Introduction

Hepatitis B virus (HBV) represents a major health problem with 400 million carriers worldwide. Infection with HBV leads to different forms outcomes, which can be broadly divided into three categories: acute, fulminate and chronic. The factors that lead to these different forms states are poorly understood but are believed to include the genetics of HBV strains. A classification into eight major strains (referred to as genotypes A-H) is currently used ***(Cacciola et al., 2002).***

HBV is characterized by a compact, circular DNA genome of about 3.2kb in length with four partially-overlapping Open Reading Frames (ORFs) and no non coding regions, suggesting that all regulatory signals are within protein-encoding regions ***(Kidd-Ljunggren et al., 2002).*** The extreme compactness of the genome leads to the expectation of significant selective constraints. Nevertheless HBV is genetically diverse and several genotypes (A-H) and sub-genotypes have been described ***(Kramvis and Kew, 2005).***

The mutation rate of HBV is commonly estimated around $4.2 * 10^{-5}$ substitutions per site per year among the non-overlapping part of the four ORFs ***(Bollyky and Holmes, 1999; Fares and Holmes, 2002).*** This rate is particularly high for DNA viruses (around 104 times higher than most DNA viruses) and closer to that observed for RNA viruses. This can be explained by the replication mechanism, via a reverse transcription step, that makes the virus prone to mutations ***(Kramvis and Kew, 2005).***

The various HBV strains observed today have been shaped by different evolutionary forces, including mutation, selection and recombination. High mutation rates and possible extensive recombination may be involved in the creation of new HBV strains. The virus also interacts with its environment, composed of different hosts from various human populations, a situation that might lead to the creation of different viral sub-populations.

Each human population (or on a smaller scale human community) has its own cultural habits which might influence the course of the infection and the transmission of the virus between individuals. These differences between human communities may contribute to the genotypic diversity within and between HBV populations. Differences in the immune system of each individual select for different viral quasi-species, further increasing the genotypic diversity. The structure existing within the host population might have led to an associated structure of HBV populations.

We aimed to understanding the mutations of HBsAg and HBCoreAg major immunodominant region nucleotide sequence; through highly sensitive diagnostic assays can be achieved for detection of HBV in clinical specimens**. So the main aims of this study were:**

- To determine HBV genotype in Egypt by comparing the nucleotide and amino acid sequences of Egyptian patient with hepatitis sequence retrieved from GenBank.
- To investigate the genetic heterogeneity of HBsAg sequences in our population.

- To analyze and compare the HBCoreAg sequence from our studied population with related GenBank sequences.
- To discuss the genetic variability of the HBCoreAg with the circulating Egyptian HBV strains.