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Detection and Analysis of drug resistance mutations in polymerase gene of hepatitis B virus

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Abstract

Despite the effectiveness of antiviral therapy using nucleos(t)ide analogues (NAs), drug resistance is still a major obstacle for the long term efficacy of antiviral therapy in chronic hepatitis B. Mutations can occur spontaneously and naturally in HBV reverse transcriptase (RT) region as minor viral population in naive patients and can emerge as major viral population, conferring drug resistance and treatment failure. The aim of this study was to analyze mutations within the HBV polymerase gene in treatment naive Moroccan patients with CHB. A total of 123 treatment-naïve HBV-infected individuals were included in this study. The HBV polymerase gene was analyzed by PCR and direct sequencing. HBV RT region mutations and amino acid changes were analyzed in BioEdit, by comparing the obtained sequences with a set of HBV reference sequences, HBV genotypes were determined using Geno2pheno HBV Database. Sixty- samples were successfully amplified by PCR. Our results showed low frequencies of classical primary drug resistance mutations (3%), (13%) of non-classical pre-treatment mutations, and a high frequency of nonclassical putative NA resistance mutations (65%). Among these, 56% were lamivudine resistance mutations, and 44% adefovir resistance mutations. A single primary resistance mutation to adefovir, „A194T‟ was detected in 2/60 CHB patients, two pretreatment mutations in 8/60 patients, and 11 putative resistance mutations in 39/60 patients. These results confirm that HBV mutations which confer resistance against currently available anti-HBV NA, may already exist in patients who have never received NA treatment.

Keywords: CHB, mutations, nucleos(t)ide analogues, RT.

Biography:

I completed my PhD since May 21th, 20219 from Chouaib Doukkali University in Morocco and Institut Pasteur du Maroc. I‟m actually a postdoctoral fellow candidate. I have seven publications in reputed journals.

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