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Serologic markers and molecular epidemiology of HBV in an HIV infected cohort from Cameroon

By

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Abstract

Hepatitis B virus (HBV) and human immunodeficiency virus (HIV) are generally transmitted through similar routes and are of global public health concern, especially in sub-Saharan Africa. Hence, it is crucial to regularly assess the prevalence of HBV in HIV infected patients to generate data relevant for the management of HIV/HBV infections. The objective of this study was to determine the prevalence of HBV serologic markers, mutations associated with resistance to Lamivudine, and HBV genotypes in HIV–infected individuals from Cameroon. Plasma from 455 HIV infected antiretroviral drug naïve patients from the Southwest and Littoral Regions of Cameroon were investigated for serologic markers of HBV infection. HBV polymerase gene was amplified by nested polymerase chain reaction, directly sequenced, and analyzed for viral genotypes and mutations associated with resistance to Lamivudine. The observed prevalences for serologic markers for HBV infection were as follows: HBsAg (25.5%), anti-HBsAg (13.3%), anti-HBc (36.3%), anti-HBs + anti-HBc (20.8%), HBsAg+HBeAg (15.2%). Occult HBV DNA was detected in 6.5% of the HBsAg negative patients. Out of 46 available HBV polymerase sequences, 7 (15.2%) harboured one or more lamivudine associated resistance mutations, and HBV genotypes noted were E (72%) and A (28%).The observations suggest that a high proportion of the HIV infected study population are co-infected with HBV. The detection of HBV variants resistant to lamivudine in HIV infected drug naïve individuals may have implications for the clinical management of HIV/HBV infected patients.

Keywords: HBVs; Seroprevalence; Occult HBV; Genotype; Lamivudine resistance