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Commentary

# Brief Note on Hepatitis B

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## DESCRIPTION

Humans frequently contract the Hepatitis B Virus (HBV), which currently has no known cure. It is a major contributor to global morbidity and mortality, and it has managed to persist in humans and the versatility of its few protein products in thwarting immune identification and clearance. The formation of clinically significant mutations in the viral genome that arise as a result of host immune selection, as well as those selected by the administration of antiviral medication or immunization, are all covered in detail.

Blood from HBV infected individuals contains three different types of viral particles and entire virion is the 42 nm diameter classic dane particle virion layers consist of an inner nucleocapsid made of dimers of hepatitis B core antigen and an outer envelope covered in hepatitis B surface antigen (HBsAg) proteins (HBcAg) with 180 or 240 core proteins and T3 or T4 symmetry, HBcAg exists as two separate populations with diameters of 32 nm and 36 nm, respectively.

The HBV genome and its closely related endogenous DNA polymerase are both contained within the nucleocapsid. Additionally, there are two non-infectious sub viral particles in the sera, both of which are made entirely of HBsAg the role of these sub viral particles is unclear, although they likely serve as immune decoys. One is a smaller, spherical structure with a 17–25 nm diameter, while the other is filamentous with a 20–nm diameter and variable length.

The HBV genome is a Relaxed Circular (RC) DNA molecule that is circular and partially double-stranded a 226 base pair overlap between the 5' ends of the two DNA strands, which include the 11 nucleotide repeat sequences known as DR1 and DR2, holds the two DNA strands in a circular configuration depending on the genotype, the length of the genome varies between 3181 and 3221 bases. The minus DNA strand does not form a full circle and has a gap between its 3' and 5' ends that is filled by the plus DNA strand. The 5' end of the negative strand is covalently attached to the viral polymerase. An 18-base oligoribo nucleotide forms the 5'end of the (+) strand and is capped in the similar way to standard messenger RNA. Because the 3' end of the plus strand is not fixed, there is a single-stranded gap region of variable length that can range in size from 20 to 80 percent of the overall genomic length. The endogenous viral DNA polymerase can fill in this region. The minus strand comprises four overlapping Open Reading Frames (ORF), of which the longest encodes the whole viral genome.

The precore and the X ORFs overlap partially with the polymerase ORF, which overlaps completely with the envelope ORF (Pre-S1, Pre-S2 and S) the ORFs overlap in a frame-shifted fashion, indicating that the virus strand is read around one and a half times during transcription. Four mRNA transcripts of varying Kilo Base (kb) length are produced from the covalently closed circular DNA, which serves as the virus' transcriptional template these transcripts are the pre-S1 (2.4 kb), pre-S2/S, and X. Each transcript's expression is regulated by a different gene promoter, including the enhancer basal core, large surface antigen (Pre-S1), major surface antigen.

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