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 adw2 and only four to ayw2. 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.