genome of two isolates, the BCP/PC and the complete S regions of 43 and 38 isolates, respectively were sequenced. Following phylogenetic analysis of the S region, 38 isolates clustered with subgenotype A1, whereas two isolates clustered with genotype D, one with subgenotype D1 and another as an outlier of the clade containing subgenotype D6 and the D/E recombinant. When the complete genome of the latter isolate was sequenced it clustered with D6. The majority of isolates belonged to serological subtype *adw*2 and only four to *ayw*2. Three distinct groups of subgenotype A1, distinguished by different amino acid motifs, circulate in Kenya: two in the African cluster and a monophyletic clade in the "Asian" cluster. HBeAg-negativity was a result of G1896A in genotype D isolates, whereas in subgenotype A1, the HBeAg-negativity was a result of mutations in the Kozak region (1809–1812) or precore start codon (1814–1816). Mutations at positions 1762 and 1764 occurred more frequently in HCC patients ($p < 0.05$). In conclusion, subgenotypes A1, D1 and D6 circulate in liver disease patients in Kenya, with A1 predominating.