Introduction

Hepatitis virus B (HBV) was a major causative agent of chronic hepatitis and can cause liver cirrhosis and hepatocellular carcinoma **(AK1 ABe *et aI*,1999).**

There were more than 300 million chronic carriers of hepatitis B virus (HBV) world wide. Chronicity may result in an asymptomatic carrier state, reactive fulminant hepatitis, mild and aggressive hepatitis and the development of liver cirrhosis or hepatocellular carcinoma **(Caplin *et al*, 1999).**

Human hepatitis B virus which was a protype member of the family hepadnaviridea, was a circular partially double stranded DNA virus of approximately 3200 nt **(Lieven *et al*, 2000).**

This highly compact genome contained four major open reading frames (ORFS) encoding the envelope (pre S1, pre S2 and surface Ag "HBS-Ag"), core (pre core precursor protein, HBe-Ag and HBc-Ag) polymerase (HBpol) and (HBx) proteins respectively. By using subtype specific antibodies against HBS-Ag, nine different serological subtypes were defined ،reflecting the genetic variability of HBV, of the defined determinants, one was common to all subtypes (a determinant), but also two pairs of mutually exclusive sub determinants (d or y, and w or r) were commonly found. By using this tool in epidemiological studies, nine serological subtypes had been identified **(Lieven *et al*, 2000).**

Genotypically, HBV genomes had been classified into six groups, designated from A - F, based on an inter group divergence of 8% or more in the complete nucleotide sequence. Genotype A , D, E were most common in Europe, North and Central America and Africa ،genotype B

and C were most prevalent in the Far East, and genotype F occurs almost exclusively in South America. **(Norder *et al*, 1992).**

Virus titers during the course of infection can vary dramatically, often being too low for detection by conventional methods, serological analysis of viral proteins was not a reliable indicator for the HBV -DNA titers because there may be very few virons or none at all, but very high levels of subviral particles devoid of viral DNA in patients sera. **(Nassal & SChaller, 1996).**

Quantification and sensitive determination of the viral DNA by PCR can provide indirect evidence for the level of viral replication, the degree of infectivity and the changes of viral DNA titers during the course of infection, moreover monitoring of the changes in viral titers during treatment with antiviral drugs and development of drug resistance. **(Gunther *et al* ,1998).**

Aim of the work

The aim of this work is to determine the most common HBV genotype in Egypt.