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Editorial

Sequencing Analysis of Hepatitis

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INTRODUCTION

Hepatitis B Virus (HBV) could also be a noncytopathic DNA virus that infects approximately 350 million people worldwide and should be a number one explanation for liver cirrhosis and hepatoma. The evolutionary dynamics of HBV are characterized by high mutation rates due to the error-prone polymerase (RT) and rapid replication rates. Thus, an outsized number of viral variants are constantly generated, creating great genetic diversity on which survival operates.

Heterogeneous populations of viruses are often mentioned as viral quasispecies. The massive heterogeneity present in HBV quasispecies has crucial biological consequences. It has been identified as an important believe regard to the clinical features of the infection (transmission, persistence, and liver damage) and it's going to influence the outcomes of treatment and be important within the development of resistance to nucleoside/nucleotide analogue (NA) antiviral therapy.

SEQUENCING ANALYSIS

It was previously demonstrated that the virus is present in serum of some patients without immunological evidence of HBV infection. Here the demonstration of sequence analysis explains that the serum of such a patient contained a mixed HBV population. In comparison with HBV genomes of various genotypes twenty-two nucleotide variations were found altogether clones sequenced in parallel. One nucleotide variation was detected within the enhancer I [1-5].

Twelve of the twenty-two nucleotide variations caused altogether fifteen changes of aminoalkanoic acid sequence in known or predicted viral proteins. The proteins of the P open reading frame, which are most vital for viral replication, were suffering from nine aminoalkanoic acid substitutions. Three aminoalkanoic acid substitutions concerned the merchandise of the X gene, a transcriptional transactivator of varied viral and cellular promoters.

Cloning of Sanger dideoxy sequencing and therefore the PCR products are widely utilized in analyzing the heterogeneity of viral quasispecies and determination of antiviral-associated drug resistance mutations, which has been used because the reference technique to review viral populations. However, this procedure is time-consuming, laborious, and costly, only a few researchers have studied viral populations in considerable detail, and no more than 100 clones were obtained within a patient sample.

Furthermore, the preferred selection of deficient viral genomes can result in the molecular cloning. Thus, we'd have missed many aspects of the viral population supported the dominant sequences, and therefore the full intrapopulation heterogeneity is difficult to characterize. Next-generation sequencing (NGS) technologies have changed things dramatically. They allow for massive parallel picoliter-scale amplification and detection of individual DNA molecules which has made it possible to generate hundreds of thousands of clonal sequence reads, providing the potential to scale back the time and complexity for DNA sequencing without the necessity for cloning.

Although it remains unclear whether any of the PBMC-integrated HBV DNA sequences are actively transcribed, the presence of a near-full-length X open reading frame and its promoter suggests such a possibility. The X protein plays a key role in the liver carcinogenesis. However, because the eventually translated X protein would be truncated, its transactivating capabilities are likely to be diminished.

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