

COMPARISON OF HBV RIBONUCLEASE H DOMAIN IN NAÏVE AND DRUG RESISTANT PATIENTS

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Abstract. Nucleotide or nucleoside analog (NA) drug resistance has increasingly become a problem in HBV treatment. Due to the similarity between HBV polymerase and HIV-1 reverse transcriptase, knowledge obtained from HIV research might be applied to the treatment of HBV infection. A previous study has shown that HIV-1 ribonuclease H (RNase H) mutation may contribute to nucleoside reverse transcriptase inhibitor (NRTI) resistance. Therefore, we hypothesized that it might be possible to have a mutation in the HBV RNase H domain of HBV NA drug resistant patients. A one-year cross-sectional study was conducted at a single university hospital. Serum samples were collected from HBV infection treatment naïve and suspected HBV NA drug resistant patients. To confirm HBV NA drug resistance, genotype specific resistance was examined. The HBV genotype and RNase H domain were sequenced and compared. In total, 37 HBV-infected patients were finally analyzed. Of these, 24 were considered sensitive to the drug and 13 resistant, as determined by the genotypic resistance method. Comparison between the two groups showed they had comparable baseline characteristics; no mutation in the HBV RNase H domain was detected. Possibly due to the small sample size, no significant mutations were found in the HBV RNase H domain of either group of HBV-infected patients. Further research of a larger patient group is needed to confirm these initial findings.

Key words: hepatitis B virus, ribonuclease H domain, drug resistant, mutation, nucleos(t)ide analog drug

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