

Hepatitis B Virus

Chronic hepatitis B virus (HBV) affects $\geq 5\%$ of the world's population -- it is the primary cause of cirrhosis and hepatocellular carcinoma and the ninth leading cause of death worldwide. In the United States, ~1 million persons are chronically infected with HBV. Because treatment of chronic active HBV can prevent cirrhosis and liver cancer, effective therapy and universal immunization are highly desirable goals. To treat HBV, it is very important to understand the epidemiology, natural history, and serologic markers of the disease.

A variety of immunologic and molecular assays are available for diagnosing viral hepatitis and monitoring treatment

response.

Tests for antibodies and antigens are available for hepatitis A-E, including those specific for hepatitis B core, surface, and e proteins. Techniques for antibody detection include enzyme immunoassay (EIA) and recombinant immunoblot assay (RIBA[®]). EIA technology is also used for antigen testing. Branched DNA (bDNA), solution hybridization-hybrid capture (Digene), transcription-mediated amplification (TMA), and polymerase chain reaction (PCR) are used for DNA and RNA testing to determine the presence of viremia and measure the viral load. HCV and HBV genotypes can also be determined with hybridization or

sequencing-based assays.

Such tests, singly or combined with other markers could lead to Diagnosis of Acute or Chronic Infection, Demonstration of Carrier Status, Recovery or Differentiation between active and resolved infection, to Assistance on treatment decisions and therapeutic monitoring, eg.: In chronic HBV infection, the baseline ALT level is associated with the likelihood of treatment response; elevated ALT in the presence of a positive HBV DNA assay is an indication for treatment initiation.

Quantitative HBV DNA assays can help assess the likelihood of response to treatment, monitor response to therapy, and predict the emer-

gence of resistance to antiviral agents.

The HBV genotyping assay is used to determine the HBV genotype, which is important for epidemiologic studies and may be associated with the clinical course and response to therapy. The HBV genotype can also detect the emergence of mutations associated with resistance to antiviral drugs.

Multiple tests for HBsAg and Anti-HBs, HBeAg and Anti-HBe, HBeAg and Anti-HBe, and HBV DNA may be required to completely characterize an individual patient's infection. Clinical and diagnostic applications of each are available to further clarify which diagnostic assays are needed in the diagnosis and management of viral hepatitis

HBV - DNA, PCR

The presence of serum HBV DNA is sensitive and specific for viral replication. Hybridization or signal amplification (branched DNA) assays detect 10^5 to 10^6 viral equivalents/mL, while the more sensitive polymerase chain reaction (PCR)-based assays detect 10^2 to 10^3 viral equivalents/mL. Recovery from acute HBV and HBeAg seroconversion in chronic HBV is associated with the disappearance of HBV DNA by non-PCR-based assays. PCR-based assays may remain positive for many years, which suggests the persistence of small numbers of virions that are contained by the host immune system. The main use of HBV DNA assays is to assess chronic active HBV patients for treatment and to evaluate their response.

Detection of Hepatitis B Virus (HBV) DNA in serum allows monitoring of HBV replication and assessing responses to antiviral treatment. HBV DNA quantification measures virus replication and can be used as a prognosis indicator of liver disease and an index of response to antiviral drugs.

HBV - Genotype

Purposes: Detect hepatitis B virus (HBV) mutations associated with resistance to antiviral agents; and Identify HBV genotype (A-G) for epidemiology and prognostic purposes

The HBV genotype assay assesses the viral genotype from 2 perspectives.

First, the assay examines antiviral resistance-associated mutations within and outside of the YMDD motif of the HBV DNA polymerase.

Second, the assay categorizes isolates according to the 7 established HBV genotypes (A-G). These genotypes are classified according to

sequence variations in the HBV "S" gene and have distinct geographic distributions. Genotypes B and C are common in Asia, while genotypes A and D are more common in Europe and the United States.

Determining the HBV subtype (A-G) is useful for epidemiological studies. In addition, the HBV genotype may be associated with the clinical course of CHB and response to therapy. Because of differences in the length of the pre-S1 region, the exact locations of resistance-associated mutations differ among HBV genotypes.

