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Mutational Analysis of Hepatitis B Virus Precore Region Molecular Variants in Ile-ife, Nigeria

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ABSTRACT

Abstract

Introduction

Evolution of phenotypic diversity among viruses occurs as an escape mechanism against host immune pressure or drug selective pressure. Among HIV/HBV co-infected individuals, various HBV basal core promoter (BCP)/precore (PC) region molecular mutants had been reported with associated phenotypic defect in HBeAg production. The emergence of HBeAg negative variants of HBV in HIV co-infected individuals have profound implication on the diagnosis, management and prognosis of this subset of individuals. This includes delayed clearance of HBV, early development of adverse hepatic events such as liver cirrhosis and hepatocellular carcinoma . Currently, little is known about HBV BCP/PC region genomic heterogeneity in HIV/HBV co-infected patients in Nigeria. Therefore, this study was focussed on investigating evidence of precore/core region genomic variability among HIV/HBV co-infected patients in Nigeria.

Materials and methods

A total of 40 patients (20 HIV/HBV co-infected and 20 HBV mono-infected samples) were enrolled into the study and subsequently tested for HBsAg, HBeAg and HBeAb using specific Enzyme-Linked Immunosorbent Assay (ELISA).The BCP/PC genome regions (nucleotides 1653-1959) were amplified using a nested PCR assay and then subjected to BCP/PC mutational analysis in genome sitesaffecting HBeAg expression especially at the BCP transcriptional and PC Translational stop codon sites.

Results

Overall, 5(83.3%) of the six exploitable sequences after analysis showed various BCP/PC mutations. Only 1(16.6%) sequence from an HIV/HBV co-infected patient had the BCP transcriptional (double mutation; A1762T/G1764A) mutant. Analysis of the PC translational stop codon showed4 (66.6%) having the G1896A mutants while 33.3% (2) had G1899A mutants.

Conclusion

This study has broadened the available evidence of BCP/PC region molecular mutants among HIV/HBV co-infected patients in Nigeria and assessed the difference of mutation prevalence in comparison with HBV mono-infected cohort . We therefore recommend that HIV/HBV co-infected patients be routinely screened for hepatitis B virus precore region mutants to improve their patient outcome.

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